

>gi\_3319923\_emb\_CAA11304\_ (AJ223389) Hev b 3 [Hevea
brasiliensis] >gi\_3319925\_emb\_CAA11305\_ (AJ223390) Hev b 3
[Hevea brasiliensis] >gi\_3818475 (AF051317) small rubber
particle protein [Hevea brasiliensis]

Seq. No. 233984

Seq. ID LIB3272-026-P1-K1-B6

Method BLASTX
NCBI GI g167367
BLAST score 407
E value 5.0e-40
Match length 108
% identity 73

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 233985

Seq. ID LIB3272-026-P1-K1-B7

Method BLASTX
NCBI GI g4490728
BLAST score 352
E value 2.0e-33
Match length 99

% identity 67

NCBI Description (AL035709) putative protein [Arabidopsis thaliana]

Seq. No. 233986

Seq. ID LIB3272-026-P1-K1-B8

Method BLASTX
NCBI GI g2119927
BLAST score 454
E value 1.0e-45
Match length 95
% identity 93

NCBI Description translation elongation factor G, chloroplast - soybean

Seq. No. 233987

Seq. ID LIB3272-026-P1-K1-B9

Method BLASTX
NCBI GI g2984709
BLAST score 147
E value 1.0e-09
Match length 50
% identity 56

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 233988

Seq. ID LIB3272-026-P1-K1-C2

Method BLASTX
NCBI GI g4262225
BLAST score 264
E value 4.0e-23
Match length 99
% identity 47

NCBI Description (AC006200) putative phosphatidic acid phosphatase

[Arabidopsis thaliana]

Seq. No. 233989



89

thaliana]

% identity

NCBI Description

```
LIB3272-026-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2146797
BLAST score
                   442
E value
                   5.0e-44
Match length
                  116
                   43
% identity
                  protein disulfide-isomerase (EC 5.3.4.1) - Castor bean
NCBI Description
                  >gi_1134968 (U41385) protein disulphide isomerase PDI
                   [Ricinus communis] >gi_1587210_prf__2206331A protein
                  disulfide isomerase [Ricinus communis]
                   233990
Seq. No.
Seq. ID
                  LIB3272-026-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q4538967
BLAST score
                   302
E value
                  2.0e-27
Match length
                  80
% identity
                   72
                  (AL049488) major intrinsic protein (MIP)-like [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                   233991
                  LIB3272-026-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3158474
BLAST score
                   581
E value
                   3.0e-60
Match length
                  122
% identity
                   92
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
Seq. No.
                  233992
Seq. ID
                  LIB3272-026-P1-K1-D5
Method
                  BLASTX
NCBI GI
                   q119640
                   176
BLAST score
E value
                   6.0e-13
Match length
                  78
% identity
                   51
                  1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOG (PROTEIN
NCBI Description
                  E8) >gi_82109_pir__S01642 ripening protein E8 - tomato
                   >gi 19199 emb CAA31789 (X13437) E8 protein [Lycopersicon
                  esculentum]
Seq. No.
                   233993
Seq. ID
                  LIB3272-026-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q3309084
BLAST score
                   386
E value
                   2.0e-37
Match length
                  88
```

(AF076252) calcineurin B-like protein 2 [Arabidopsis



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Seq. No.
                    233994
- Seq. ID
                    LIB3272-026-P1-K1-E11
 Method
                    BLASTX
 NCBI GI
                    q3776005
 BLAST score
                    587
 E value
                    1.0e-64
 Match length
                    134
                    93
 % identity
 NCBI Description
                   (AJ010466) RNA helicase [Arabidopsis thaliana]
 Seq. No.
                    233995
 Seq. ID
                    LIB3272-026-P1-K1-E3
 Method
                    BLASTX
 NCBI GI
                    q70644
 BLAST score
                    533
 E value
                    1.0e-54
 Match length
                    108
                    19
 % identity
 NCBI Description
                   ubiquitin precursor - common sunflower (fragment)
                    233996
 Seq. No.
                    LIB3272-026-P1-K1-F1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q629483
 BLAST score
                    321
 E value
                    1.0e-29
 Match length
                    112
 % identity
                    60
                    gene 1-Sc3 protein - European white birch
 NCBI Description
                    >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                    >gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
                    pendula]
 Seq. No.
                    233997
 Seq. ID
                    LIB3272-026-P1-K1-F4
 Method
                    BLASTX
 NCBI GI
                    g484656
 BLAST score
                    471
 E value
                    2.0e-47
 Match length
                    102
 % identity
                    87
                    monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
 NCBI Description
                    cucumber >gi_452165_dbj_BAA05408_ (D26392)
                    monodehydroascorbate reductase [Cucumis sativus]
 Seq. No.
                    233998
 Seq. ID
                    LIB3272-026-P1-K1-F6
 Method
                    BLASTX
 NCBI GI
                    g1709498
 BLAST score
                    513
 E value
                    3.0e-52
 Match length
                    122
                    77
 % identity
                    OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
 NCBI Description
```

[Arabidopsis thaliana]

>gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis
thaliana >gi\_887390\_emb\_CAA61411\_ (X89008) osmotin



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233999
Seq. No.
Seq. ID
                    LIB3272-026-P1-K1-F8
Method
                    BLASTX
NCBI GI
                    g3063396
BLAST score
                    279
                    2.0e-25
E value
Match length
                    54
% identity
                     93
NCBI Description
                   (AB012947) vcCyP [Vicia faba]
                    234000
Seq. No.
                    LIB3272-026-P1-K1-G10
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2511691
                    225
BLAST score
                    1.0e-18
E value
                    78
Match length
% identity
                    58
NCBI Description
                   (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]
                    234001
Seq. No.
                    LIB3272-026-P1-K1-G12
Seq. ID
Method
                    BLASTX
                    g3450889
NCBI GI
BLAST score
                    387
E value
                     2.0e-37
Match length
                    109
% identity
                     72
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
                    234002
Seq. No.
                    LIB3272-026-P1-K1-G2
Seq. ID
Method
                    BLASTX
NCBI GI
                    q113621
BLAST score
                     511
E value
                     5.0e-52
Match length
                    118
% identity
                     85
NCBI Description
                    FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
                    >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
                    4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
                     cytoplasmic aldolase [Zea mays]
Seq. No.
                    234003
Seq. ID
                    LIB3272-026-P1-K1-G3
```

Method BLASTX NCBI GI g4432864 BLAST score 539 E value 2.0e-55 127 Match length 77 % identity

(AC006300) hypothetical protein [Arabidopsis thaliana] NCBI Description

234004 Seq. No.



LIB3272-026-P1-K1-G7 Seq. ID BLASTX Method g1710780 NCBI GI BLAST score 397 E value 6.0e-39 Match length 98 77 % identity 40S RIBOSOMAL PROTEIN S9 (S7) >gi\_1321917\_emb\_CAA65433\_ NCBI Description (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina] 234005 Seq. No. LIB3272-026-P1-K1-H1 Seq. ID Method BLASTX NCBI GI g417148 BLAST score 345 E value 1.0e-32 122 Match length 55 % identity PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A) NCBI Description (G2-4) >gi 99912 pir A33654 heat shock protein 26A soybean >gi\_169981 (M20363) Gmhsp26-A [Glycine max] 234006 Seq. No. LIB3272-026-P1-K1-H10 Seq. ID Method BLASTX NCBI GI g3776577 BLAST score 199 2.0e-15 E value 95 Match length 42 % identity NCBI Description (AC005388) T22H22.24 [Arabidopsis thaliana] 234007 Seq. No. LIB3272-026-P1-K1-H11 Seq. ID Method BLASTX NCBI GI q2347189 BLAST score 341 4.0e-32 E value Match length 84 79 % identity NCBI Description (AC002338) hypothetical protein [Arabidopsis thaliana] >gi 3150399 (AC004165) hypothetical protein [Arabidopsis thaliana] Seq. No. 234008 Seq. ID LIB3272-026-P1-K1-H9 Method BLASTX NCBI GI q267069 BLAST score 336

E value 9.0e - 32Match length 70 % identity

NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi\_320183\_pir\_\_JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi\_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916

(M84697) alpha-4 tubulin [Arabidopsis thaliana]



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234009
 Seq. No.
                   LIB3272-027-P1-K1-A10
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q2648355
 BLAST score
                   148
                    2.0e-09
 E value
                   138
 Match length
 % identity
                    32
                   (AE000955) 2-nitropropane dioxygenase (ncd2) [Archaeoglobus
 NCBI Description
                    fulgidus]
 Seq. No.
                   234010
                   LIB3272-027-P1-K1-A2
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q1362055
 BLAST score
                    360
                    3.0e-34
 E value
                    79
 Match length
                    90
 % identity
 NCBI Description
                   phosphogluconate dehydrogenase (decarboxylating) (EC
                    1.1.1.44) - alfalfa >gi_603221 (U18239) 6-phosphogluconate
                    dehydrogenase [Medicago sativa subsp. sativa]
 Seq. No.
                    234011
.Seq. ID
                    LIB3272-027-P1-K1-A4
 Method
                    BLASTX
 NCBI GI
                    q132944
 BLAST score
                    653
                    1.0e-68
 E value
 Match length
                    128
                    93
 % identity
                   60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal
 NCBI Description
                    protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                    (M32655) ribosomal protein [Arabidopsis thaliana]
 Seq. No.
                    234012
                    LIB3272-027-P1-K1-A5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q4371284
 BLAST score
                    678
 E value
                    1.0e-71
 Match length
                    142
 % identity
                    91
                    (AC006260) putative plasma membrane intrinsic protein 2B
 NCBI Description
                    [Arabidopsis thaliana]
                    234013
 Seq. No.
                    LIB3272-027-P1-K1-A6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g547712
 BLAST score
                    695
 E value
                    1.0e-73
 Match length
                    143
 % identity
                    95
```

>gi\_542153\_pir\_\_S38358 translation initiation factor eIF-4A

NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)



234014



```
- rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic
initiation factor 4A [Oryza sativa]
```

Seq. No. LIB3272-027-P1-K1-A7 Seq. ID Method BLASTX g3868758 NCBI GI BLAST score 420 2.0e-41

E value Match length 105 % identity 73

(D89802) elongation factor 1B gamma [Oryza sativa] NCBI Description

234015 Seq. No.

LIB3272-027-P1-K1-B2 Seq. ID

BLASTX Method g1352681 NCBI GI BLAST score 217 E value 2.0e-17 Match length 117 48 % identity

PROTEIN PHOSPHATASE 2C (PP2C) >gi\_1076391\_pir\_\_S55457 NCBI Description

phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis

thaliana >gi\_633028\_dbj\_BAA07287\_ (D38109) protein

phosphatase 2C [Arabidopsis thaliana]

Seq. No. 234016

LIB3272-027-P1-K1-B4 Seq. ID

Method BLASTX NCBI GI g2129670 BLAST score 450 E value 8.0e-45 Match length 132 65 % identity

phosphoinositide-specific phospholipase C - Arabidopsis NCBI Description

thaliana >gi\_857374\_dbj\_BAA09432\_ (D50804) phosphoinositide

specific phospholipase C [Arabidopsis thaliana]

234017 Seq. No.

Seq. ID LIB3272-027-P1-K1-B8

Method BLASTX NCBI GI q3413511 BLAST score 553 6.0e-57 E value Match length 137 % identity

NCBI Description (AJ000265) glucose-6-phosphate isomerase [Spinacia

oleracea]

234018 Seq. No.

LIB3272-027-P1-K1-B9 Seq. ID

Method BLASTX NCBI GI q2274915 BLAST score 410 E value 4.0e-40Match length 113 % identity 69

Seq. No.

Seq. ID

234024

LIB3272-027-P1-K1-D11



```
NCBI Description (AJ000081) beta-1,3-glucanase [Citrus sinensis]
                  234019
Seq. No.
Seq. ID
                  LIB3272-027-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g122770
BLAST score
                  442
                  5.0e-44
E value
Match length
                  112
% identity
                  79
NCBI Description HEMOGLOBIN II >gi_99509_pir__S13378 hemoglobin II - swamp
                  oak >gi_18015_emb_CAA37898_ (X53950) hemoglobin [Casuarina
                  glauca]
Seq. No.
                  234020
                  LIB3272-027-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267075
                  751
BLAST score
E value
                  4.0e-80
Match length
                  144
                  95
% identity
NCBI Description TUBULIN BETA-2 CHAIN >gi_388254_emb_CAA38614_ (X54845)
                  beta-tubulin 2 [Pisum sativum]
                  234021
Seq. No.
                  LIB3272-027-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  139
E value
                  2.0e-19
Match length
                  86
                  69
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                  234022
Seq. ID
                  LIB3272-027-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q3881978
BLAST score
                  325
E value
                   4.0e-30
Match length
                  83
% identity
NCBI Description (Y11348) annexin-like protein [Medicago sativa]
                  234023
Seq. No.
Seq. ID
                  LIB3272-027-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2388575
BLAST score
                  239
E value
                  4.0e-20
Match length
                  133
                  39
% identity
NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]
```



```
Method BLASTX
NCBI GI g120669
BLAST score 513
E value 3.0e-52
Match length 102
% identity 93
```

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

 Seq. No.
 234025

 Seq. ID
 LIB3272-027-P1-K1-D12

 Method
 BLASTX

Method BLASTX
NCBI GI g120669
BLAST score 332
E value 5.0e-31
Match length 71
% identity 89

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 234026

Seq. ID LIB3272-027-P1-K1-D2

Method BLASTX
NCBI GI g2662343
BLAST score 594
E value 1.0e-61
Match length 113
% identity 100

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 234027

Seq. ID LIB3272-027-P1-K1-D3

Method BLASTX
NCBI GI g3510540
BLAST score 365
E value 6.0e-35
Match length 85
% identity 74

NCBI Description (AF038815) expansin [Prunus armeniaca]

Seq. No. 234028

Seq. ID LIB3272-027-P1-K1-D4

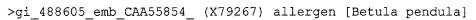
Method BLASTX
NCBI GI g1168696
BLAST score 213
E value 5.0e-17
Match length 66
% identity 56

NCBI Description ALLERGEN BET V 3 (BET V III) >gi 629480 pir S45011

allergen Bet v III - European white birch

>gi 1076247 pir S46233 allergen - European white birch





234029 Seq. No. LIB3272-027-P1-K1-D6 Seq. ID Method BLASTX NCBI GI q4210948 BLAST score 473 2.0e-47 E value 94 Match length 94 % identity NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis] 234030 Seq. No. LIB3272-027-P1-K1-D7 Seq. ID Method BLASTX NCBI GI g3643602 BLAST score 263 5.0e-23E value Match length 103 54 % identity (AC005395) putative tonoplast intrinsic protein NCBI Description [Arabidopsis thaliana] 234031 Seq. No. LIB3272-027-P1-K1-D8 Seq. ID Method BLASTX NCBI GI q3023186 BLAST score 535 8.0e-55 E value 131 Match length 79 % identity NCBI Description 14-3-3-LIKE PROTEIN 9 >qi 1771180 emb CAA67373.1 (X98865) 14-3-3 protein [Lycopersicon esculentum] 234032 Seq. No. LIB3272-027-P1-K1-E1 Seq. ID Method BLASTX NCBI GI g3023281 379 BLAST score E value 2.0e-36 Match length 105 % identity 70 HIGH AFFINITY AMMONIUM TRANSPORTER NCBI Description

>gi 2065194 emb CAA64475 (X95098) ammonium transporter

[Lycopersicon esculentum]

Seq. No. 234033

Seq. ID LIB3272-027-P1-K1-E10

Method BLASTX
NCBI GI g1279654
BLAST score 384
E value 4.0e-37
Match length 108
% identity 71

NCBI Description (X97351) peroxidase [Populus balsamifera subsp.

trichocarpa]

Method

BLASTX



```
234034
 Seq. No.
 Seq. ID
                    LIB3272-027-P1-K1-E5
 Method
                    BLASTX
 NCBI GI
                    q2244806
 BLAST score
                    277
                    2.0e-24
 E value
                    88
 Match length
                    59
 % identity
 NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    234035
                    LIB3272-027-P1-K1-E6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q1729971
 BLAST score
                    270
                    1.0e-23
 E value
                    69
 Match length
                    70
 % identity
 NCBI Description TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                    (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                    rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                    sativa]
                    234036
 Seq. No.
                    LIB3272-027-P1-K1-E7
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3789911
 BLAST score
                    156
                    2.0e-10
 E value
 Match length
                    87
 % identity
                    40
                   (AF081802) developmental protein DG1118 [Dictyostelium
 NCBI Description
                    discoideum]
 Seq. No.
                    234037
 Seq. ID
                    LIB3272-027-P1-K1-E8
 Method
                    BLASTX
- NCBI GI
                    g1707018
 BLAST score
                    212
 E value
                    2.0e-17
 Match length
                    55
 % identity
                    75
 NCBI Description (U78721) CutA isolog [Arabidopsis thaliana]
 Seq. No.
                    234038
 Seq. ID
                    LIB3272-027-P1-K1-F1
 Method
                    BLASTX
 NCBI GI
                    g992706
 BLAST score
                    543
 E value
                    9.0e-56
 Match length
                    105
 % identity
                    91
 NCBI Description (U33758) UBC13 [Arabidopsis thaliana]
 Seq. No.
                    234039
 Seq. ID
                    LIB3272-027-P1-K1-F10
```

BLAST score

E value

282

3.0e-25



```
NCBI GI
                  g167367
BLAST score
                  562
                  6.0e-58
E value
                  146
Match length
                  76
% identity
                 (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                  234040
Seq. No.
                  LIB3272-027-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120669
BLAST score
                  628
                  1.0e-65
E value
                  128
Match length
                  93
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi 19566_emb_CAA42905_ (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                  234041
                  LIB3272-027-P1-K1-F2
Seq. ID
Method
                  BLASTX
                  g2501850
NCBI GI
BLAST score
                  728
E value
                  2.0e-77
Match length
                  145
                  95
% identity
NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
Seq. No.
                  234042
                  LIB3272-027-P1-K1-F3
Seq. ID
Method
                  BLASTX
                  g3759184
NCBI GI
BLAST score
                  301
E value
                  2.0e-27
                  141
Match length
% identity
                  51
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   234043
Seq. ID
                  LIB3272-027-P1-K1-F4
Method
                  BLASTX
NCBI GI
                   g2511691
BLAST score
                  430
E value
                   2.0e-42
Match length
                  112
% identity
                  74
NCBI Description (Z99953) cysteine proteinase precursor [Phaseolus vulgaris]
Seq. No.
                   234044
                  LIB3272-027-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3377952
```

Match length

% identity

98 70



```
Match length
                    68
% identity
                    76
NCBI Description
                   (AJ009878) cysteine proteinase [Cicer arietinum]
Seq. No.
                   234045
Seq. ID
                   LIB3272-027-P1-K1-F8
                   BLASTX
Method
NCBI GI
                   q4150974
BLAST score
                   337
                   9.0e-32
E value
Match length
                   92
                   65
% identity
NCBI Description
                   (AJ224331) cystatin [Castanea sativa]
                   234046
Seq. No.
Seq. ID
                   LIB3272-027-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   q2765837
BLAST score
                   156
                   2.0e-10
E value
                   41
Match length
                   71
% identity
                   (Z96936) NAP16kDa protein [Arabidopsis thaliana]
NCBI Description
                   234047
Seq. No.
                   LIB3272-027-P1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3184098
BLAST score
                   166
E value
                   1.0e-11
Match length
                   122
% identity
                   34
NCBI Description
                   (AL023777) coenzyme a synthetase [Schizosaccharomyces
                   pombe]
                   234048
Seq. No.
                   LIB3272-027-P1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1703108
BLAST score
                 · - 702
E value
                   2.0e-74
Match length
                   144
                   98
% identity
NCBI Description ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
                   thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
                   234049
Seq. No.
                   LIB3272-027-P1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g122007
BLAST score
                   338
                   1.0e-31
E value
```



```
NCBI Description HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley
                  >gi_20448_emb_CAA37828 (X53831) H2A histone protein (AA 1
                  - 149) [Petroselinum crispum]
Seq. No.
                  234050
                  LIB3272-027-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1657948
BLAST score
                  489
E value
                  2.0e-49
Match length
                  126
% identity
                  77
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
                  234051
Seq. No.
Seq. ID
                  LIB3272-027-P1-K1-H1
Method
                  BLASTX
                  g4468153
NCBI GI
BLAST score
                  600
                  2.0e-62
E value
Match length
                  144
                  79
% identity
NCBI Description (AJ132000) sucrose synthase [Craterostigma plantagineum]
Seq. No.
                  234052
                  LIB3272-027-P1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1107526
BLAST score
                  249
E value
                  1.0e-21
Match length
                  70
% identity
                  63
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
                  234053
Seq. No.
Seq. ID
                  LIB3272-027-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q481236
BLAST score
                  260
E value
                  1.0e-22
Match length
                  67
% identity
                  79
NCBI Description hypothetical protein - Madagascar periwinkle
                  >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide
                  [Catharanthus roseus]
Seq. No.
                  234054
Seq. ID
                  LIB3272-027-P1-K1-H12
```

Method BLASTX NCBI GI q4481934 BLAST score 155 E value 2.0e-10 Match length 103 % identity 19

NCBI Description (AL035640) CDA peptide synthetase I [Streptomyces

coelicolor]



```
234055
Seq. No.
Seq. ID
                  LIB3272-027-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q2924779
BLAST score
                  539
E value
                  2.0e-55
Match length
                  127
% identity
                  83
NCBI Description
                  (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
                  thaliana] >gi_2981616_dbj_BAA25248_ (AB008854)
                  3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                  >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA
                  thiolase [Arabidopsis thaliana]
Seq. No.
                  234056
                  LIB3272-027-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g508304
BLAST score
                  260
E value
                  1.0e-22
                  96
Match length
% identity
                  55
NCBI Description (L22305) corC [Medicago sativa]
                  234057
Seq. No.
Seq. ID
                  LIB3272-027-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q508304
BLAST score
                  175
                  5.0e-13
E value
Match length
                  62
% identity
                  61
NCBI Description (L22305) corC [Medicago sativa]
                  234058
Seq. No.
Seq. ID
                  LIB3272-027-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q4539292
BLAST score
                  485
E value
                  6.0e-49
Match length
                  118
% identity
                 (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  234059
Seq. ID
                  LIB3272-028-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g1076501
BLAST score
                  288
E value
                  7.0e-26
```

Match length 82 % identity 66

NCBI Description cell wall protein - alfalfa >gi 3818416 (AF028841) proline-rich cell wall protein [Medicago sativa]

Seq. No. 234060



LIB3272-028-P1-K1-A11 Seq. ID Method BLASTX g4006850 NCBI GI BLAST score 434 E value 5.0e-43Match length 133 60 % identity (Z99707) cytochrome like protein [Arabidopsis thaliana] NCBI Description Seq. No. 234061 Seq. ID LIB3272-028-P1-K1-A12 Method BLASTX NCBI GI g416649 BLAST score 383 5.0e-37 E value Match length 119 % identity 64 PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN NCBI Description PGNT1/PCNT110) >gi 100303 pir S16267 auxin-induced protein (clone pGNT1) - common tobacco >gi 19789 emb CAA39709 (X56268) auxin-induced protein [Nicotiana tabacum] >gi\_19795\_emb\_CAA39705 (X56264) auxin-induced protein [Nicotiana tabacum] 234062 Seq. No. Seq. ID LIB3272-028-P1-K1-A2 Method BLASTX NCBI GI g416664 BLAST score 149 E value 1.0e-09 Match length 37 % identity 78 NCBI Description PLASMA MEMBRANE ATPASE 4 (PROTON PUMP) >gi\_485504 pir S33548 H+-transporting ATPase (EC 3.6.1.35) type 4, plasma membrane - curled-leaved tobacco >gi\_19704 emb CAA47275 (X66737) plasma membrane H+-ATPase [Nicotiana plumbaginifolia] Seq. No. 234063 LIB3272-028-P1-K1-A3 Seq. ID Method BLASTX NCBI GI q3360289 BLAST score 384 E value 4.0e-37 Match length 139 % identity 55 NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays] Seq. No. 234064 Seq. ID LIB3272-028-P1-K1-A4 Method BLASTX

Method BLASTX
NCBI GI g1657948
BLAST score 460
E value 5.0e-46
Match length 120
% identity 76

Seq. ID



```
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
Seq. No.
                  234065
Seq. ID
                  LIB3272-028-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q4417279
BLAST score
                  477
                  5.0e-48
E value
Match length
                  134
                  67
% identity
NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  234066
                  LIB3272-028-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  a1703375
BLAST score
                  643
                  2.0e-67
E value
Match length
                  127
% identity
                  99
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
                  DcARF1 [Daucus carota]
                  234067
Seq. No.
                  LIB3272-028-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4056457
BLAST score
                  527
                  7.0e-54
E value
Match length
                  126
% identity
                  79
NCBI Description (AC005990) ESTs gb_234051 and gb_F13722 come from this
                  gene. [Arabidopsis thaliana]
                  234068
Seq. No.
Seq. ID
                  LIB3272-028-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q508304
BLAST score
                  261
E value
                  9.0e-23
Match length
                  61
% identity
                  80
NCBI Description (L22305) corC [Medicago sativa]
Seq. No.
                   234069
Seq. ID
                  LIB3272-028-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2911042
BLAST score
                  352
E value
                  2.0e-33
Match length
                  91
                  78
% identity
                 (AL021961) Phosphoglycerate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  234070
```

33810

LIB3272-028-P1-K1-B11



```
BLASTX
Method
                   g1928981
NCBI GI
                   574
BLAST score
                   2.0è-59
E value
Match length
                   120
% identity
                   63
                   (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   234071
Seq. No.
                   LIB3272-028-P1-K1-B2
Seq. ID
                   BLASTX
Method
                   g1346802
NCBI GI
                   173
BLAST score
                   2.0e-12
E value
                   34
Match length
                   91
% identity
                   PROFILIN 1 >gi 1076516 pir S49351 profilin - kidney bean
NCBI Description
                   >gi 556836 emb CAA57508 (\overline{X8}1982) profilin [Phaseolus
                   vulgaris]
                   234072
Seq. No.
                  LIB3272-028-P1-K1-B3
Seq. ID
                   BLASTX
Method
                   g1408471
NCBI GI
                   503
BLAST score
                    4.0e-51
E value
Match length
                   113
                   81
% identity
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   234073
Seq. No.
                   LIB3272-028-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                    q2984709
BLAST score
                    442
                    7.0e-44
E value
Match length
                    91
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                    234074
Seq. No.
                   LIB3272-028-P1-K1-B8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g120669
BLAST score
                    557
E value
                    2.0e-57
Match length
                    109
% identity
                    95
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                    >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
```

>gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]



```
Seq. No.
                  234075
                  LIB3272-028-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  g3413167
NCBI GI
                  192
BLAST score
                  1.0e-14
E value
Match length
                  38
                  100
% identity
                  (AJ010225) elongation factor 1-alpha [Cicer arietinum]
NCBI Description
                  234076
Seq. No.
Seq. ID
                  LIB3272-028-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q3868853
BLAST score
                  269
E value
                  1.0e-23
                  78
Match length
% identity
                  69
                  (AB013853) GPI-anchored protein [Vigna radiata]
NCBI Description
Seq. No.
                  234077
                  LIB3272-028-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1703375
BLAST score
                  602
                  1.0e-62
E value
Match length
                  117
                  100
% identity
NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
                  DcARF1 [Daucus carota]
                  234078
Seq. No.
                  LIB3272-028-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  g2583134
NCBI GI
BLAST score
                  227
                  9.0e-19
E value
Match length
                  106
% identity
                   49
NCBI Description (AC002387) putative proline-rich protein [Arabidopsis
                  thaliana]
                   234079
Seq. No.
                  LIB3272-028-P1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1173055
BLAST score
                   589
                   4.0e-61
E value
                  118
Match length
                   99
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497
                   ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819
                   RL5 ribosomal protein - alfalfa >gi_463252 emb_CAA55090_
                   (X78284) RL5 ribosomal protein [Medicago sativa]
```

234080 LIB3272-028-P1-K1-C8 Seq. ID

Seq. No.



```
Method
                  BLASTX
NCBI GI
                  q1703375
BLAST score
                  156
E value
                  2.0e-17
Match length
                  95
                  63
% identity
                 ADP-RIBOSYLATION FACTOR 1 >gi 965483 dbj BAA08259 (D45420)
NCBI Description
                  DcARF1 [Daucus carota]
                  234081
Seq. No.
Seq. ID
                  LIB3272-028-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g3337356
BLAST score
                  612
E value
                  7.0e-64
Match length
                  135
                  89
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
                  234082
Seq. No.
Seq. ID
                  LIB3272-028-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q3980393
BLAST score
                  399
E value
                   7.0e - 39
Match length
                  122
% identity
                   61
NCBI Description
                  (AC004561) putative glutathione S-transferase [Arabidopsis
                  thaliana]
Seq. No.
                  234083
Seq. ID
                  LIB3272-028-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2465434
BLAST score
                  520
E value
                   4.0e-53
Match length
                  115
% identity
NCBI Description (AF022142) flavanone 3beta-hydroxylase [Petunia x hybrida]
Seq. No.
                  234084
Seq. ID
                  LIB3272-028-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g549063
BLAST score
                   487
E value
                   3.0e-49
Match length
                  112
% identity
                  82
```

TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

234085 Seq. No.

Seq. ID LIB3272-028-P1-K1-D2

Method BLASTX



```
g4104242
NCBI GI
BLAST score
                   632
E value
                   3.0e-66
Match length
                   137
% identity
                   87
NCBI Description
                   (AF034266) palmitoyl-acyl carrier protein thioesterase
                   [Gossypium hirsutum]
Seq. No.
                   234086
Seq. ID
                   LIB3272-028-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g2129726
BLAST score
                   560
E value
                   9.0e-58
Match length
                   120
% identity
                   87
NCBI Description
                  RNA polymerase II third largest chain RPB35.5A -
                   Arabidopsis thaliana >gi 514318 (L34770) RNA polymerase II
                   third largest subunit [Arabidopsis thaliana]
                   >gi_4544370_gb_AAD22281.1_AC006920_5 (AC006920) RNA
                   polymerase II, third largest subunit [Arabidopsis thaliana]
Seq. No.
                   234087
Seq. ID
                  LIB3272-028-P1-K1-D5
Method
                  BLASTX
NCBI GI
                   g4261517
BLAST score
                   361
E value
                   2.0e-34
Match length
                   85
% identity
                   78
NCBI Description
                 (AF117334) cysteine proteinase inhibitor [Ipomoea batatas]
                   234088
Seq. No.
Seq. ID
                  LIB3272-028-P1-K1-D7
Method
                  BLASTX
NCBI GI
                   g2129915
BLAST score
                  507
E value
                   1.0e-51
Match length
                  131
% identity
                   72
NCBI Description
                  ferredoxin precursor - sweet orange
                   >gi_1360725_emb_CAA87068_ (Z46944) non-photosynthetic
                  ferredoxin [Citrus sinensis]
Seq. No.
                   234089
Seq. ID
                  LIB3272-028-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g1850546
BLAST score
                  407
E value
                  8.0e-40
Match length
                  104
                  79
```

% identity

NCBI Description (U88045) syntaxin related protein AtVam3p [Arabidopsis

thaliana]

Seq. No. 234090

Seq. ID LIB3272-028-P1-K1-D9



Method BLASTX NCBI GI g4033424 BLAST score 485 E value 6.0e-49Match length 111 83 % identity SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE NCBI Description PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic pyrophosphatase [Zea mays] Seq. No. 234091 Seq. ID LIB3272-028-P1-K1-E10 Method BLASTX g3184098 NCBI GI BLAST score 252 E value 1.0e-21 Match length 135 43 % identity (AL023777) coenzyme a synthetase [Schizosaccharomyces NCBI Description pombe] Seq. No. 234092 LIB3272-028-P1-K1-E11 Seq. ID Method BLASTX NCBI GI g2245066 BLAST score 544 E value 7.0e-56 Match length 136 % identity 68 NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana] Seq. No. 234093 LIB3272-028-P1-K1-E3 Seq. ID Method BLASTX NCBI GI q167367 BLAST score 525 E value 1.0e-53 Match length 131 % identity 78 NCBI Description (L08199) peroxidase [Gossypium hirsutum] Seq. No. 234094 Seq. ID LIB3272-028-P1-K1-E4 Method BLASTX NCBI GI g2506467 BLAST score 353 E value 2.0e-33

Match length 115 % identity 64

NCBI Description LICHENASE PRECURSOR (ENDO-BETA-1, 3-1, 4 GLUCANASE)

>gi 170263 (M23120) beta-glucanase precursor [Nicotiana

plumbaginifolia]

Seq. No. 234095

Seq. ID LIB3272-028-P1-K1-E5

Method BLASTX NCBI GI g1709498



```
BLAST score
                  515
E value
                  2.0e-52
                  112
Match length
% identity
                  83
                  OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                  >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
                  thaliana >qi 887390 emb CAA61411 (X89008) osmotin
                   [Arabidopsis thaliana]
                  234096
Seq. No.
                  LIB3272-028-P1-K1-E7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g167367
                  464
BLAST score
                  1.0e-46
E value
                  120
Match length
% identity
                  76
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  234097
Seq. No.
                  LIB3272-028-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  g3915031
NCBI GI
BLAST score
                  700
E value
                  3.0e-74
                  132
Match length
                  99
% identity
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                   (STEAROYL-ACP DESATURASE) >gi 1217628 emb CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
Seq. No.
                  234098
Seq. ID
                  LIB3272-028-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g2129579
BLAST score
                  748
                  8.0e-80
E value
Match length
                  136
% identity
                   94
                  Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400)
NCBI Description
                  Dwarf1 [Arabidopsis thaliana]
                  234099
Seq. No.
                  LIB3272-028-P1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g20186
BLAST score
                  491
E value
                  1.0e-49
```

96 Match length 55 % identity

NCBI Description (X65016) calmodulin [Oryza sativa]

>gi\_3336950\_emb\_CAA74307\_ (Y13974) calmodulin [Zea mays] >gi 4103961 (AF030034) calmodulin [Phaseolus vulgaris]

Seq. No. 234100

LIB3272-028-P1-K1-F5 Seq. ID



```
BLASTX
Method
NCBI GI
                  g464986
                  522
BLAST score
                  3.0e-53
E value
                  ~96
Match length
                  99
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
                   \overline{6.3.2.19}) \overline{\text{UBC9}} - Arabidopsis thaliana
                  >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                   enzyme E2 [Arabidopsis thaliana]
                   >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
                  234101
Seq. No.
Seq. ID
                  LIB3272-028-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  g2924521
                  183
BLAST score
                  1.0e-13
E value
                  109
Match length
                   43
% identity
NCBI Description
                  (AL022023) putative protein [Arabidopsis thaliana]
                  234102
Seq. No.
                  LIB3272-028-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585241
BLAST score
                  193
                   1.0e-14
E value
                   98
Match length
                   45
% identity
NCBI Description
                  HISTONE H1 >gi 629668 pir S45662 histone H1 - tomato
                   >gi 424100 (U03391) histone H1 [Lycopersicon esculentum]
                   234103
Seq. No.
Seq. ID
                  LIB3272-028-P1-K1-F9
Method
                  BLASTX
NCBI GI
                   g1841870
BLAST score
                   344
                   2.0e-32
E value
                   93
Match length
% identity
                   75
NCBI Description (U87222) elongation factor 1-beta [Pimpinella brachycarpa]
Seq. No.
                   234104
                   LIB3272-028-P1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2829896
```

BLAST score 395 E value 2.0e-38 Match length 133 % identity 56



```
(AC002311) highly similar to auxin-regulated protein GH3,
NCBI Description
                  gp_X60033_18591 [Arabidopsis thaliana]
Seq. No.
                  234105
                  LIB3272-028-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129915
BLAST score
                  506
                  2.0e-51
E value
Match length
                  133
                  70
% identity
                  ferredoxin precursor - sweet orange
NCBI Description
                  >gi 1360725 emb CAA87068 (Z46944) non-photosynthetic
                  ferredoxin [Citrus sinensis]
                  234106
Seq. No.
Seq. ID
                  LIB3272-028-P1-K1-G3
                  BLASTX
Method
NCBI GI
                  q441457
BLAST score
                   611
                   9.0e-64
E value
Match length
                  115
                   98
% identity
                  (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                   234107
Seq. ID
                  LIB3272-028-P1-K1-G8
Method
                  BLASTX
                   q4263517
NCBI GI
BLAST score
                   328
                   1.0e-30
E value
                   116
Match length
% identity
                   57
                  (AC004044) similar to PHZF, catalyzing the hydroxylation of
NCBI Description
                   phenazine-1-carboxylic acid to
                   2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis
                   thaliana]
                   234108
Seq. No.
                   LIB3272-028-P1-K1-G9
Seq. ID
                   BLASTX
Method
                   g3759184
NCBI GI
BLAST score
                   268
                   2.0e-23
E value
                   95
Match length
                   59
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                   234109
Seq. No.
                   LIB3272-028-P1-K1-H1
Seq. ID
Method
                   BLASTX
                   g2909583
NCBI GI
BLAST score
                   342
                   3.0e-32
E value
```

33818

135

53

Match length

% identity



```
(AL021926) oxcA [Mycobacterium tuberculosis]
NCBI Description
                  234110
Seq. No.
                  LIB3272-028-P1-K1-H10
Seq. ID
Method
                  BLASTX
                  g2677828
NCBI GI
BLAST score
                  477
E value
                  5.0e-48
                  134
Match length
                  67
% identity
                  (U93166) cysteine protease [Prunus armeniaca]
NCBI Description
                  234111
Seq. No.
                  LIB3272-028-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  g4193388
NCBI GI
                  492
BLAST score
E value
                  8.0e-50
                  116
Match length
                  84
% identity
                  (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                  brasiliensis]
                  234112
Seq. No.
                  LIB3272-028-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1843628
BLAST score
                   391
                   6.0e-38
E value
                  99
Match length
                   45
% identity
NCBI Description (U88061) SNF5 homolog BSH [Arabidopsis thaliana]
                  234113
Seq. No.
                  LIB3272-028-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3687243
BLAST score
                   245
E value
                   8.0e-21
Match length
                   61
                   79
% identity
NCBI Description
                   (AC005169) putative ribosomal protein [Arabidopsis
                   thaliana]
                   234114
Seq. No.
Seq. ID
                   LIB3272-028-P1-K1-H6
Method
                  BLASTX
NCBI GI
                   g1703375
BLAST score
                   599
E value
                   2.0e-62
Match length
                   119
                   98
% identity
                  ADP-RIBOSYLATION FACTOR 1 >qi 965483 dbj BAA08259 (D45420)
NCBI Description
                   DcARF1 [Daucus carota]
```

33819

234115

LIB3272-029-P1-K1-A1

Seq. No.

Seq. ID



```
Method
                   BLASTX
                   g125271
NCBI GI
BLAST score
                   289
                   3.0e-28
E value
Match length
                   134
                   53
% identity
                   CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA)
NCBI Description
                   >gi_100860_pir__S19726 casein kinase II (EC 2.7.1.-) alpha
                   chain - maize >gi_3318993_pdb_1A60_ Protein Kinase Ck2
                   (Catalytic Subunit) From Zea Mays >gi_22117_emb_CAA43659_
                   (X61387) casein kinase II alpha subunit [Zea mays]
                   234116
Seq. No.
Seq. ID
                   LIB3272-029-P1-K1-A2
Method
                   BLASTX
                   g3927830
NCBI GI
                   265
BLAST score
                   4.0e-23
E value
                   80
Match length
                   57
% identity
                  (AC005727) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   234117
Seq. No.
                   LIB3272-029-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3868758
                   339
BLAST score
                   6.0e - 32
E value
                   93
Match length
                   67
% identity
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                   234118
Seq. No.
                   LIB3272-029-P1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3043428
BLAST score
                   474
                   1.0e-47
E value
Match length
                   104
% identity
                  (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
NCBI Description
                   234119
Seq. No.
                   LIB3272-029-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2970051
BLAST score
                   426
E value
                   5.0e-42
                   107
Match length
% identity
                   76
NCBI Description (AB012110) ARG10 [Vigna radiata]
```

Seq. No. 234120

Seq. ID LIB3272-029-P1-K1-B4

Method BLASTX
NCBI GI g1255954
BLAST score 465



E value 1.0e-46 Match length 110 % identity 76

NCBI Description (Z70677) thioredoxin [Ricinus communis]

Seq. No. 234121

Seq. ID LIB3272-029-P1-K1-C1

Method BLASTX
NCBI GI g1076389
BLAST score 495
E value 4.0e-50
Match length 108
% identity 92

NCBI Description protein phosphatase 2A pDF1 - Arabidopsis thaliana

>gi 683502 emb CAA57528 (X82002) protein phosphatase 2A 65

kDa regulatory subunit [Arabidopsis thaliana]

Seq. No. 234122

Seq. ID LIB3272-029-P1-K1-C12

Method BLASTX
NCBI GI g1174592
BLAST score 497
E value 2.0e-50
Match length 96
% identity 94

NCBI Description TUBULIN ALPHA-1 CHAIN >gi 2119270 pir\_\_S60233 alpha-tubulin

- garden pea >gi 525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 234123

Seq. ID LIB3272-029-P1-K1-C2

Method BLASTX
NCBI GI g629483
BLAST score 326
E value 3.0e-30
Match length 125
% identity 54

NCBI Description gene 1-Sc3 protein - European white birch

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula] >gi\_1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula

pendula]

Seq. No. 234124

Seq. ID LIB3272-029-P1-K1-C3

Method BLASTX
NCBI GI g3759184
BLAST score 202
E value 7.0e-16
Match length 105
% identity 51

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 234125

Seq. ID LIB3272-029-P1-K1-C4

Method BLASTX NCBI GI g3334147 BLAST score 613



```
E value
                   6.0e-64
Match length
                  142
                  84
% identity
                  ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I
NCBI Description
                  chitinase [Gossypium hirsutum]
                  234126
Seq. No.
                  LIB3272-029-P1-K1-C8
Seq. ID
Method
                  BLASTX
                  g3608136
NCBI GI
BLAST score
                  231
                   2.0e-35
E value
Match length
                  89
                   90
% identity
                  (AC005314) defender against cell death [Arabidopsis
NCBI Description
                  thaliana]
                   234127
Seq. No.
                  LIB3272-029-P1-K1-D10
Seq. ID
Method
                   BLASTX
                   g3377813
NCBI GI
BLAST score
                   190
                   2.0e-14
E value
                   61
Match length
% identity
                   57
NCBI Description (AF076275) No definition line found [Arabidopsis thaliana]
Seq. No.
                   234128
                  LIB3272-029-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3158376
BLAST score
                   151
                   5.0e-16
E value
                   121
Match length
                   50
% identity
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                   234129
                   LIB3272-029-P1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4467153
BLAST score
                   483
E value
                   1.0e-48
Match length
                   104
                   82
% identity
                  (AL035540) putative thaumatin-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   234130
Seq. ID
                   LIB3272-029-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q2501555
BLAST score
                   315
E value
                   5.0e-29
Match length
                   114
% identity
```

NCBI Description POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi\_549984 (U13148)

Method

BLASTX



## possible apospory-associated protein [Pennisetum ciliare]

```
Seq. No.
                  234131
Seq. ID
                  LIB3272-029-P1-K1-D6
Method
                  BLASTX
                  g2119934
NCBI GI
BLAST score
                  486
                  5.0e-49
E value
Match length
                  101
% identity
                  92
NCBI Description translation initiation factor eIF-4A.7 - common tobacco
Seq. No.
                  234132
                  LIB3272-029-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2583081
BLAST score
                  216
E value
                  2.0e-17
Match length
                  93
                  46
% identity
NCBI Description
                  (AF026977) microsomal glutathione S-transferase 3 [Homo
                  sapiens]
Seq. No.
                  234133
                  LIB3272-029-P1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1213450
BLAST score
                  250
                  2.0e-21
E value
Match length
                  86
% identity
                  57
                  (U48963) isopentenyl pyrophosphate isomerase [Clarkia
NCBI Description
                  breweri]
                   234134
Seq. No.
Seq. ID
                  LIB3272-029-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  190
E value
                   9.0e-15
Match length
                  85
% identity
                   56
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   234135
Seq. ID
                  LIB3272-029-P1-K1-E12
Method
                  BLASTX
NCBI GI
                   g3096939
BLAST score
                   392
E value
                   5.0e-38
                  116
Match length
% identity
                   64
                 (AL023094) putative protein [Arabidopsis thaliana]
NCBI Description
                   234136
Seq. No.
Seq. ID
                  LIB3272-029-P1-K1-E2
```

```
NCBI GI
                  g1666173
                  470
BLAST score
                  4.0e-47
E value
Match length
                  112
                  83
% identity
                  (Y09106) transcription factor [Nicotiana plumbaginifolia]
NCBI Description
                  234137
Seq. No.
                  LIB3272-029-P1-K1-E3
Seq. ID
Method
                  BLASTX
                  g2119278
NCBI GI
BLAST score
                  611
                  1.0e-63
E value
Match length
                  114
% identity
                  96
NCBI Description tubulin beta-1 chain - rice
Seq. No.
                  234138
                  LIB3272-029-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3393062
BLAST score
                  455
E value
                  2.0e-45
Match length
                  136
% identity
                  57
NCBI Description (Y17386) putative In2.1 protein [Triticum aestivum]
Seq. No.
                  234139
                  LIB3272-029-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g549063
                   409
BLAST score
E value
                  5.0e-40
                  121
Match length
                   67
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
```

factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

234140 Seq. No.

Seq. ID LIB3272-029-P1-K1-E6

Method BLASTX NCBI GI g2827702 576 BLAST score E value 1.0e-59 145 Match length 74 % identity

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

234141 Seq. No.

LIB3272-029-P1-K1-E8 Seq. ID

Method BLASTX NCBI GI g514324 417 BLAST score 5.0e-41 E value Match length 120

Seq. No.



% identity NCBI Description (L34773) RNA polymerase subunit [Arabidopsis thaliana] >gi 2462755 (AC002292) RNA polymerase subunit (isoform B) [Arabidopsis thaliana] >gi 1586550 prf 2204246B RNA polymerase [Arabidopsis thaliana] Seq. No. 234142 LIB3272-029-P1-K1-F1 Seq. ID Method BLASTX NCBI GI q300264 BLAST score 248 E value 3.0e-21 Match length 98 58 % identity NCBI Description (S59747) HSP68=68 kda heat-stress DnaK homolog [Solanum

tuberosum=potatoes, Peptide Mitochondrial, 682 aa] [Solanum tuberosum]

Seq. No. LIB3272-029-P1-K1-F10 Seq. ID Method BLASTX NCBI GI q2369766 BLAST score 389 E value 1.0e-37 Match length 126 % identity 62

NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]

LIB3272-029-P1-K1-F11 Seq. ID Method BLASTX NCBI GI q2498885 BLAST score 142 E value 7.0e-18Match length 113 % identity 49

NCBI Description PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A

>gi\_1296664\_emb\_CAA65774\_ (X97064) Sec23 protein [Homo

sapiens]

234143

234144

Seq. No. 234145 Seq. ID

LIB3272-029-P1-K1-F12

Method BLASTX NCBI GI g3915031 BLAST score 713 E value 1.0e-75Match length 137 % identity 98

NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR

(STEAROYL-ACP DESATURASE) >gi\_1217628\_emb\_CAA65232

(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase

[Gossypium hirsutum]

Seq. No. 234146

LIB3272-029-P1-K1-F5 Seq. ID

Method BLASTX NCBI GI g464986



```
BLAST score
                   427
                   3.0e-42
E value
Match length
                   91
                   88
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                   enzyme E2 [Arabidopsis thaliana]
                   >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
Seq. No.
                   234147
                   LIB3272-029-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1778376
BLAST score
                   519
E value
                   6.0e-53
Match length
                   141
                   68
% identity
NCBI Description (U81288) PsRT17-1 [Pisum sativum]
Seq. No.
                   234148
                   LIB3272-029-P1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q445612
BLAST score
                   208
                   1.0e-16
E value
Match length
                   90
                   52
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
Seq. No.
                   234149
                   LIB3272-029-P1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2501449
BLAST score
                   398
E value
                   9.0e-39
                   78
Match length
% identity
                   97
NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >gi 1668773 emb CAA67922
                   (X99608) ubiquitin-like protein [Oryza sativa]
Seq. No.
                   234150
                   LIB3272-029-P1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120669
BLAST score
                   489
E value
                   2.0e-49
```

Match length 104 89 % identity

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 66014 pir DEJMG glyceraldehyde-3-phosphate



dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora >gi\_19566\_emb\_CAA42905\_ (X60347) glyceraldehyde 3-phosphate dehydrogenase [Magnolia liliiflora]

```
Seq. No.
                  234151
Seq. ID
                  LIB3272-029-P1-K1-G2
                  BLASTX
Method
NCBI GI
                  q1173055
                  661
BLAST score
                   1.0e-69
E value
                  137
Match length
                   95
% identity
                   60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__$42497
NCBI Description
                  ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819
                  RL5 ribosomal protein - alfalfa >gi_463252_emb_CAA55090_
                   (X78284) RL5 ribosomal protein [Medicago sativa]
                   234152
Seq. No.
Seq. ID
                  LIB3272-029-P1-K1-G5
                   BLASTX
Method
                   q1107526
NCBI GI
                   445
BLAST score
                   3.0e-44
E value
Match length
                   113
                   74
% identity
                  (X87931) SIEP1L protein [Beta vulgaris]
NCBI Description
                   234153
Seq. No.
Seq. ID
                   LIB3272-029-P1-K1-G6
Method
                   BLASTX
                   q4455227
NCBI GI
BLAST score
                   351
                   3.0e-33
E value
Match length
                   79
% identity
                   82
NCBI Description (AL035440) SNF8 like protein [Arabidopsis thaliana]
                   234154
Seq. No.
                   LIB3272-029-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1724102
                   505
BLAST score
                   3.0e-51
E value
                   117
Match length
% identity
                   83
                  (U79766) S-adenosyl-L-homocystein hydrolase; SAH
NCBI Description
                   [Mesembryanthemum crystallinum]
                   234155
Seq. No.
                   LIB3272-029-P1-K1-G8
Seq. ID
                   BLASTX
Method
                   g3122673
NCBI GI
                   525
BLAST score
                   1.0e-53
E value
                   131
Match length
                   79
% identity
```

NCBI Description 60S RIBOSOMAL PROTEIN L15 >gi\_2245027\_emb\_CAB10447\_



## (Z97341) ribosomal protein [Arabidopsis thaliana]

```
234156
Seq. No.
                  LIB3272-029-P1-K1-G9
Seq. ID
                  BLASTX
Method
                  g464986
NCBI GI
                  534
BLAST score
                  1.0e-54
E value
                  117
Match length
                  85
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi 421857 pir S32674 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >qi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis thaliana]
                  >qi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
                  ligase UBC9 [Arabidopsis thaliana]
                  234157
Seq. No.
                  LIB3272-029-P1-K1-H1
Seq. ID
                  BLASTX
Method
                  g4006881
NCBI GI
                  277
BLAST score
                  1.0e-24
E value
                  115
Match length
                  55
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                  234158
Seq. No.
Seq. ID
                  LIB3272-029-P1-K1-H10
Method
                  BLASTX
                  g1263291
NCBI GI
                  638
BLAST score
                  7.0e-67
E value
                  120
Match length
% identity
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
                  234159
Seq. No.
                  LIB3272-029-P1-K1-H11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1220196
BLAST score
                  550
                  1.0e-56
E value
Match length
                  120
                  88
% identity
NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
Seq. No.
                  234160
                  LIB3272-029-P1-K1-H12
Seq. ID
                  BLASTX
Method
                  g3759184
NCBI GI
```

33828

254

BLAST score



```
5.0e-22
- E value
 Match length
                    84
                    62
 % identity
                   (AB018441) phi-1 [Nicotiana tabacum]
 NCBI Description
 Seq. No.
                    234161
                    LIB3272-029-P1-K1-H2
 Seq. ID
                    BLASTX
 Method
                    a167367
 NCBI GI
                    640
 BLAST score
                    4.0e-67
 E value
                    138
 Match length
                    91
 % identity
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                    234162
 Seq. No.
 Seq. ID
                    LIB3272-029-P1-K1-H4
 Method
                    BLASTX
 NCBI GI
                    q3600039
 BLAST score
                    283
                    8.0e-49
 E value
                    140
 Match length
                    68
 % identity
                   (AF080119) similar to Schizosaccharomyces pombe isp4
 NCBI Description
                    protein (GB:D14061) [Arabidopsis thaliana]
                    234163
 Seq. No.
                    LIB3272-029-P1-K1-H7
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2921512
                    455
 BLAST score
                    2.0e-45
 E value
                    112
 Match length
 % identity
                   (AF037460) GF14 protein [Fritillaria agrestis]
 NCBI Description
                    234164
 Seq. No.
                    LIB3272-030-P1-K1-A1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q1705812
 BLAST score
                    449
                    1.0e-44
 E value
 Match length
                    136
                    62
 % identity
                   ACIDIC CHITINASE PRECURSOR >gi 1150686 emb CAA92207
 NCBI Description
                    (Z68123) acidic chitinase [Vitis vinifera]
                    234165
 Seq. No.
                    LIB3272-030-P1-K1-A10
 Seq. ID
 Method
                    BLASTX
                    g2347098
 NCBI GI
 BLAST score
                    512
                    4.0e-52
 E value
```

107 Match length 93 % identity

(U76845) ubiquitin-specific protease [Arabidopsis thaliana] NCBI Description >qi 4490742 emb CAB38904.1 (AL035708) ubiquitin-specific



## protease (AtUBP3) [Arabidopsis thaliana]

```
234166
Seq. No.
Seq. ID
                  LIB3272-030-P1-K1-A11
Method
                  BLASTX
                  g2924521
NCBI GI
BLAST score
                  178
E value
                  5.0e-13
                  109
Match length
% identity
                  43
                  (AL022023) putative protein [Arabidopsis thaliana]
NCBI Description
                  234167
Seq. No.
                  LIB3272-030-P1-K1-A12
Seq. ID
                  BLASTX
Method
                  g2078350
NCBI GI
BLAST score
                  604
                  6.0e-63
E value
Match length
                  134
                   90
% identity
                  (U95923) transaldolase [Solanum tuberosum]
NCBI Description
Seq. No.
                  234168
Seq. ID
                  LIB3272-030-P1-K1-A2
Method
                  BLASTX
                  q4539457
NCBI GI
                  198
BLAST score
                   3.0e-15
E value
Match length
                   55
% identity
                   65
                  (AL049500) heat shock transcription factor-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   234169
                   LIB3272-030-P1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1848212
BLAST score
                   451
E value
                   5.0e-45
Match length
                   87
% identity
                   44
                  (Y11209) protein disulfide-isomerase precursor [Nicotiana
NCBI Description
                   tabacum]
Seq. No.
                   234170
                   LIB3272-030-P1-K1-A7
Seq. ID
                   BLASTX
Method
                   g3249066
NCBI GI
                   381
BLAST score
                   9.0e-37
E value
Match length
                   128
                   66
% identity
                  (AC004473) Similar to S. cerevisiae SIK1P protein
NCBI Description
                   gb_984964. ESTs gb_F15433 and gb_AA395158 come from this
                   gene. [Arabidopsis thaliana]
```

Seq. No. 234171



```
LIB3272-030-P1-K1-B1
Seq. ID
Method
                   BLASTX
                   a3869088
NCBI GI
BLAST score
                   581
                   3.0e-60
E value
Match length
                   112
% identity
                  (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
NCBI Description
Seq. No.
                   234172
                   LIB3272-030-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   a118564
BLAST score
                   466
E value
                   7.0e-47
Match length
                   104
                   85
% identity
                   GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE
NCBI Description
                   REDUCTASE) (HPR) (GDH) >gi_65955_pir__DEKVG glycerate dehydrogenase (EC 1.1.1.29) - cucumber
                   >gi_18264_emb_CAA41434_ (X58542) NADH-dependent
                   hydroxypyruvate reductase [Cucumis sativus]
                   >gi_18275_emb_CAA32764_ (X14609) NAPH-dependent
                   hydroxypyruvate reductase (AA 1 - 382) [Cucumis sativus]
Seq. No.
                   234173
                   LIB3272-030-P1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2766452
BLAST score
                   173
E value
                   1.0e-12
Match length
                   51
% identity
NCBI Description
                  (AF029858) cytochrome P450 CYP71E1 [Sorghum bicolor]
Seq. No.
                   234174
                   LIB3272-030-P1-K1-B5
Seq. ID
Method
                   BLASTX
                   g3559811
NCBI GI
BLAST score
                   168
E value
                   7.0e-16
Match length
                   88
% identity
                   45
NCBI Description (AJ010735) gr1-protein [Arabidopsis thaliana]
Seq. No.
                   234175
Seq. ID
                   LIB3272-030-P1-K1-B6
                   BLASTX
Method
NCBI GI
                   g1706326
BLAST score
                   635
E value
                   1.0e-66
                   135
Match length
                   87
% identity
                  PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC)
NCBI Description
                   >gi 2146786_pir__S65470 pyruvate decarboxylase (EC 4.1.1.1)
```

(clone PDC1) - Garden pea >gi\_1177603\_emb\_CAA91444\_
(Z66543) pyruvate decarboxylase [Pisum sativum]

Seq. No.

Seq. ID

234181

LIB3272-030-P1-K1-C3



```
234176
Seq. No.
Seq. ID
                  LIB3272-030-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g1666173
BLAST score
                  144
E value
                  3.0e-09
Match length
                  48
% identity
                  67
                  (Y09106) transcription factor [Nicotiana plumbaginifolia]
NCBI Description
                  234177
Seq. No.
                  LIB3272-030-P1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3236235
BLAST score
                  525
                  1.0e-53
E value
Match length
                  139
                  73
% identity
                  (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >qi 4056501 (AC005896) unknown protein [Arabidopsis
                  thaliana]
Seq. No.
                  234178
                  LIB3272-030-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q167367
BLAST score
                  721
                  1.0e-76
E value
Match length
                  137
% identity
                  99
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                  234179
Seq. ID
                  LIB3272-030-P1-K1-C11
Method
                  BLASTX
                  q3023847
NCBI GI
BLAST score
                  285
                   3.0e - 33
E value
Match length
                  83
% identity
                   62
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                   PROTEIN >gi 2385376 emb CAA69934 (Y08678) G protein beta
                   subunit-like [Medicago sativa]
Seq. No.
                   234180
                  LIB3272-030-P1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4115731
BLAST score
                  183
E value
                  1.0e-13
Match length
                  84
% identity
                   44
NCBI Description (AB017507) Apg12 [Homo sapiens]
```



```
BLASTX
Method
                   g4521249
NCBI GI
                   433
BLAST score
                   6.0e-43
E value
                   114
Match length
                   74
% identity
                   (AB013912) DNA helicase [Mus musculus]
NCBI Description
                   234182
Seq. No.
                   LIB3272-030-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1169009
BLAST score
                   684
                   3.0e-72
E value
                   134
Match length
                   90
% identity
                   CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_542009_pir__S40146
                   catechol O-methyltransferase (EC \overline{2.1.1.6}) - \overline{\text{cider}} tree
                   >gi_437777_emb_CAA52814_ (X74814) 0-Methyltransferase
                   [Eucalyptus gunnii]
                   234183
Seq. No.
                   LIB3272-030-P1-K1-C8
Seq. ID
                   BLASTX
Method
                   g2244740
NCBI GI
BLAST score
                   167
                   9.0e-12
E value
                   44
Match length
                   75
% identity
                  (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]
NCBI Description
                   234184
Seq. No.
                   LIB3272-030-P1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q404670
BLAST score
                   385
                   3.0e-37
E value
Match length
                   130
% identity
                   59
                   (L21154) phytochrome A [Arabidopsis thaliana] >gi_3482934
NCBI Description
                    (AC003970) phytochrome A [Arabidopsis thaliana]
                   234185
Seq. No.
                   LIB3272-030-P1-K1-D11
Seq. ID
Method
                   BLASTX
                   g3237190
NCBI GI
BLAST score
                   144
```

3.0e-09 E value Match length 56 % identity

NCBI Description (AB014760) cystein proteinase inhibitor [Cucumis sativus]

234186 Seq. No.

LIB3272-030-P1-K1-D12 Seq. ID

Method BLASTX



```
NCBI GI
                  g2541876
BLAST score
                  159
E value
                  8.0e-11
Match length
                  79
                   49
% identity
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                  234187
Seq. ID
                  LIB3272-030-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q4371284
BLAST score
                  565
                   2.0e-58
E value
Match length
                   125
% identity
                   (AC006260) putative plasma membrane intrinsic protein 2B
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   234188
                  LIB3272-030-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4115377
BLAST score
                   270
                   9.0e-24
E value
Match length
                   85
                   69
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
                   234189
Seq. No.
                   LIB3272-030-P1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3763925
BLAST score
                   332
E value
                   4.0e-31
Match length
                   70
                   87
% identity
NCBI Description (AC004450) putative Af10-protein [Arabidopsis thaliana]
                   234190
Seq. No.
                   LIB3272-030-P1-K1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g585973
BLAST score
                   499
E value
                   1.0e-50
Match length
                   123
                   83
% identity
                  FRUCTOKINASE >gi 626018 pir S39997 fructokinase (EC
NCBI Description
                   2.7.1.4) - potato >gi 2\overline{97015} emb CAA78283 (Z12823)
                   fructokinase [Solanum tuberosum] >gi 1095321 prf 2108342A
                   fructokinase [Solanum tuberosum]
                   234191
Seq. No.
```

Seq. ID LIB3272-030-P1-K1-E3

Method BLASTX NCBI GI g3128177 BLAST score 486

BLAST score

Match length

E value

151

88

8.0e-10



```
4.0e-49
E value
                  120
Match length
% identity
                  81
                  (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
                  234192
Seq. No.
                  LIB3272-030-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3024020
BLAST score
                  617
E value
                  2.0e-64
Match length
                  121
                  96
% identity
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 2225881_dbj BAA20877_ (AB004824) eukaryotic initiation
                  factor 5A3 [Solanum tuberosum]
                  234193
Seq. No.
                  LIB3272-030-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  q2914706
NCBI GI
BLAST score
                   481
E value
                   2.0e-48
Match length
                  104
                   82
% identity
                  (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
                   234194
Seq. No.
                  LIB3272-030-P1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1653033
BLAST score
                   293
                   2.0e-26
E value
Match length
                   76
                   75
% identity
NCBI Description (D90910) hypothetical protein [Synechocystis sp.]
Seq. No.
                   234195
                   LIB3272-030-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1709498
BLAST score
                   516
                   1.0e-52
E value
                   113
Match length
                   82
% identity
                   OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                   >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
                   thaliana >gi 887390 emb CAA61411 (X89008) osmotin
                   [Arabidopsis thaliana]
                   234196
Seq. No.
                   LIB3272-030-P1-K1-F6
Seq. ID
                   BLASTX
Method
                   g225024
NCBI GI
```

% identity

59



```
% identity
NCBI Description calmodulin [Chlamydomonas reinhardtii]
                   234197
Seq. No.
                   LIB3272-030-P1-K1-F7
Seq. ID
                   BLASTX
Method
                   q3128228
NCBI GI
BLAST score
                   626
E value
                   2.0e-65
                   128
Match length
                   91
% identity
                   (AC004077) putative ribosomal protein L18A [Arabidopsis
NCBI Description
                   thaliana] >gi_3337376 (AC004481) putative ribosomal protein
                   L18A [Arabidopsis thaliana]
                   234198
Seq. No.
                   LIB3272-030-P1-K1-F8
Seq. ID
Method
                   BLASTX
                   q167367
NCBI GI
BLAST score
                   328
E value
                   1.0e-30
                   82
Match length
% identity
                   77
                   (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                   234199
Seq. No.
Seq. ID
                   LIB3272-030-P1-K1-F9
                   BLASTX
Method
NCBI GI
                   q125887
BLAST score
                   194
E value
                    5.0e-15
Match length
                   102
                    46
% identity
                   ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
NCBI Description
                   >gi_82092_pir__S04765 LAT52 protein precursor - tomato
>gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
                    esculentum]
                    234200
Seq. No.
                    LIB3272-030-P1-K1-G11
Seq. ID
Method
                    BLASTX
NCBI GI
                    g217909
                    328
BLAST score
                    1.0e-30
E value
Match length
                    74
% identity
                    88
NCBI Description (D14044) glycolate oxidase [Cucurbita sp.]
                    234201
Seq. No.
                    LIB3272-030-P1-K1-G3
Seq. ID
                    BLASTX
Method
NCBI GI
                    g3212854
                    272
BLAST score
                    5.0e-24
E value
                    126
Match length
```

33836

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. ID



```
234202
Seq. No.
                  LIB3272-030-P1-K1-G4
Seq. ID
                  BLASTX
Method
                  g2642432
NCBI GI
                  171
BLAST score
                  4.0e-12
E value
                  83
Match length
                  51
% identity
                  (AC002391) putative elicitor response element binding
NCBI Description
                  protein (WRKY3) [Arabidopsis thaliana]
                   234203
Seq. No.
                  LIB3272-030-P1-K1-G6
Seq. ID
Method
                  BLASTX
                   q3164222
NCBI GI
                   236
BLAST score
                   8.0e-20
E value
                   63
Match length
                   65
% identity
                   (AB008518) RMA1 [Arabidopsis thaliana] >gi_4206205
NCBI Description
                   (AF071527) RMA1 RING zinc finger protein [Arabidopsis
                   thaliana]
                   234204
Seq. No.
                   LIB3272-030-P1-K1-G7
Seq. ID
                   BLASTX
Method
                   q3128209
NCBI GI
                   332
BLAST score
                   5.0e-31
E value
Match length
                   94
                   69
% identity
NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]
                   234205
Seq. No.
                   LIB3272-030-P1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1402912
BLAST score
                   424
                   7.0e-42
E value
Match length
                   122
% identity
                   66
NCBI Description (X98317) peroxidase [Arabidopsis thaliana]
                   234206
Seq. No.
                   LIB3272-030-P1-K1-G9
Seq. ID
Method
                   BLASTX
                   q2275210
NCBI GI
                   180
BLAST score
                   2.0e-13
E value
                   97
Match length
                   44
 % identity
                   (AC002337) peptidyl-prolyl cis-trans isomerase isolog
NCBI Description
                   [Arabidopsis thaliana]
                   234207
 Seq. No.
```

LIB3272-030-P1-K1-H1

NCBI GI



```
BLASTX
 Method
                    q862931
. NCBI GI
 BLAST score
                    356
                    6.0e - 34
 E value
                    106
 Match length
                    69
 % identity
 NCBI Description (U27179) acidic glucanase [Medicago sativa subsp. sativa]
 Seq. No.
                    234208
                    LIB3272-030-P1-K1-H10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g136057
 BLAST score
                    177
                    3.0e-13
 E value
 Match length
                    59
                    61
  % identity
                    TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
 NCBI Description
                    >gi 99499 pir__A32187 (S)-tetrahydroberberine oxidase -
                    Coptis japonica >gi 556171 (J04121) triosephosphate
                    isomerase [Coptis japonica]
                    234209
  Seq. No.
                    LIB3272-030-P1-K1-H12
  Seq. ID
  Method
                    BLASTX
  NCBI GÍ
                    q2440044
  BLAST score
                    319
                    8.0e-30
  E value
  Match length
                    65
  % identity
                     91
                    (AJ001293) major intrinsic protein PIPB [Craterostigma
  NCBI Description
                    plantagineum]
                     234210
  Seq. No.
                    LIB3272-030-P1-K1-H2
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     q1928981
                     537
  BLAST score
                     4.0e-55
  E value
                     114
  Match length
                     93
  % identity
  NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                     oleracea var. botrytis]
                     234211
  Seq. No.
                     LIB3272-030-P1-K1-H3
  Seq. ID
                     BLASTX
  Method
                     q2829871
  NCBI GI
  BLAST score
                     129
                     4.0e-09
  E value
                     93
  Match length
  % identity
  NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]
                     234212
  Seq. No.
  Seq. ID
                     LIB3272-030-P1-K1-H9
                     BLASTX
  Method
                     q1107526
```

Seq. ID

Method

NCBI GI



```
235
BLAST score
                  6.0e-20
E value
Match length
                  70
% identity
                  61
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
                  234213
Seq. No.
                  LIB3272-031-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1653767
BLAST score
                  434
E value
                  5.0e-43
Match length
                  134
                  59
% identity
NCBI Description (D90916) oligopeptidase A [Synechocystis sp.]
                  234214
Seq. No.
                  LIB3272-031-P1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g131385
BLAST score
                  438
                  2.0e-43
E value
Match length
                  130
                  70
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN)
                  234215
Seq. No.
                  LIB3272-031-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548852
                  361
BLAST score
                  2.0e-34
E value
Match length
                  82
% identity
                   80
                  40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal
NCBI Description
                   protein S21 - rice >gi_303839_dbj BAA02158 (D12633) 40S
                   subunit ribosomal protein [Oryza sativa]
                   234216
Seq. No.
                  LIB3272-031-P1-K1-A7
Seq. ID
                  BLASTX
Method
                   g1709498
NCBI GI
BLAST score
                   514
E value
                   2.0e-52
                  129
Match length
                   74
% identity
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                   >gi 1362001 pir S57524 osmotin precursor - Arabidopsis
                   thaliana >gi 887390 emb CAA61411 (X89008) osmotin
                   [Arabidopsis thaliana]
                   234217
Seq. No.
```

33839

LIB3272-031-P1-K1-B12

BLASTX

q3158376



```
442
BLAST score
                  6.0e-44
E value
Match length
                  120
                  75
% identity
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
                  234218
Seq. No.
                  LIB3272-031-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3319882
BLAST score
                  518
                  8.0e-53
E value
Match length
                  139
                  76
% identity
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                  arietinum]
                  234219
Seq. No.
                  LIB3272-031-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3869088
BLAST score
                  643
E value
                   2.0e-67
Match length
                  123
                   100
% identity
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                   234220
Seq. No.
                  LIB3272-031-P1-K1-B5
Seq. ID
Method
                  BLASTX
                   g3288821
NCBI GI
                   422
BLAST score
                   1.0e-48
E value
                   123
Match length
% identity
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                   transaminase [Arabidopsis thaliana]
                   234221
Seq. No.
                   LIB3272-031-P1-K1-B6
Seq. ID
                   BLASTX
Method
                   g1172995
NCBI GI
                   238
BLAST score
                   5.0e-20
E value
                   95
Match length
                   54
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal
                   protein L22 - rat >gi 710295 emb CAA55204 (X78444)
                   ribosomal protein L22 [Rattus norvegicus]
                   >gi_1093952_prf__2105193A ribosomal protein L22 [Rattus
                   norvegicus]
                   234222
 Seq. No.
Seq. ID
                   LIB3272-031-P1-K1-B7
Method
                   BLASTX
```

33840

q1170747

361

NCBI GI

BLAST score



2.0e-34 E value 77 Match length 92 % identity LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345 NCBI Description (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi\_167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum] 234223 Seq. No. LIB3272-031-P1-K1-C10 Seq. ID Method BLASTX NCBI GI g1483218 190 BLAST score 2.0e-14 E value 79 Match length 53 % identity (X99793) induced upon wounding stress [Arabidopsis NCBI Description thaliana] 234224 Seq. No. LIB3272-031-P1-K1-C12 Seq. ID BLASTX Method q585204 NCBI GI BLAST score 513 3.0e-52 E value 100 Match length % identity 94 GLUTAMINE SYNTHETASE ROOT ISOZYME 4 (GLUTAMATE--AMMONIA NCBI Description LIGASE) (GS107) >gi\_481809\_pir\_\_S39480 glutamate--ammonia ligase (EC 6.3.1.2) 1-4, cytosolic - maize >gi 434330 emb\_CAA46722\_ (X65929) glutamine synthetase [Zea mays] 234225 Seq. No. Seq. ID LIB3272-031-P1-K1-C2 Method BLASTX NCBI GI q2262115 BLAST score 266 3.0e-23E value Match length 114 % identity 46 NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana] 234226 Seq. No. LIB3272-031-P1-K1-C4 Seq. ID Method BLASTX NCBI GI g3355477 417 BLAST score 5.0e-41E value 139 Match length 43 % identity (AC004218) putative P-glycoprotein, pgpl [Arabidopsis

NCBI Description

thaliana]

234227 Seq. No.

LIB3272-031-P1-K1-C5 Seq. ID

BLASTX Method

E value

Match length

3.0e-29

86



```
q2738248
NCBI GI
                  508
BLAST score
E value
                  1.0e-51
Match length
                  138
                  76
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  234228
                  LIB3272-031-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3980393
                  262
BLAST score
                   6.0e-27
E value
Match length
                   102
                   64
% identity
                  (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                   thaliana]
                   234229
Seq. No.
                   LIB3272-031-P1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2388689
BLAST score
                   217
                   2.0e-17
E value
Match length
                   84
                   55
% identity
NCBI Description (AF016633) GH1 protein [Glycine max]
                   234230
Seq. No.
                   LIB3272-031-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1657948
BLAST score
                   385
E value
                   2.0e-37
Match length
                   104
                   74
% identity
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
                   234231
Seq. No.
                   LIB3272-031-P1-K1-D2
Seq. ID
                   BLASTX
Method
                   g4049354
NCBI GI
                   689
BLAST score
                   7.0e-73
E value
Match length
                   137
                   96
% identity
NCBI Description (AL034567) glycine hydroxymethyltransferase (EC
                   2.1.2.1) - like protein [Arabidopsis thaliana]
                   234232
Seq. No.
                   LIB3272-031-P1-K1-D3
Seq. ID
                   BLASTX
Method
                   g2213597
NCBI GI
BLAST score
                   317
```



```
% identity
NCBI Description (AC000348) T7N9.17 [Arabidopsis thaliana]
                   234233
Seq. No.
                   LIB3272-031-P1-K1-D4
Seq. ID
Method
                   BLASTX
                   g728880
NCBI GI
                   181
BLAST score
E value
                   2.0e-13
                   98
Match length
                   43
% identity
                   N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG
NCBI Description
                   >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl
                    transferase related protein [Homo sapiens]
                    234234
Seq. No.
                   LIB3272-031-P1-K1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                    q495725
                    603
BLAST score
                    8.0e-63
E value
Match length
                    133
                    85
% identity
                   (L25042) acetyl-CoA carboxylase [Medicago sativa]
NCBI Description
                    234235
Seq. No.
                    LIB3272-031-P1-K1-D6
Seq. ID
                    BLASTX
Method
                    g123620
NCBI GI
BLAST score
                    552
                    6.0e-57
E value
Match length
                    114
                    96
% identity
                    HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi_100224_pir__S14950
NCBI Description
                    heat shock cognate protein 70 - tomato
                    >gi_19258_emb_CAA37971_ (X54030) heat shock protein cognate
                    70 [Lycopersicon esculentum]
                    234236
Seq. No.
                    LIB3272-031-P1-K1-E1
Seq. ID
                    BLASTX
Method
                    g3702332
NCBI GI
                    199
BLAST score
                    2.0e-24
E value
Match length
                    98
                    66
 % identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                    234237
 Seq. No.
                    LIB3272-031-P1-K1-E10
 Seq. ID
                    {\tt BLASTX}
 Method
                    g167367
 NCBI GI
                    542
 BLAST score
```

33843

9.0e-56

119 89

E value Match length

% identity

Match length

% identity

89

87



```
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                   234238
 Seq. No.
                   LIB3272-031-P1-K1-E11
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2160166
 BLAST score
                   293
 E value
                   2.0e-26
 Match length
                   128
                    52
 % identity
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
                    234239
 Seq. No.
                   LIB3272-031-P1-K1-E4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g3582342
 BLAST score
                   247
                    4.0e-21
 E value
 Match length
                    133
 % identity
                    42
                    (AC005496) putative flavonol 3-o-glucosyltransferase
 NCBI Description
                    [Arabidopsis thaliana]
 Seq. No.
                    234240
Seq. ID
                    LIB3272-031-P1-K1-E7
 Method
                   BLASTX
 NCBI GI
                    q131770
 BLAST score
                    239
 E value
                    2.0e-20
 Match length
                    82
                    55
 % identity
                    40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
 NCBI Description
                    (VEGETATIVE SPECIFIC PROTEIN V12) >gi 70880_pir__R3D024
                    ribosomal protein S9.e - slime mold (Dictyostelium
                    discoideum) >qi 7353 emb CAA29844 (X06636) rp1024 protein
                    [Dictyostelium discoideum]
                  ~ 234241
 Seq. No.
                    LIB3272-031-P1-K1-F1
 Seq. ID
                    BLASTX
 Method
                    g3023847
 NCBI GI
                    328
 BLAST score
 E value
                    3.0e-51
                    113
 Match length
 % identity
                    35
                    GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
 NCBI Description
                    PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta
                    subunit-like [Medicago sativa]
 Seq. No.
                    234242
 Seq. ID
                    LIB3272-031-P1-K1-F10
                    BLASTX
 Method
                    g2267567
 NCBI GI
 BLAST score
                    405
 E value
                    1.0e-39
```



```
(AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                  x hortorum] >gi_2267569 (AF009004) glycine-rich RNA binding
                  protein 2 [Pelargonium x hortorum]
                  234243
Seq. No.
                  LIB3272-031-P1-K1-F11
Seq. ID
                  BLASTX
Method
                  g3913996
NCBI GI
                   422
BLAST score
                  1.0e-41
E value
                   119
Match length
                   70
% identity
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR
NCBI Description
                  >gi_2208927_dbj_BAA20482_ (D85610) ATP-dependent protease
                   Lon [Spinacia oleracea]
                   234244
Seq. No.
                   LIB3272-031-P1-K1-F2
Seq. ID
                   BLASTX
Method
                   g2267567
NCBI GI
                   391
BLAST score
                   6.0e-38
E value
                   87
Match length
                   85
% identity
                   (AF009003) glycine-rich RNA binding protein 1 [Pelargonium
NCBI Description
                   x hortorum] >gi 2267569 (AF009004) glycine-rich RNA binding
                   protein 2 [Pelargonium x hortorum]
                   234245
Seq. No.
                   LIB3272-031-P1-K1-F3
Seq. ID
                   BLASTX
Method
                   g2982311
NCBI GI
                   250
BLAST score
                   2.0e-21
E value
                   92
Match length
                   59
 % identity
                   (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea
NCBI Description
                   mariana]
                   234246
 Seq. No.
                   LIB3272-031-P1-K1-F4
 Seq. ID
 Method
                   BLASTX
                   g2811025
 NCBI GI
                   202
 BLAST score
                   1.0e-19
 E value
 Match length
                   90
 % identity
                   61
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_1944181_dbj_BAA19607_
                   (AB002695) aspartic endopeptidase [Cucurbita pepo]
```

234247 Seq. No.

LIB3272-031-P1-K1-F5 Seq. ID

BLASTX Method g2507421 NCBI GI 467 BLAST score 7.0e-47E value 97 Match length

BLAST score

Match length

E value

231

6.0e-25 108

```
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277
NCBI Description
                   (U81042) translation initiation factor [Arabidopsis
                  thaliana] >gi 4490709_emb_CAB38843.1_ (AL035680)
                  translation initiation factor [Arabidopsis thaliana]
                  234248
Seq. No.
                  LIB3272-031-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3201612
BLAST score
                  172
                  2.0e-12
E value
                  60
Match length
% identity
NCBI Description (AC004669) putative 2A6 protein [Arabidopsis thaliana]
                  234249
Seq. No.
                  LIB3272-031-P1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3695408
                  295
BLAST score
                   1.0e-26
E value
Match length
                  86
% identity
                   72
                  (AF096373) contains similarity to Solanum lycopersicum
NCBI Description
                   (tomato) wound-induced protein (GB:X59882) [Arabidopsis
                   thaliana] >gi 4538956 emb CAB39780.1 (AL049488) probable
                  wound-induced protein [Arabidopsis thaliana]
                   234250
Seq. No.
                   LIB3272-031-P1-K1-G12
Seq. ID
Method
                  BLASTX
                   q1107526
NCBI GI
BLAST score
                   341
E value
                   4.0e-32
Match length
                   92
                   73
% identity
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
                   234251
Seq. No.
                   LIB3272-031-P1-K1-G3
Seq. ID
                   BLASTX
Method
                   g1345501
NCBI GI
                   246
BLAST score
                   4.0e-21
E value
                   74
Match length
                   70
% identity
NCBI Description (X59517) glycolytic glyceraldehyde 3-phosphate
                   dehydrogenase [Antirrhinum majus]
Seq. No.
                   234252
Seq. ID
                   LIB3272-031-P1-K1-G5
                   BLASTX
Method
                   g537313
NCBI GI
```

```
% identity
NCBI Description (L36159) unknown protein [Medicago sativa]
                  234253
Seq. No.
                  LIB3272-031-P1-K1-G6
Seq. ID
Method
                  BLASTX
                  q3845257
NCBI GI
BLAST score
                  161
E value
                  5.0e-11
                  100
Match length
% identity
                  (AE001413) predicted integral membrane protein [Plasmodium
NCBI Description
                  falciparum]
                  234254
Seq. No.
                  LIB3272-031-P1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3142698
                  509
BLAST score
                  9.0e-52
E value
Match length
                  137
                  68
% identity
                  (AF064542) protein farnesyltransferase subunit A
NCBI Description
                   [Arabidopsis thaliana]
                  234255
Seq. No.
                  LIB3272-031-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q322750
                  151
BLAST score
E value
                   3.0e-11
                  77
Match length
                   56
% identity
                  ubiquitin / ribosomal protein CEP52 - wood tobacco
NCBI Description
                   >qi 170217 (M74100) ubiquitin fusion protein [Nicotiana
                   sylvestris]
                   234256
Seq. No.
                   LIB3272-031-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4539459
BLAST score
                   400
                   5.0e-39
E value
Match length
                   114
                   67
% identity
                  (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                   234257
Seq. No.
                   LIB3272-031-P1-K1-H2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3123515
BLAST score
                   663
                   8.0e-70
E value
```

NCBI Description (Y08761) Mago Nashi-like protein [Euphorbia lagascae]

136

93

Match length

% identity



```
234258
Seq. No.
                  LIB3272-031-P1-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3759184
                  274
BLAST score
                  3.0e-24
E value
                  135
Match length
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                  234259
Seq. No.
                  LIB3272-031-P1-K1-H6
Seq. ID
Method
                  BLASTX
                  q1359896
NCBI GI
BLAST score
                  381
                  6.0e - 37
E value
Match length
                  105
                  67
% identity
                  (Z26250) NADPH-ferrihemoprotein reductase [Helianthus
NCBI Description
                  tuberosus]
                  234260
Seq. No.
                  LIB3272-031-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3851636
                  583
BLAST score
                  2.0e-60
E value
                  133
Match length
                  83
% identity
                   (AF098519) unknown [Avicennia marina] >gi_4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   234261
Seq. No.
                  LIB3272-031-P1-K1-H9
Seq. ID
Method
                  BLASTX
                   g1703446
NCBI GI
                  230
BLAST score
                   2.0e-19
E value
                  79
Match length
                   59
% identity
                  L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
NCBI Description
                   >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana
                   >qi 735918 emb CAA84367 (Z34884) asparaginase [Arabidopsis
                   thaliana]
Seq. No.
                   234262
                   LIB3272-032-P1-K1-A1
Seq. ID
                   BLASTX
Method
                   g2879867
NCBI GI
                   403
BLAST score
E value
                   2.0e-39
Match length
                   110
                   69
% identity
                  (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
NCBI Description
```

33848

pombe]

234263

Seq. No.



```
LIB3272-032-P1-K1-A11
Seq. ID
                  BLASTX
Method
                  q3882081
NCBI GI
                  521
BLAST score
                  3.0e-53
E value
                  108
Match length
                   36
% identity
NCBI Description (AJ012552) polyubiquitin [Vicia faba]
                  234264
Seq. No.
                  LIB3272-032-P1-K1-A12
Seq. ID
                  BLASTX
Method
                   q4539292
NCBI GI
                   461
BLAST score
                   3.0e-46
E value
                   95
Match length
                   88
% identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                   thaliana]
                   234265
Seq. No.
                   LIB3272-032-P1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1408471
                   437
BLAST score
                   2.0e-43
E value
                   98
Match length
                   79
% identity
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
                   234266
Seq. No.
                   LIB3272-032-P1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3033380
                   442
BLAST score
                   6.0e-44
E value
                   112
Match length
                   76
 % identity
                   (AC004238) putative coatomer epsilon subunit [Arabidopsis
NCBI Description
                   thaliana]
                   234267
 Seq. No.
                   LIB3272-032-P1-K1-A6
 Seq. ID
                   BLASTX
 Method
                   g3046700
 NCBI GI
                   211
 BLAST score
                   4.0e-17
 E value
                   65
 Match length
                   66
 % identity
                   (AJ005261) cytidine deaminase [Arabidopsis thaliana]
 NCBI Description
                   >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase
                   [Arabidopsis thaliana] >gi 4191787 (AC005917) putative
                   cytidine deaminase [Arabidopsis thaliana]
```

Seq. No. 234268



```
LIB3272-032-P1-K1-A8
Seq. ID
                  BLASTX
Method -
                  q2285792
NCBI GI
BLAST score
                  383
                   4.0e-37
E value
                  118
Match length
                   64
% identity
                   (AB004568) cyanase [Arabidopsis thaliana]
NCBI Description
                   >gi 3287503 dbj_BAA31224_ (AB015748) cyanase [Arabidopsis
                   thaliana]
                   234269
Seq. No.
                  LIB3272-032-P1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3158376
                   463
BLAST score
                   2.0e-46
E value
                   123
Match length
                   76
% identity
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
                   234270
Seq. No.
                   LIB3272-032-P1-K1-B12
Seq. ID
Method
                   BLASTX
                   q2677828
NCBI GI
BLAST score
                   424
E value
                   8.0e-42
Match length
                   111
                   70
% identity
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
                   234271
Seq. No.
                   LIB3272-032-P1-K1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3759184
BLAST score
                   270
                   8.0e-24
E value
                   112
Match length
                   53
 % identity
 NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                   234272
 Seq. No.
                   LIB3272-032-P1-K1-B4
 Seq. ID
                   BLASTX
 Method
                   g3914361
 NCBI GI
                   371
 BLAST score
                   6.0e-36
 E value
                   85
 Match length
                   80
 % identity
 NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                   >gi 2281951 emb_CAB06620_ (Z84822) phospholipase D
                   [Nicotiana tabacum]
```

Seq. No. 234273

Seq. ID LIB3272-032-P1-K1-B7

Method BLASTX



```
q2583134
NCBI GI
                  179
BLAST score
                  3.0e-13
E value
Match length
                  105
% identity
                   (AC002387) putative proline-rich protein [Arabidopsis
NCBI Description
                  thaliana]
                  234274
Seq. No.
                  LIB3272-032-P1-K1-C10
Seq. ID
Method
                  BLASTX
                   q1199772
NCBI GI
                   344
BLAST score
                   2.0e-32
E value
Match length
                   119
                   62
% identity
                   (D83226) extensin like protein [Populus nigra]
NCBI Description
                   >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein
                   [Populus nigra]
                   234275
Seq. No.
                   LIB3272-032-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1107526
                   413
BLAST score
E value
                   1.0e-40
                   119
Match length
                   66
% identity
                  (X87931) SIEP1L protein [Beta vulgaris]
NCBI Description
                   234276
Seq. No.
                   LIB3272-032-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1928981
BLAST score
                   485
E value
                   5.0e-49
                   109
Match length
                   89
% identity
                   (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   234277
Seq. No.
                   LIB3272-032-P1-K1-C3
Seq. ID
                   BLASTX
Method
                   g4115337
NCBI GI
BLAST score
                   394
                   3.0e-38
E value
                   82
Match length
                   16
 % identity
NCBI Description (L81141) ubiquitin [Pisum sativum]
                   234278
 Seq. No.
                   LIB3272-032-P1-K1-C5
 Seq. ID
                   BLASTX
Method
                   g543867
 NCBI GI
                   374
 BLAST score
```

33851

6.0e-36

E value



```
106
Match length
                  79
% identity
                  ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor - sweet potato
                  >gi 303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit
                  [Ipomoea batatas]
Seq. No.
                  234279
                  LIB3272-032-P1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g886100
                  304
BLAST score
E value
                  3.0e-29
                  100
Match length
                  74
% identity
                  (U27347) putative water channel protein; plasmalemma
NCBI Description
                  intrinsic protein; similar to Arabidopsis Pip2a gene
                  product, PIR Accession Number S44084 [Glycine max]
                  234280
Seq. No.
                  LIB3272-032-P1-K1-C9
Seq. ID
                  BLASTX
Method
                  q2583121
NCBI GI
BLAST score
                  162
                  4.0e-11
E value
                  66
Match length
                  56
% identity
                  (AC002387) putative phosphotransferase [Arabidopsis
NCBI Description
                  thaliana]
                  234281
Seq. No.
Seq. ID
                  LIB3272-032-P1-K1-D11
                  BLASTX
Method
NCBI GI
                  q3643609
BLAST score
                  419
                  3.0e-41
E value
                  132
Match length
                   63
% identity
                  (AC005395) putative Cys3His zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
                  234282
Seq. No.
Seq. ID
                  LIB3272-032-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g3094012
BLAST score
                  235
                   9.0e-20
E value
                  75
Match length
                   65
% identity
```

NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]

Seq. No. 234283

Seq. ID LIB3272-032-P1-K1-D4

Method BLASTX q498040 NCBI GI BLAST score 335



```
2.0e-31
 E value
Match length
                     90
% identity
                     71
                    (L33793) ORF [Senecio odorus]
 NCBI Description
                     234284
  Seq. No.
  Seq. ID
                     LIB3272-032-P1-K1-D5
 Method
                     BLASTX
 NCBI GI
                     q2879867
 BLAST score
                     393
                     3.0e - 38
 E value
 Match length
                     111
  % identity
                     68
                    (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
 NCBI Description
                     pombe]
                     234285
  Seq. No.
  Seq. ID
                     LIB3272-032-P1-K1-D6
 Method
                     BLASTX
 NCBI GI
                     g1172555
 BLAST score
                     466
  E value
                     9.0e-47
 Match length
                     103
 % identity
                     86
                     34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
 NCBI Description
                     (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                     (POM 34) >gi_629720_pir__S46936 34K porin - potato >gi_1076682_pir__A55364_porin (clone pPOM-34) - potato
                     mitochondrion >gi 516166 emb_CAA56599_ (X80386) 34 kDA
                     porin [Solanum tuberosum]
                     234286
  Seq. No.
  Seq. ID
                     LIB3272-032-P1-K1-D7
  Method
                     BLASTX
  NCBI GI
                     g3860272
  BLAST score
                     486
  E value
                     4.0e-49
  Match length
                     99
  % identity
                     94
                     (AC005824) putative suppressor protein [Arabidopsis
  NCBI Description
                     thaliana] >gi 4314399 gb AAD15609 (AC006232) putative skd1
                     protein [Arabidopsis thaliana]
                     234287
  Seq. No.
  Seq. ID
                     LIB3272-032-P1-K1-D9
  Method
                     BLASTX
  NCBI GI
                     q3024020
  BLAST score
                     650
                     2.0e-68
  E value
  Match length
                     129
                     94
  % identity
                     INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
  NCBI Description
```

>gi\_2225881\_dbj\_BAA20877\_ (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

234288 Seq. No.

LIB3272-032-P1-K1-E1 Seq. ID



```
BLASTX
Method
NCBI GI
                   g629483
BLAST score
                   317
E value
                   3.0e-29
Match length
                   113
                   57
% identity
                   gene 1-Sc3 protein - European white birch
NCBI Description
                   >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
>gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
                   pendula]
                   234289
Seq. No.
                   LIB3272-032-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3901014
BLAST score
                   235
E value
                   1.0e-19
Match length
                   55
                    76
% identity
                   (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
Seq. No.
                    234290
                    LIB3272-032-P1-K1-E11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2558962
BLAST score
                    360
                    2.0e-34
E value
Match length
                    96
                    77
% identity
NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]
Seq. No.
                    234291
                    LIB3272-032-P1-K1-E12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2244765
BLAST score
                    160
                    7.0e-11
E value
                    108
Match length
                    24
% identity
NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]
                    234292
Seq. No.
                    LIB3272-032-P1-K1-E2
Seq. ID
                    BLASTX
Method
NCBI GI
                    q729470
                    268
BLAST score
                    1.0e-23
E value
                    83
Match length
                    63
% identity
NCBI Description MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
                    (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
```

>gi\_542089\_pir\_\_JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi 297798 emb CAA79702 (Z21493) mitochondrial formate dehydrogenase precursor

[Solanum tuberosum]



```
234293
Seq. No.
                   LIB3272-032-P1-K1-E3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q401189
                   513
BLAST score
                   3.0e-52
E value
                   109
Match length
                   89
% identity
                   WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP)
NCBI Description
                   (TURGOR-RESPONSIVE PROTEIN 7A) >gi_485511_pir__S33617
                   trg-31 protein - garden pea >gi_20\overline{4}26_emb_CAA\overline{7}9159_(Z18288) trg-31 [Pisum sativum]
                   234294
Seq. No.
                   LIB3272-032-P1-K1-E4
Seq. ID
Method
                   BLASTX
                   g1076660
NCBI GI
                   188
BLAST score
                   4.0e-14
E value
Match length
                   47
                   79
% identity
                   D13F(MYBST1) protein - potato >gi_786426_bbs_159122
NCBI Description
                    (S74753) MybSt1=Myb-related transcriptional activator
                    {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                   leaf, Peptide, 342 aa] [Solanum tuberosum]
Seq. No.
                   234295
                   LIB3272-032-P1-K1-E9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3646373
BLAST score
                   596
                   5.0e-62
E value
Match length
                   116
                   93
% identity
NCBI Description (AJ011078) RGP1 protein [Oryza sativa]
                    234296
Seq. No.
                   LIB3272-032-P1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI .
                   g3759184
                   285
BLAST score
                    2.0e-25
E value
                   125
Match length
                    50
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                    234297
Seq. No.
Seq. ID
                   LIB3272-032-P1-K1-F12
                   BLASTX
Method
NCBI GI
                    g4454097
                   277
BLAST score
                    1.0e-24
E value
                    67
Match length
% identity
```

Seq. No. 234298

33855

NCBI Description (X85206) hybrid proline-rich protein [Catharanthus roseus]



```
LIB3272-032-P1-K1-F2
Seq. ID
Method
                   BLASTX
                   g1709498
NCBI GI
                   377
BLAST score
                   2.0e-36
E value
Match length
                   85
                   80
% identity
                   OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                   >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
                   tha\overline{\text{liana}} > \overline{\text{gi}}_88\overline{73}90_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
                   234299
Seq. No.
                   LIB3272-032-P1-K1-F3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2791834
                   509
BLAST score
                   3.0e-52
E value
                   111
Match length
                   96
% identity
                   (AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
                   234300
Seq. No.
                   LIB3272-032-P1-K1-F5
Seq. ID
                   BLASTX
Method
                   q2507281
NCBI GI
BLAST score
                   634
                   2.0e-66
E value
Match length
                   114
                   99
% identity
NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_
                    (X97380) atran2 [Arabidopsis thaliana]
                   234301
Seq. No.
                   LIB3272-032-P1-K1-F7
Seq. ID
                   BLASTX
Method
                   q3915165
NCBI GI
BLAST score
                    484
                    5.0e-49
E value
Match length
                   106
                    89
% identity
                   TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi 2792520
NCBI Description
                    (AF042320) tryptophan synthase beta subunit [Camptotheca
                    acuminata] >gi_2801771 (AF042321) tryptophan synthase beta
                    [Camptotheca acuminata]
                    234302
Seq. No.
Seq. ID
                    LIB3272-032-P1-K1-F8
Method
                    BLASTX
                    q3860333
NCBI GI
                    392
BLAST score
                    4.0e-38
E value
Match length
                    99
```

% identity

NCBI Description (AJ012693) basic blue copper protein [Cicer arietinum]

Seq. No. 234303

% identity



```
LIB3272-032-P1-K1-F9
Seq. ID
                  BLASTX
Method
                  g2130149
NCBI GI
                  438
BLAST score
                  1.0e-43
E value
                  96
Match length
% identity
                  91
                  translation elongation factor eEF-1 alpha chain - maize
NCBI Description
                  (fragment)
                  234304
Seq. No.
                  LIB3272-032-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130073
BLAST score
                  483
                  9.0e-49
E value
Match length
                  103
                  92
% identity
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                   cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                   C-1 [Oryza sativa] \overline{>gi_790970_dbj_BAA08830_} (D50301)
                  aldolase C-1 [Oryza sativa]
                   234305
Seq. No.
                  LIB3272-032-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1724102
                  475
BLAST score
                   6.0e-48
E value
Match length
                  95
                   96
% identity
NCBI Description (U79766) S-adenosyl-L-homocystein hydrolase; SAH
                   [Mesembryanthemum crystallinum]
Seq. No.
                   234306
                  LIB3272-032-P1-K1-G4
Seq. ID
                  BLASTX
Method
                   g115610
NCBI GI
BLAST score
                   388
                   1.0e-37
E value
                   82
Match length
                   95
% identity
NCBI Description PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE)
                   >gi_68030_pir__QYNT phosphoenolpyruvate carboxylase (EC
                   4.1.1.31) - common tobacco >gi 22589_emb CAA41758_ (X59016)
                   phosphoenolpyruvate carboxylase [Nicotiana tabacum]
                   234307
Seq. No.
Seq. ID
                   LIB3272-032-P1-K1-G5
                   BLASTX
Method
NCBI GI
                   q3132675
                   464
BLAST score
                   1.0e-46
E value
Match length
                   91
```

NCBI Description (AF061740) asparagine synthetase [Elaeagnus umbellata]



```
234308
Seq. No.
Seq. ID
                   LIB3272-032-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g1001312
                   270
BLAST score
E value
                   8.0e-24
Match length
                   84
% identity
                   63
NCBI Description (D64006) hypothetical protein [Synechocystis sp.]
                   234309
Seq. No.
                   LIB3272-032-P1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q549063
BLAST score
                   140
E value
                   7.0e-09
Match length
                   69
                   51
% identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
                   234310
Seq. No.
                   LIB3272-032-P1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q441457
BLAST score
                   290
                   3.0e-26
E value
Match length
                   65
% identity
                   80
                   (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon
NCBI Description
                   esculentum]
Seq. No.
                   234311
Seq. ID
                   LIB3272-032-P1-K1-H11
Method
                   BLASTX
                   g3687243
NCBI GI
BLAST score
                   235
                   9.0e-20
E value
                    59
Match length
% identity
                   (AC005169) putative ribosomal protein [Arabidopsis
NCBI Description
                   thaliana]
                    234312
Seq. No.
Seq. ID
                   LIB3272-032-P1-K1-H2
                   BLASTX
Method
NCBI GI
                   g2501578
BLAST score
                   489
E value
                    1.0e-49
                   104
Match length
                    95
% identity
```

NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi\_2129913\_pir\_\_S60047 ethylene-responsive protein 1 - Para rubber tree

>gi\_1209317 (M88254) ethylene-inducible protein [Hevea

brasiliensis]

Method

NCBI GI BLAST score BLASTX q1431629

352



```
234313
Seq. No.
                  LIB3272-032-P1-K1-H5
Seq. ID
                  BLASTX
Method
                  g2894599
NCBI GI
                  533
BLAST score
                  1.0e-54
E value
Match length
                  115
% identity
                  81
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  234314
                  LIB3272-032-P1-K1-H6
Seq. ID
Method
                  BLASTX
                  g2842486
NCBI GI
                  331
BLAST score
                  6.0e - 31
E value
                  105
Match length
% identity
                  65
NCBI Description (AL021749) putative protein [Arabidopsis thaliana]
Seq. No.
                  234315
                  LIB3272-032-P1-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3868758
BLAST score
                  412
                  2.0e-40
E value
                  99
Match length
                  77
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                  234316
Seq. No.
                  LIB3272-033-P1-K1-A1
Seq. ID
                  BLASTX
Method
                  g4210948
NCBI GI
                  470
BLAST score
                   3.0e-47
E value
                  99
Match length
                   91
% identity
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
                   234317
Seq. No.
Seq. ID
                  LIB3272-033-P1-K1-A10
                  BLASTX
Method
NCBI GI
                   g3023190
                   278
BLAST score
E value
                   9.0e-25
                   95
Match length
                   64
% identity
NCBI Description 14-3-3-LIKE PROTEIN 16R >gi_1888459_emb CAA72381_ (Y11685)
                   14-3-3 protein [Solanum tuberosum]
                   234318
Seq. No.
Seq. ID
                   LIB3272-033-P1-K1-A11
```

```
2.0e-33
E value
Match length
                  95
%'identity
                  68
                  (X99348) pectinacetylesterase precursor [Vigna radiata]
NCBI Description
                  234319
Seq. No.
                  LIB3272-033-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3158376
BLAST score
                  425
E value
                  6.0e-42
Match length
                  118
                  74
% identity
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
                  234320
Seq. No.
                  LIB3272-033-P1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2583108
                  227
BLAST score
                  9.0e-19
E value
                  91
Match length
% identity
                  55
                  (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
                  234321
Seq. No.
                  LIB3272-033-P1-K1-A5
Seq. ID
                  BLASTX
Method
                  g464986
NCBI GI
BLAST score
                  469
                  4.0e-47
E value
                  87
Match length
                  98
% identity
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi 421857_pir__S32674 ubiquitin--protein ligase (EC
                  6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
```

ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi\_600391\_emb\_CAA51201\_ (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi\_4455355\_emb\_CAB36765.1 (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

234322 Seq. No.

LIB3272-033-P1-K1-A6 Seq. ID

Method BLASTX NCBI GI g1666234 551 BLAST score 8.0e-57 E value 103 Match length % identity

(U76193) actin [Pisum sativum] >gi\_1724143 (U81049) actin NCBI Description

[Pisum sativum]

Seq. No. 234323

NCBI GI

g82263



```
LIB3272-033-P1-K1-A7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3598857
BLAST score
                  268
                   1.0e-23
E value
Match length
                  114
                   47
% identity
NCBI Description
                  (AF072447) short-chain alcohol dehydrogenase [Ipomoea
                  trifida]
Seq. No.
                  234324
                  LIB3272-033-P1-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3334320
BLAST score
                  493
                   6.0e-50
E value
                  108
Match length
% identity
                   92
                  40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
NCBI Description
                  ribosome-associated protein p40 [Glycine max]
                   234325
Seq. No.
Seq. ID
                  LIB3272-033-P1-K1-B12
Method
                  BLASTX
                   q4217999
NCBI GI
BLAST score
                   618
                   1.0e-64
E value
Match length
                   124
                   89
% identity
                  (AC006135) putative ubiquitin--protein ligase
NCBI Description
                   (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
                   234326
Seq. No.
Seq. ID
                   LIB3272-033-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   q421924
BLAST score
                   356
                   7.0e-34
E value
                   107
Match length
% identity
                   64
NCBI Description peroxidase (EC 1.11.1.7) - tomato >gi_296910_emb_CAA50597_
                   (X71593) peroxidase [Lycopersicon esculentum]
Seq. No.
                   234327
                   LIB3272-033-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4105698
BLAST score
                   196
E value
                   3.0e-15
Match length
                   69
% identity
NCBI Description (AF049870) small hydrophobic protein [Arabidopsis thaliana]
                   234328
Seq. No.
Seq. ID
                   LIB3272-033-P1-K1-B6
Method
                   BLASTX
```



```
BLAST score
E value
                  3.0e-30
Match length
                  62
                  100
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                  c1 precursor (clone pC(1)3II) - potato
Seq. No.
                  234329
                  LIB3272-033-P1-K1-B9
Seq. ID
                  BLASTX
Method
                  g3947719
NCBI GI
BLAST score
                  249
E value
                  2.0e-21
Match length
                  53
                  92
% identity
                   (AJ012653) ribosomal protein S28 [Prunus persica]
NCBI Description
                  >gi 3947721 emb CAA10102 (AJ012654) ribosomal protein S28
                   [Prunus persica] >gi 3947723 emb_CAA10103_ (AJ012655)
                  ribosomal protein S28 [Prunus persica]
                  234330
Seq. No.
                  LIB3272-033-P1-K1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4263711
                  240
BLAST score
                   3.0e-20
E value
Match length
                  88
                   51
% identity
                  (AC006223) putative CCR4-associated transcription factor
NCBI Description
                   [Arabidopsis thaliana]
                   234331
Seq. No.
Seq. ID
                   LIB3272-033-P1-K1-C11
                   BLASTX
Method
                   q3980393
NCBI GI
BLAST score
                   388
                   1.0e-37
E value
                   107
Match length
% identity
                   67
                  (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                   thaliana]
                   234332
Seq. No.
Seq. ID
                   LIB3272-033-P1-K1-C12
Method
                   BLASTX
                   q3687654
NCBI GI
BLAST score
                   238
                   4.0e-20
E value
Match length
                   96
                   54
% identity
NCBI Description (AF047975) putative ethylene receptor; ETR2 [Arabidopsis
                   thaliana]
```

Seq. No. 234333

Seq. ID LIB3272-033-P1-K1-C3

Method BLASTX NCBI GI g3193316



BLAST score 179 Evalue 4.0e-13 Match length 111 % identity 46

NCBI Description (AF069299) contains similarity to nucleotide sugar

epimerases [Arabidopsis thaliana]

Seq. No. 234334

Seq. ID LIB3272-033-P1-K1-C4

Method BLASTX
NCBI GI g1076393
BLAST score 360
E value 2.0e-34
Match length 94
% identity 80

NCBI Description RCI14A protein - Arabidopsis thaliana

>gi 540559 emb CAA52237 (X74140) RCI14A [Arabidopsis

thaliana]

Seq. No. 234335

Seq. ID LIB3272-033-P1-K1-C5

Method BLASTX
NCBI GI g4097579
BLAST score 513
E value 3.0e-52
Match length 105
% identity 91

NCBI Description (U64922) NTGP1 [Nicotiana tabacum]

Seq. No. 234336

Seq. ID LIB3272-033-P1-K1-C7

Method BLASTX
NCBI GI g4510376
BLAST score 205
E value 3.0e-16
Match length 69

% identity 55

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 234337

Seq. ID LIB3272-033-P1-K1-C8

Method BLASTX
NCBI GI g122770
BLAST score 443
E value 4.0e-44
Match length 112
% identity 79

NCBI Description HEMOGLOBIN II >gi\_99509\_pir\_\_S13378 hemoglobin II - swamp

oak >gi 18015 emb CAA37898 (X53950) hemoglobin [Casuarina

glauca]

Seq. No. 234338

Seq. ID LIB3272-033-P1-K1-C9

Method BLASTX
NCBI GI g3879192
BLAST score 274
E value 3.0e-24



Match length % identity 48 (Z50795) weak similarity with yeast cat8 regulatory protein NCBI Description (Swiss Prot accession number P39113); cDNA EST EMBL: Z14554 comes from this gene; cDNA EST EMBL: T02057 comes from this gene; cDNA EST EMBL: D75504 comes from this gene; Seq. No. 234339 LIB3272-033-P1-K1-D1 Seq. ID Method BLASTX NCBI GI g3236242 BLAST score 439 1.0e-43 E value Match length 103 % identity 84 (AC004684) putative ribosomal protein L36 [Arabidopsis NCBI Description thaliana] Seq. No. 234340 Seq. ID LIB3272-033-P1-K1-D10 Method BLASTX NCBI GI q3522945 263 BLAST score 5.0e-23 E value Match length 116 % identity 44 NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana] 234341 Seq. No. Seq. ID LIB3272-033-P1-K1-D11 Method BLASTX NCBI GI g4126401 420 BLAST score 2.0e-41 E value Match length 95 % identity NCBI Description (AB011795) flavanone 3-hydroxylase [Citrus sinensis] Seq. No. 234342 Seq. ID LIB3272-033-P1-K1-D2 Method BLASTX NCBI GI q549063 BLAST score 447 E value 1.0e-44Match length 103 82 % identity TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description >gi\_1072464\_pir A38958 IgE-dependent histamine-releasing factor homolog - rice >gi 303835 dbj BAA02151 (D12626) 21kd polypeptide [Oryza sativa] 234343 Seq. No.

LIB3272-033-P1-K1-D4 Seq. ID

Method BLASTX NCBI GI q445613 BLAST score 400 5.0e-39 E value

NCBI Description

thaliana]



```
107
Match length
                  74
% identity
NCBI Description ribosomal protein L7 [Solanum tuberosum]
Seq. No.
                  234344
                  LIB3272-033-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3763932
BLAST score
                  561
E value
                  6.0e-58
                  126
Match length
                  86
% identity
                  (AC004450) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  234345
                  LIB3272-033-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g886100
BLAST score
                  529
E value
                   3.0e-54
Match length
                  123
% identity
                  83
                  (U27347) putative water channel protein; plasmalemma
NCBI Description
                   intrinsic protein; similar to Arabidopsis Pip2a gene
                  product, PIR Accession Number S44084 [Glycine max]
                   234346
Seq. No.
                  LIB3272-033-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1657948
                   507
BLAST score
E value
                   1.0e-51
Match length
                  114
                   87
% identity
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
                   234347
Seq. No.
Seq. ID
                  LIB3272-033-P1-K1-E1
Method
                  BLASTX
NCBI GI
                   g1928981
BLAST score
                   535
                   7.0e-55
E value
                  114
Match length
                   93
% identity
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   234348
Seq. No.
Seq. ID
                  LIB3272-033-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g2262173
BLAST score
                   321
                   8.0e-30
E value
Match length
                   122
% identity
```

33865

(ACO02329) NADPH thioredoxin reductase [Arabidopsis

Seq. ID Method 234354

BLASTX

LIB3272-033-P1-K1-F5



```
234349
Seq. No.
                  LIB3272-033-P1-K1-E3
Seq. ID
                 BLASTX
Method
NCBI GI
                  g746510
                  219
BLAST score
                  8.0e-18
E value
Match length
                  57
% identity
                  65
                 (U23517) similar to ubiquitin conjugating enzyme
NCBI Description
                  [Caenorhabditis elegans]
                  234350
Seq. No.
                  LIB3272-033-P1-K1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3522952
BLAST score
                  340
E value
                  4.0e-32
Match length
                  99
% identity
                  66
NCBI Description (AC004411) putative alcohol dehydrogenase [Arabidopsis
                  thaliana]
                  234351
Seq. No.
                  LIB3272-033-P1-K1-F11
Seq. ID
Method
                  BLASTX
                  g3695023
NCBI GI
                  301
BLAST score
                  2.0e-27
E value
                  105
Match length
                  58
% identity
NCBI Description (AF055850) unknown [Arabidopsis thaliana]
                  234352
Seq. No.
                  LIB3272-033-P1-K1-F2
Seq. ID
                  BLASTX
Method
                  q4455293
NCBI GI
BLAST score
                  366
E value
                  5.0e-35
Match length
                  89
% identity
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
                  234353
Seq. No.
Seq. ID
                  LIB3272-033-P1-K1-F4
                  BLASTX
Method
NCBI GI
                  a543905
                  397
BLAST score
                  1.0e-38
E value
Match length
                  97
                  80
% identity
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
                  brassinosteroid-regulated protein [Glycine max]
```

```
NCBI GI
                    g2271477
 BLAST score
                    321
                    8.0e-30
 E value
 Match length
                    76
 % identity
                   (AF009631) AP47/50p [Arabidopsis thaliana]
 NCBI Description
                    234355
 Seq. No.
 Seq. ID
                    LIB3272-033-P1-K1-F6
                    BLASTX
 Method
 NCBI GI
                    q3063449
 BLAST score
                    336
                    1.0e-31
 E value
 Match length
                    90
 % identity
                    72
 NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]
                    234356
 Seq. No.
 Seq. ID
                    LIB3272-033-P1-K1-G10
 Method
                    BLASTX
· NCBI GI
                    q4335763
 BLAST score
                    251
 E value
                    1.0e-21
 Match length
                    90
                    50
 % identity
 NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
                    234357
 Seq. No.
                    LIB3272-033-P1-K1-G11
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1055130
 BLAST score
                    238
                    4.0e-20
 E value
 Match length
                    118
  % identity
                    43
                    (U39998) coded for by C. elegans cDNA yk92b11.3; coded for
 NCBI Description
                    by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA
                    yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by
                    C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA
                    yk78c2.3
                    234358
  Seq. No.
                    LIB3272-033-P1-K1-G12
  Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g1928981
 BLAST score
                    498
 E value
                    1.0e-50
                    106
 Match length
                    93
  % identity
 NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                    oleracea var. botrytis]
```

Seq. ID LIB3272-033-P1-K1-G3

Method BLASTX
NCBI GI g1928981
BLAST score 549



```
2.0e-56
E value
Match length
                  114
% identity
                  95
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
Seq. No.
                  234360
Seq. ID
                  LIB3272-033-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1352461
BLAST score
                  491
E value
                  1.0e-49
Match length
                  113
% identity
                  81
NCBI Description IN2-2 PROTEIN
                  234361
Seq. No.
                  LIB3272-033-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885884
BLAST score
                  538
E value
                  3.0e-55
Match length
                  105
% identity
                  92
NCBI Description (AF093630) 60S ribosomal protein L21 [Oryza sativa]
Seq. No.
                  234362
                  LIB3272-033-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1694621
BLAST score
                  329
                  9.0e-31
E value
Match length
                  102
% identity
                  67
NCBI Description (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
                  234363
Seq. No.
Seq. ID
                  LIB3272-033-P1-K1-G7
                  BLASTX
Method
                  g3834310
NCBI GI
BLAST score
                  466
E value
                  8.0e-47
Match length
                  89
                  100
% identity
NCBI Description (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
                  gb D83004 from Homo sapiens. ESTs gb T88233, gb Z24464,
                  gb N37265, gb H36151, gb Z34711, gb AA040983, and gb T22122
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  234364
                  LIB3272-033-P1-K1-G8
Seq. ID
                  BLASTX
Method
                  g3176662
NCBI GI
BLAST score
                  497
E value
                  2.0e-50
                  121
Match length
```

33868

71

% identity



```
(AC004393) Similar to mannosyl-oligosaccharide glucosidase
NCBI Description
                  gb X87237 from Homo sapiens. [Arabidopsis thaliana]
Seq. No.
                  234365
                  LIB3272-033-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3367522
BLAST score
                  197
E value
                  3.0e-15
Match length
                  105
% identity
                  46
                  (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  234366
Seq. No.
                  LIB3272-033-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1657948
BLAST score
                  504
E value
                  3.0e-51
Match length
                  115
% identity
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
Seq. No.
                  234367
                  LIB3272-033-P1-K1-H12 =
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3395432
BLAST score
                  394
E value
                  2.0e-38
Match length
                  120
% identity
                  56
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                  234368
                  LIB3272-034-P1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3252868
BLAST score
                  160
E value
                  3.0e-11
Match length
                  42
% identity
NCBI Description (AF033536) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                  234369
Seq. ID
                  LIB3272-034-P1-K1-A12
                  BLASTX
Method
NCBI GI
                  q421989
BLAST score
                  177
                  2.0e-13
E value
                  51
Match length
```

[Hordeum vulgare]

Seq. No. 234370



```
LIB3272-034-P1-K1-A4
Seq. ID
                  BLASTX
Method
                  g3386615
NCBI GI
                  157
BLAST score
                  1.0e-10
E value
                  54
Match length
                  63
% identity
                  (AC004665) putative phosphomannomutase [Arabidopsis
NCBI Description
                  thaliana]
                  234371
Seq. No.
                  LIB3272-034-P1-K1-A5
Seq. ID
Method
                  BLASTX
                  g3395431
NCBI GI
                  209
BLAST score
                  1.0e-16
E value
                  76
Match length
                  49
% identity
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                  234372
Seq. No.
                  LIB3272-034-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g549063
BLAST score
                  211
E value
                  4.0e-17
                  70
Match length
% identity
                  63
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                  21kd polypeptide [Oryza sativa]
                  234373
Seq. No.
                  LIB3272-034-P1-K1-A9
Seq. ID
                  BLASTX
Method
                  q419789
NCBI GI
                  482
BLAST score
E value
                  1.0e-48
Match length
                  121
                  79
% identity
NCBI Description hypothetical protein - potato
                   234374
Seq. No.
                  LIB3272-034-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3914430
                   491
BLAST score
E value
                   8.0e-50
                   98
Match length
% identity
NCBI Description PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
                   CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                   >gi 2285800 dbj BAA21650 (D78172) 26S proteasome beta
```

subunit [Spinacia oleracea]



```
LIB3272-034-P1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2088654
                  433
BLAST score
                  7.0e-43
E value
                  97
Match length
                  87
% identity
                  (AF002109) 60S acidic ribosomal protein PO isolog
NCBI Description
                   [Arabidopsis thaliana]
                  234376
Seq. No.
                  LIB3272-034-P1-K1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1107526
BLAST score
                  491
                  1.0e-49
E value
Match length
                  122
% identity
                  75
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
                  234377
Seq. No.
Seq. ID
                  LIB3272-034-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g1166450
BLAST score
                  161
E value
                   3.0e-11
Match length
                   33
                   88
% identity
NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]
                   234378
Seq. No.
                   LIB3272-034-P1-K1-B9
Seq. ID
                  BLASTX
Method
NCBI GI
                   q927025
BLAST score
                   339
E value
                   6.0e-32
                   77
Match length
                   55
% identity
NCBI Description (L44134) SPF1-like DNA-binding protein [Cucumis sativus]
                   234379
Seq. No.
                   LIB3272-034-P1-K1-C1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3242720
BLAST score
                   185
                   8.0e-14
E value
                   54
Match length
                   61
% identity
                  (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
NCBI Description
                   thaliana]
                   234380
Seq. No.
                   LIB3272-034-P1-K1-C10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4406780
```

405

1.0e-39

BLAST score E value

BLAST score

E value

299

2.0e-27



```
Match length
% identity
                   68
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                   234381
Seq. No.
Seq. ID
                   LIB3272-034-P1-K1-C12
Method
                   BLASTX
                   g1709498
NCBI GI
                   491
BLAST score
                   1.0e-49
E value
                   107
Match length
                   82
% identity
                   OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                   >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
                   tha\overline{1}iana g\overline{1}88\overline{73}90_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
Seq. No.
                   234382
                   LIB3272-034-P1-K1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3522937
                   329
BLAST score
                   1.0e-30
E value
                   69
Match length
                   83
% identity
NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]
                   234383
Seq. No.
                   LIB3272-034-P1-K1-C4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g629602
                   157
BLAST score
                   1.0e-10
E value
                   48
Match length
                   65
% identity
NCBI Description probable imbibition protein - wild cabbage
                   >gi 488787 emb CAA55893_ (X79330) putative imbibition
                   protein [Brassica oleracea]
                   234384
Seq. No.
Seq. ID
                   LIB3272-034-P1-K1-C6
                   BLASTX
Method
NCBI GI
                   q730536
                   247
BLAST score
                   2.0e-29
E value
                   74
Match length
                   93
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal
                   protein subunit L17 [Nicotiana tabacum]
                   234385
Seq. No.
                   LIB3272-034-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2274915
```

% identity

NCBI Description

65



```
Match length
 % identity
                    73
                   (AJ000081) beta-1,3-glucanase [Citrus sinensis]
 NCBI Description
                    234386
 Seq. No.
 Seq. ID
                   LIB3272-034-P1-K1-C9
 Method
                   BLASTX
 NCBI GI
                    g3080428
 BLAST score
                    321
                    9.0e-30
 E value
 Match length
                    98
 % identity
                    56
 NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
                    234387
 Seq. No.
 Seq. ID
                   LIB3272-034-P1-K1-D1
 Method
                    BLASTX
 NCBI GI
                    g2088652
 BLAST score
                    470
                    3.0e-47
 E value
                    114
 Match length
% identity
                    76
 NCBI Description
                   (AF002109) 26S proteasome regulatory subunit S12 isolog
                    [Arabidopsis thaliana] >gi 2351376 (U54561) translation
                    initiation factor eIF2 p47 subunit homolog [Arabidopsis
                    thaliana]
 Seq. No.
                    234388
 Seq. ID
                    LIB3272-034-P1-K1-D12
 Method
                   BLASTX
 NCBI GI
                    g2507281
 BLAST score
                    649
 E value
                    3.0e-68
 Match length
                    116
                    100
 % identity
 NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >qi 1668706 emb CAA66048
                    (X97380) atran2 [Arabidopsis thaliana]
 Seq. No.
                    234389
 Seq. ID
                    LIB3272-034-P1-K1-D2
 Method
                    BLASTX
 NCBI GI
                    g1777386
 BLAST score
                    203
 E value
                    6.0e-16
 Match length
                    117
 % identity
                    41
 NCBI Description (U39301) caffeic acid O-methyltransferase [Pinus taeda]
 Seq. No.
                    234390
                    LIB3272-034-P1-K1-D3
 Seq. ID
 Method
                    BLASTX
                    g4455223
 NCBI GI
 BLAST score
                    141
 E value
                    1.0e-08
 Match length
                    43
```

33873

(AL035440) putative DNA binding protein [Arabidopsis



## thaliana]

```
234391
Seq. No.
Seq. ID
                  LIB3272-034-P1-K1-D4
                  BLASTX
Method
NCBI GI
                  q3334147
BLAST score
                  500
E value
                  9.0e-51
Match length
                  126
% identity
                  78
NCBI Description ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I
                  chitinase [Gossypium hirsutum]
Seq. No.
                  234392
Seq. ID .
                  LIB3272-034-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2879867
BLAST score
                  396
E value
                  1.0e-38
Match length
                  106
                  71
% identity
                  (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
NCBI Description
                  pombe]
Seq. No. Seq. ID
                  234393
                  LIB3272-034-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g508304
BLAST score
                  244
E value
                  9.0e-21
Match length
                  58
                  79
% identity
NCBI Description (L22305) corC [Medicago sativa]
                  234394
Seq. No.
Seq. ID
                  LIB3272-034-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1173209
BLAST score
                  633
E value
                  2.0e-66
Match length
                  129
                  98
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_541835_pir__S41193 ribosomal
                  protein S16 protein - upland cotton
                  >gi 439654 emb CAA53567 (X75954) RS16 protein, 40S subunit
                  [Gossypium hirsutum]
Seq. No.
                  234395
Seq. ID
                  LIB3272-034-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g1350944
BLAST score
                  367
E value
                  3.0e-35
Match length
                  76
% identity
                  96
```

NCBI Description 40S RIBOSOMAL PROTEIN S17



```
234396
Seq. No.
                  LIB3272-034-P1-K1-E6
Seq. ID
Method
                  BLASTX
                  q3122673
NCBI GI
BLAST score
                  412
                  2.0e-40
E value
                  112
Match length
                  75
% identity
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027_emb_CAB10447_
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                  234397
Seq. No.
                  LIB3272-034-P1-K1-E7
Seq. ID
Method
                  BLASTX
                   q543867
NCBI GI
                   369
BLAST score
                   2.0e-35
E value
Match length
                   104
                   78
% identity
                  ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                   >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC
                   3.6-1.34) gamma chain precursor - sweet potato
                   >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit
                   [Ipomoea batatas]
                   234398
Seq. No.
                   LIB3272-034-P1-K1-E8
Seq. ID
                   BLASTX
Method
                   g1332579
NCBI GI
BLAST score
                   580
                   4.0e-60
E value
                   117
Match length
                   10
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                   234399
Seq. No.
                   LIB3272-034-P1-K1-E9
Seq. ID
                   BLASTX
Method
                   g4220477
NCBI GI
                   279
BLAST score
                   7.0e-25
E value
                   114
Match length
                   56
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
                   234400
Seq. No.
                   LIB3272-034-P1-K1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2583134
BLAST score
                   243
                   1.0e-20
E value
                   123
Match length
 % identity
                   (AC002387) putative proline-rich protein [Arabidopsis
```

thaliana]

NCBI Description

Method

NCBI GI

BLASTX

q2829927



```
LIB3272-034-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82264
BLAST score
                  178
E value
                  5.0e-13
Match length
                  36
                  92
% identity
                  ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome
NCBI Description
                  c1 precursor (clone pC(1)8I) - potato (fragment)
                  >qi 498789 emb CAA56109 (X79597) cytochrome c1 [Solanum
                  tuberosum]
                  234402
Seq. No.
                  LIB3272-034-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1199778
BLAST score
                   381
E value
                   8.0e-37
Match length
                  110
% identity
                   68
                  (D83225) peroxidase [Populus nigra]
NCBI Description
Seq. No.
                   234403
                   LIB3272-034-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q508304 -
BLAST score
                   164
E value
                   2.0e-11
Match length
                   65
% identity
                   51
NCBI Description (L22305) corC [Medicago sativa]
                   234404
Seq. No.
                   LIB3272-034-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3004565
                   150
BLAST score
                   1.0e-09
E value
                   52
Match length
                   81
% identity
                 (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   234405
Seq. No.
Seq. ID
                   LIB3272-034-P1-K1-F5
Method
                   BLASTX
                   g2384760
NCBI GI
BLAST score
                   283
                   6.0e-34
E value
                   81
Match length
                   91
% identity
                  (AF016897) GDP dissociation inhibitor protein OsGDI2 [Oryza
NCBI Description
                   sativa]
                   234406
Seq. No.
Seq. ID
                   LIB3272-034-P1-K1-F6
```



```
158
BLAST score
                  5.0e-11
E value
                  45
Match length
                  71
% identity
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
                  234407
Seq. No.
                  LIB3272-034-P1-K1-F7
Seq. ID
                  {\tt BLASTX}
Method
                  g3643609
NCBI GI
                  382
BLAST score
                  6.0e-37
E value
Match length
                  124
% identity
                  63
                  (AC005395) putative Cys3His zinc finger protein
NCBI Description
                  [Arabidopsis thaliana]
                  234408
Seq. No.
                  LIB3272-034-P1-K1-F8
Seq. ID
                  BLASTX
Method
                  g3928095
NCBI GI
BLAST score
                  171
                  3.0e-12
E value
Match length
                  109
% identity
                  38
NCBI Description (AC005770) putative protein kinase [Arabidopsis thaliana]
                  234409
Seq. No.
                  LIB3272-034-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3212869
                  570
BLAST score
E value
                  5.0e-59
                  120
Match length
% identity
                  87
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                  234410
Seq. No.
Seq. ID
                  LIB3272-034-P1-K1-G2
                  BLASTX
Method
                  g3158474
NCBI GI
BLAST score
                  324
                   5.0e-36
E value
Match length
                  91
% identity
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
                   234411
Seq. No.
Seq. ID
                  LIB3272-034-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g322750
                  615
BLAST score
                   3.0e-64
E value
Match length
                  120
                   98
% identity
NCBI Description ubiquitin / ribosomal protein CEP52 - wood tobacco
                   >gi 170217 (M74100) ubiquitin fusion protein [Nicotiana
```



## sylvestris]

```
Seq. No.
                  234412
                  LIB3272-034-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2654208
BLAST score
                  279
                  7.0e-25
E value
Match length
                  97
                  68
% identity
NCBI Description
                  (AF035456) heat shock 70 protein [Spinacia oleracea]
                  >gi 2773050 (AF039083) heat shock 70 protein [Spinacia
                  oleracea]
Seq. No.
                  234413
Seq. ID
                  LIB3272-034-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q2894599
BLAST score
                  355
E value
                  9.0e - 34
Match length
                  101
                  65
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  234414
Seq. ID
                  LIB3272-034-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q2245064
BLAST score
                  144
                  5.0e-09
E value
Match length
                  99
                  40
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
                  234415
Seq. No.
Seq. ID
                  LIB3272-034-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g1297359
BLAST score
                  679
E value
                  9.0e-72
Match length
                  127
% identity
                  100
NCBI Description (U53701) alcohol dehydrogenase 2d [Gossypium hirsutum]
Seq. No.
                  234416
Seq. ID
                  LIB3272-034-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2146746
BLAST score
                  257
                  3.0e-22
E value
Match length
                  58
                  91
% identity
NCBI Description protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi 166819 (L05562) protein kinase [Arabidopsis thaliana]
```

Seq. No. 234417

Seq. ID LIB3272-034-P1-K1-H11



```
BLASTX
Method
                  g1928981
NCBI GI
BLAST score
                  394
                  1.0e-38
E value
Match length
                  90
                  53
% identity
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                  oleracea var. botrytis]
                  234418
Seq. No.
                  LIB3272-034-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1332579
BLAST score
                  665
E value
                  4.0e-70
Match length
                  134
                  10
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                  234419
                  LIB3272-034-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4103324
BLAST score
                  529
E value
                   4.0e-54
Match length
                  111
% identity
                   92
                  (AF022716) GDP-mannose pyrophosphorylase [Solanum
NCBI Description
                  tuberosum]
                  234420
Seq. No.
                  LIB3272-034-P1-K1-H6
Seq. ID
                  BLASTX
Method
                  g475048
NCBI GI
                  527
BLAST score
                  6.0e-54
E value
                  115
Match length
                   58
% identity
NCBI Description (X72581) tonoplast intrinsic protein gamma (gamma-TIP)
                   [Arabidopsis thaliana]
                   234421
Seq. No.
Seq. ID
                  LIB3272-034-P1-K1-H8
Method
                  BLASTX
NCBI GI
                   g585973
BLAST score
                   602
E value
                   1.0e-62
                   130
Match length
                   91
% identity
                  FRUCTOKINASE >gi 626018 pir S39997 fructokinase (EC
NCBI Description
                   2.7.1.4) - potato >gi 297015 emb CAA78283 (Z12823)
                   fructokinase [Solanum tuberosum] >gi_1095321_prf__2108342A
                   fructokinase [Solanum tuberosum]
```

LIB3272-034-P1-K1-H9 Seq. ID

BLASTX Method



q3334223 NCBI GI 311 BLAST score 6.0e-29 E value Match length 71 % identity

4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD) NCBI Description

>gi\_2145039 (AF000228) p-hydroxyphenylpyruvate dioxygenase

[Arabidopsis thaliana] >gi\_2392518 (U89267)

p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi 3098559 (AF047834) 4-hydroxyphenylpyruvate dioxygenase

[Arabidopsis thaliana]

234423 Seq. No.

LIB3272-035-P1-K1-A10 Seq. ID

Method BLASTX g131015 NCBI GI 294 BLAST score 9.0e-27 E value Match length 68 74 % identity

NCBI Description

PATHOGENESIS-RELATED PROTEIN R MAJOR FORM PRECURSOR (THAUMATIN-LIKE PROTEIN E22) >gi\_100385 pir\_\_JH0230 pathogenesis-related protein R precursor - common tobacco >gi 19855 emb\_CAA33293\_ (X15224) thaumatin-like protein [Nicotiana tabacum] >gi\_19980\_emb\_CAA31235\_ (X12739) pathogenesis-related protein  $\overline{R}$  (A $\overline{A}$  1 - 226) [Nicotiana tabacum]

234424 Seq. No. LIB3272-035-P1-K1-A12 Seq. ID Method BLASTX

NCBI GI g417103 597 BLAST score 4.0e-62 E value Match length 136 % identity 88

NCBI Description HISTONE H3.2, MINOR >gi\_282871 pir S24346 histone H3.3-like protein - Arabidopsis thaliana

>gi 16324 emb\_CAA42957\_ (X60429) histone H3.3 like protein [Arabidopsis Thaliana] >gi 404825\_emb CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 ( $\overline{\text{U}}$ 09460) histone H3.2 [Medicago sativa] >gi 488569 ( $\overline{U}09461$ ) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa]  $>gi_4885\overline{7}7$  (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone

H3 [Lolium temulentum] >gi 1435157 emb\_CAA58445\_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi 4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 234425



```
LIB3272-035-P1-K1-A3
Seq. ID
                  BLASTX
Method
                  g1709498
NCBI GI
                  559
BLAST score
                  1.0e-57
E value
                  125
Match length
                  80
% identity
                  OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                  >gi 1362001 pir S57524 osmotin precursor - Arabidopsis
                  thaliana >gi 887390 emb CAA61411 (X89008) osmotin
                  [Arabidopsis thaliana]
                  234426
Seq. No.
                  LIB3272-035-P1-K1-A6
Seq. ID
                  BLASTX
Method
                  g2078350
NCBI GI
                  606
BLAST score
                  4.0e-63
E value
Match length
                  138
% identity
                  83
NCBI Description (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                  234427
                  LIB3272-035-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  q133249
NCBI GI
                  311
BLAST score
                  1.0e-28
E value
                  78
Match length
% identity
                  45
NCBI Description CHLOROPLAST 33 KD RIBONUCLEOPROTEIN PRECURSOR
                  >gi 100390 pir__S12111 ribonucleoprotein, 33K, precursor -
                   common tobacco >gi_20005_emb_CAA37879_ (X53932) 33 kDa
                  ribonucleoprotein precursor [Nicotiana tabacum]
                   234428
Seq. No.
                  LIB3272-035-P1-K1-A9
Seq. ID
                  BLASTX
Method
                  g3894159
NCBI GI
                   228
BLAST score
                   8.0e-19
E value
                  130
Match length
% identity
NCBI Description (AC005312) hypothetical protein [Arabidopsis thaliana]
                   234429
Seq. No.
                   LIB3272-035-P1-K1-B1
Seq. ID
                   BLASTX
Method
                   g1945611
NCBI GI
BLAST score
                   301
                   2.0e-27
E value
                   134
Match length
```

....

macropain) 26S subunit, non-ATPase,

45

% identity

NCBI Description

33881

(AB003103) 26S proteasome subunit p55 [Homo sapiens]

>qi 4506221 ref NP 002807.1\_pPSMD12\_ proteasome (prosome,

Match length

% identity

108



```
234430
 Seq. No.
Seq. ID
                   LIB3272-035-P1-K1-B10
                   BLASTX
Method
NCBI GI
                   g119355
BLAST score
                   506
E value
                   1.0e-51
Match length
                   112
 % identity
                   88
                   ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi 100869 pir S16257 phosphopyruvate hydratase (EC
                   4.2.1.11) - maize >gi 22273 emb CAA39454 (X55981) enolase
                   [Zea mays]
                   234431
 Seq. No.
 Seq. ID
                   LIB3272-035-P1-K1-B12
                   BLASTX
Method
NCBI GI
                   g2462929
BLAST score
                   486
                   5.0e-49
E value
                   144
Match length
 % identity
                   64
 NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]
 Seq. No.
                   234432
Seq. ID
                   LIB3272-035-P1-K1-B4
Method
                   BLASTX
 NCBI GI
                   g133867
 BLAST score
                   371
                   9.0e-36
 E value
                   91
 Match length
                   80
 % identity
 NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi 82722_pir S16577 ribosomal
                   protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                   ribosomal protein S11 [Zea mays]
                   234433
 Seq. No.
 Seq. ID
                   LIB3272-035-P1-K1-C2
 Method
                   BLASTX
 NCBI GI
                   g126770
 BLAST score
                   705
                   1.0e-74
 E value
                   134
 Match length
                   100
 % identity
 NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi_68218_pir__SYCNMU malate
                   synthase (EC 4.1.3.2) - upland cotton
                   >gi 18507 emb CAA36546 (X52305) malate synthase (AA 1-567)
                   [Gossypium hirsutum]
 Seq. No.
                   234434
 Seq. ID
                   LIB3272-035-P1-K1-C3
                   BLASTX
 Method
 NCBI GI
                   g548774
 BLAST score
                   421
 E value
                   2.0e-41
```



NCBI Description 60S RIBOSOMAL PROTEIN L7A >gi\_542158\_pir\_S38360 ribosomal protein L7a - rice >gi\_303855\_dbj\_BAA02156\_ (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No. 234435

Seq. ID LIB3272-035-P1-K1-C4

Method BLASTX
NCBI GI g2499946
BLAST score 229
E value 2.0e-22
Match length 86

% identity 73

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi\_747980 (U22260) UMP synthase [Nicotiana

tabacum]

Seq. No. 234436

Seq. ID LIB3272-035-P1-K1-C6

Method BLASTX
NCBI GI g544231
BLAST score 333
E value 1.0e-40
Match length 115
% identity 74

NCBI Description ELONGATION FACTOR 1-ALPHA 2 (EF-1-ALPHA-2) (STATIN S1)

>gi\_2144946\_pir\_\_EFHUA2 translation elongation factor eEF-1 alpha-2 chain - human >gi\_38456\_emb\_CAA50280\_ (X70940) elongation factor 1 alpha-2 [Homo sapiens] >gi\_3098311 (AF035178) elongation factor 1 A2 [Oryctolagus cuniculus] >gi\_4503475\_ref\_NP\_001949.1\_pEEF1A2\_ eukaryotic translation

elongation factor 1 alpha

Seq. No. 234437

Seq. ID LIB3272-035-P1-K1-C7

Method BLASTX
NCBI GI g1705463
BLAST score 246
E value 4.0e-21
Match length 68
% identity 68

NCBI Description BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi\_2129547\_pir\_\_S71201

biotin sythase - Arabidopsis thaliana  $>gi_10453\overline{16}$  ( $\overline{U2}4147$ ) biotin sythase [Arabidopsis thaliana]  $>gi_1403662$  (U31806) BIO2 protein [Arabidopsis thaliana]  $>gi_1769457$  (L34413)

biotin synthase [Arabidopsis thaliana] >gi\_2288983

(AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi\_1589016\_prf\_\_2209438A biotin synthase [Arabidopsis

thaliana]

Seq. No. 234438

Seq. ID LIB3272-035-P1-K1-C8

Method BLASTX
NCBI GI g584861
BLAST score 255
E value 6.0e-22
Match length 94



% identity NCBI Description CYTOCHROME P450 71A2 (CYPLXXIA2) (P-450EG4) >gi\_480396\_pir\_\_S36806 cytochrome P450 71A2 - eggplant >gi\_408140\_emb\_CAA50645\_ (X71654) P450 hydroxylase [Solanum
melongena] >gi\_441185\_dbj\_BAA03635\_ (D14990) Cytochrome P-450EG4 [Solanum melongena] 234439 Seq. No. Seq. ID LIB3272-035-P1-K1-D10 Method BLASTX NCBI GI q1173209 BLAST score 660 2.0e-69 E value Match length 140 % identity 93 40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal NCBI Description protein S16 protein - upland cotton >gi\_439654\_emb\_CAA53567\_ (X75954) RS16 protein, 40S subunit [Gossypium hirsutum] 234440 Seq. No. LIB3272-035-P1-K1-D11 Seq. ID Method BLASTX NCBI GI q3158376 BLAST score 309 E value 3.0e - 28Match length 118 % identity 56 NCBI Description (AF035385) unknown [Arabidopsis thaliana] Seq. No. 234441 Seq. ID LIB3272-035-P1-K1-D12 Method BLASTX NCBI GI q3063470 BLAST score 547 E value 3.0e-56 Match length 100 % identity 96 NCBI Description (AC003981) F22013.32 [Arabidopsis thaliana] Seq. No. 234442 Seq. ID LIB3272-035-P1-K1-D5 Method BLASTX NCBI GI g4490321 BLAST score 297 E value 7.0e-27 Match length 115 54 % identity (AJ011604) nitrate transporter [Arabidopsis thaliana] NCBI Description Seq. No. 234443 Seq. ID LIB3272-035-P1-K1-D7 Method BLASTX

Method BLASTX
NCBI GI g529353
BLAST score 214
E value 4.0e-17
Match length 105



```
% identity
                    (U12757) diphenol oxidase [Acer pseudoplatanus]
NCBI Description
                    234444
Seq. No.
                    LIB3272-035-P1-K1-D8
Seq. ID
                    BLASTX
Method
                    q1729971
NCBI GI
BLAST score
                    220
E value
                    2.0e-18
                    109
Match length
% identity
                    51
                    TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                    (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                    satival
                    234445
Seq. No.
Seq. ID
                    LIB3272-035-P1-K1-D9
Method
                    BLASTX
NCBI GI
                    q2511594
                    641
BLAST score
                    3.0e-67
E value
Match length
                    139
% identity
                    (Y13694) multicatalytic endopeptidase complex, proteasome
NCBI Description
                    precursor, beta subunit [Arabidopsis thaliana]
                    >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic
                    endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S
                    proteasome subunit PBA1 [Arabidopsis thaliana]
Seq. No.
                    234446
                    LIB3272-035-P1-K1-E11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q419781
BLAST score
                    138
                    1.0e-08
E value
                    45
Match length
                    64
% identity
NCBI Description probable cysteine proteinase precursor (clone CYP-7) -
                    common tobacco >gi_19849_emb_CAA78361_ (Z13959) tobacco
                    pre-pro-cysteine proteinase [Nicotiana tabacum]
                    234447
Seq. No.
Seq. ID
                    LIB3272-035-P1-K1-E12
Method
                    BLASTX
                    g3421102
NCBI GI
                    392
BLAST score
                    3.0e-38
E value
                    86
Match length
                    83
% identity
```

NCBI Description (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis

thaliana]

Seq. No. 234448

Seq. ID LIB3272-035-P1-K1-E2

Method BLASTX



q125271 NCBI GI BLAST score 585 E value 1.0e-60 Match length 141 78 % identity CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA) NCBI Description >gi\_100860\_pir\_\_S19726 casein kinase II (EC 2.7.1.-) alpha chain - maize >gi\_3318993\_pdb\_1A60\_ Protein Kinase Ck2 (Catalytic Subunit) From Zea Mays >gi\_22117\_emb\_CAA43659\_ (X61387) casein kinase II alpha subunit [Zea mays] 234449 Seq. No. LIB3272-035-P1-K1-E4 Seq. ID Method BLASTX NCBI GI g549063 BLAST score 377 E value 3.0e-36 Match length 114 66 % identity TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description >gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi 303835 dbj BAA02151\_ (D12626) 21kd polypeptide [Oryza sativa] Seq. No. 234450 LIB3272-035-P1-K1-E8 Seq. ID Method BLASTX NCBI GI g1171579 421 BLAST score E value 2.0e-41Match length 134 64 % identity NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum] Seq. No. 234451 LIB3272-035-P1-K1-E9 Seq. ID BLASTX Method NCBI GI q4115377 BLAST score 307 3.0e-36 E value 129 Match length 63 % identity NCBI Description (AC005967) unknown protein [Arabidopsis thaliana] Seq. No. 234452 LIB3272-035-P1-K1-F1 Seq. ID BLASTX Method NCBI GI q1928981 BLAST score 281 5.0e-50E value 112 Match length % identity

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 234453

Seq. ID LIB3272-035-P1-K1-F11

Seq. ID

Method



```
BLASTX
Method
NCBI GI
                   q2462746
BLAST score
                   359
E value
                   2.0e-34
                   88
Match length
                   77
% identity
                   (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                   thaliana]
                   234454
Seq. No.
Seq. ID
                   LIB3272-035-P1-K1-F12
Mëthod
                   BLASTX
                   a3860308
NCBI GI
                   167
BLAST score
E value
                   7.0e-12
                   47
Match length
                   70
% identity
                   (AJ012681) hypothetical protein [Cicer arietinum]
NCBI Description
                   234455
Seq. No.
                   LIB3272-035-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2244799
BLAST score
                   201
                   1.0e-15
E value
Match length
                   139
% identity
                   38
                   (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
NCBI Description
                   234456
Seq. No.
                   LIB3272-035-P1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                    g119150
BLAST score
                    671
E value
                    8.0e-71
Match length
                   128
% identity
                    99
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi_82081_pir__S10507 translation elongation factor eEF-1
alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF
                    1-alpha (AA 1-448) [Lycopersicon esculentum]
                    >gi 295810_emb_CAA37212_ (X53043) elongation factor 1-alpha
                    [Lycopersicon esculentum]
Seq. No.
                    234457
                   LIB3272-035-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2662343
BLAST score
                   509
                    6.0e-52
E value
                   104
Match length
                    93
% identity
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                    234458
Seq. No.
```

33887

LIB3272-035-P1-K1-F7

BLASTX

Seq. ID

234463

LIB3272-035-P1-K1-G8



```
NCBI GI
                   q3451072
BLAST score
                   280
E value
                   5.0e-25
Match length
                   82
% identity
                   59
NCBI Description
                 (AL031326) putative protein [Arabidopsis thaliana]
                   234459
Seq. No.
Seq. ID
                   LIB3272-035-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   q2341032
BLAST score
                   420
E value
                   2.0e-41
Match length
                   108
% identity
                   71
                  (AC000104) EST gb ATTS0956 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   234460
Seq. ID
                   LIB3272-035-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   q3287834
BLAST score
                   293
E value
                   1.0e-26
Match length
                   107
% identity
NCBI Description
                   (+)-DELTA-CADINENE SYNTHASE ISOZYME XC14 (D-CADINENE
                   {\tt SYNTHASE}) > {\tt gi\_2147016\_pir\_S68366 (+)-delta-cadinene}
                   synthase isozyme XC14 - Gossypium arboreum >gi 1045314
                   (U23205) (+)-delta-cadinene synthase isozyme XC14
                   [Gossypium arboreum]
Seq. No.
                   234461
Seq. ID
                   LIB3272-035-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g2117725
BLAST score
                   474
E value
                   4.0e-49
Match length
                   116
% identity
                   80
                   1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform
NCBI Description
                   SBE2.2 precursor - Arabidopsis thaliana (fragment)
                   >gi 726490 (U22428) starch branching enzyme class II
                   [Arabidopsis thaliana]
Seq. No.
                   234462
                   LIB3272-035-P1-K1-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1843527
BLAST score
                   700
                   4.0e-74
E value
                   140
Match length
% identity
NCBI Description
                  (U73747) annexin [Gossypium hirsutum]
```

E value

Match length

2.0e-35

137



```
Method
                  BLASTX
NCBI GI
                  g529353
BLAST score
                  188
                  2.0e-14
E value
                  58
Match length
                  55
% identity
NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]
Seq. No.
                  234464
                  LIB3272-035-P1-K1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4193388
                  218
BLAST score
E value
                  1.0e-17
                  56
Match length
                  79
% identity
                 (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                  brasiliensis]
Seq. No.
                  234465
                  LIB3272-035-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2369766
BLAST score
                  305
                  2.0e-28
E value
                  106
Match length
% identity
                  62
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
Seq. No.
                  234466
Seq. ID
                  LIB3272-035-P1-K1-H2
                  BLASTX
Method
NCBI GI
                  g3617741
BLAST score
                  665
E value
                  4.0e-70
Match length
                  137
                  91
% identity
NCBI Description (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis
                  thaliana]
Seq. No.
                  234467
Seq. ID
                  LIB3272-035-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g3860308
BLAST score
                  210
                  1.0e-16
E value
                  69
Match length
                  62
% identity
NCBI Description (AJ012681) hypothetical protein [Cicer arietinum]
                  234468
Seq. No.
                  LIB3272-035-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q480618
BLAST score
                  370
```



% identity ATAF1 protein - Arabidopsis thaliana (fragment) NCBI Description >gi 1345506 emb CAA52771 (X74755) ATAF1 [Arabidopsis thaliana] 234469 Seq. No. LIB3272-035-P1-K1-H7 Seq. ID Method BLASTX NCBI GI g4220521 476 BLAST score 7.0e-48 E value 144 Match length % identity 61 NCBI Description (AL035356) putative protein [Arabidopsis thaliana] 234470 Seq. No. LIB3272-035-P1-K1-H8 Seq. ID BLASTX Method NCBI GI g1565225 BLAST score 431 1.0e-42 E value 95 Match length 83 % identity NCBI Description (X95572) salt-tolerance protein [Arabidopsis thaliana] 234471 Seq. No. LIB3272-036-P1-K1-A1 Seq. ID BLASTX Method NCBI GI g2499946 BLAST score 548 2.0e-56 E value 125 Match length 86 % identity NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi 747980 (U22260) UMP synthase [Nicotiana tabacum] 234472 Seq. No. LIB3272-036-P1-K1-A10 Seq. ID BLASTX Method NCBI GI g462138 BLAST score 292 E value 1.0e-26 100 Match length % identity 62 NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >qi 169091 (L07500) glyceraldehyde-3-phosphate dehydrogenase [Pisum sativum] >gi\_1345567 emb\_CAA51675\_ (X73150) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Pisum sativum]

234473 Seq. No.

Seq. ID LIB3272-036-P1-K1-A11

Method BLASTX q289920 NCBI GI BLAST score 683



```
3.0e-72
E value
Match length
                  126
                  99
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  234474
Seq. No.
Seq. ID
                  LIB3272-036-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q81454
BLAST score
                  596
                  5.0e-62
E value
Match length
                  128
                  91
% identity
                  photosystem II oxygen-evolving complex protein 1 - spinach
NCBI Description
                  >gi 224916 prf 1204192A photosystem II protein 33kD
                   [Spinacia oleracea]
Seq. No.
                  234475
                  LIB3272-036-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1709498
BLAST score
                  488
E value
                   2.0e-49
Match length
                  109
% identity
                   81
                  OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                   >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis
                   thaliana >gi 887390 emb CAA61411 (X89008) osmotin
                   [Arabidopsis thaliana]
                   234476
Seq. No.
                  LIB3272-036-P1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2088652
BLAST score
                   383
                   2.0e-44
E value
                  119
Match length
% identity
                   76
                  (AF002109) 26S proteasome regulatory subunit S12 isolog
NCBI Description
                   [Arabidopsis thaliana] >gi 2351376 (U54561) translation
                   initiation factor eIF2 p47 subunit homolog [Arabidopsis
                   thaliana]
Seq. No.
                   234477
Seq. ID
                   LIB3272-036-P1-K1-A6
                   BLASTX
Method
NCBI GI
                   q549063
BLAST score
                   365
```

5.0e-35 E value 92 Match length 75

% identity TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi 303835 dbj BAA02151 (D12626)

21kd polypeptide [Oryza sativa]



```
234478
Seq. No.
                   LIB3272-036-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3986695
BLAST score
                   645
E value
                   9.0e-68
                   139
Match length
                   93
% identity
                  (AF101423) ribosomal protein L12 [Cichorium intybus]
NCBI Description
Seq. No.
                   234479
                   LIB3272-036-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q464986
BLAST score
                   493
                   7.0e-50
E value
                   92
Match length
                   98
% identity
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                   enzyme E2 [Arabidopsis thaliana]
                   >qi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
Seq. No.
                   234480
                   LIB3272-036-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2146740
BLAST score
                   408
E value
                   6.0e-40
Match length
                   111
                   72
% identity
                   inner mitochondrial membrane protein - Arabidopsis thaliana
NCBI Description
                   >gi 603056 (U18126) inner mitochondrial membrane protein
                   [Arabidopsis thaliana]
                   234481
Seq. No.
                   LIB3272-036-P1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4191788
BLAST score
                   453
                   3.0e-45
E value
Match length
                   128
% identity
```

NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate

oxidase [Arabidopsis thaliana]

Seq. No. 234482

Seq. ID LIB3272-036-P1-K1-B5

Method BLASTX NCBI GI g3334123



BLAST score 288
E value 6.0e-26
Match length 85
% identity 74

NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

>gi\_1655480\_dbj\_BAA13599\_ (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] >gi\_2924787

(AC002334) mitochondrial F1-ATPase, gamma subunit

[Arabidopsis thaliana]

Seq. No. 234483

Seq. ID LIB3272-036-P1-K1-B6

Method BLASTX
NCBI GI g1172597
BLAST score 229
E value 4.0e-19
Match length 47
% identity 94

NCBI Description WOUND-INDUCED BASIC PROTEIN >gi\_81888\_pir\_\_JS0731

wound-inducible basic protein - kidney bean >gi 169365

(L00625) basic protein [Phaseolus vulgaris]

>gi 217989 dbj BAA02299 (D12914) 5.8 kb basic protein

[Phaseolus vulgaris]

Seq. No. 234484

Seq. ID LIB3272-036-P1-K1-B7

Method BLASTX
NCBI GI g4510363
BLAST score 523
E value 2.0e-53
Match length 110
% identity 89

NCBI Description (AC007017) putative DNA-binding protein [Arabidopsis

thaliana]

Seq. No. 234485

Seq. ID LIB3272-036-P1-K1-B9

Method BLASTX
NCBI GI g2129871
BLAST score 278
E value 1.0e-24
Match length 89
% identity 62

NCBI Description proline-rich protein, 14K - kidney bean >gi 1420885

(U34333) proline-rich 14 kDa protein [Phaseolus vulgaris]

Seq. No. 234486

Seq. ID LIB3272-036-P1-K1-C10

Method BLASTX
NCBI GI g3986695
BLAST score 616
E value 2.0e-64
Match length 135

% identity 91

NCBI Description (AF101423) ribosomal protein L12 [Cichorium intybus]

Seq. No. 234487

E value

Match length

4.0e-32



```
LIB3272-036-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3334147
BLAST score
                  384
E value
                   3.0e-37
Match length
                  111
% identity
                  68
NCBI Description ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I
                  chitinase [Gossypium hirsutum]
Seq. No.
                  234488
Seq. ID
                  LIB3272-036-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2760345
BLAST score
                  584
E value
                  1.0e-60
Match length
                  116
% identity
                  25
NCBI Description (U84967) ubiquitin [Arabidopsis thaliana]
Seq. No.
                  234489
Seq. ID
                  LIB3272-036-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4455225
BLAST score
                  214
                  3.0e-17
E value
Match length
                  64
                  56
% identity
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  234490
Seq. ID
                  LIB3272-036-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g3128177
BLAST score
                  504
E value
                  3.0e-51
Match length
                  119
% identity
                  82
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  234491
Seq. ID
                  LIB3272-036-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g4103618
BLAST score
                  229
                  6.0e-19
E value
Match length
                  77
                  57
% identity
NCBI Description (AF026382) HyPRP [Fragaria x ananassa]
Seq. No.
                  234492
Seq. ID
                  LIB3272-036-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g2462758
BLAST score
                  341
```

Seq. ID

234498

LIB3272-036-P1-K1-D7



```
% identity
                  (AC002292) putative RNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  234493
Seq. No.
Seq. ID
                  LIB3272-036-P1-K1-D11
                  BLASTX
Method
NCBI GI
                  g3128209
BLAST score
                  388
                  1.0e-37
E value
                  102
Match length
                  74
% identity
NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]
Seq. No.
                  234494
Seq. ID
                  LIB3272-036-P1-K1-D12
                  BLASTX
Method
NCBI GI
                  g113217
BLAST score
                  230
E value
                  3.0e-19
                  51
Match length
% identity
                  88
NCBI Description ACTIN 1 >gi 100149 pir S07002 actin 1 - carrot
Seq. No.
                  234495
Seq. ID
                  LIB3272-036-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g3759184
BLAST score
                  262
E value
                  7.0e-23
                  112
Match length
% identity
                  55
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                  234496
Seq. No.
Seq. ID
                  LIB3272-036-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g4309698
BLAST score
                  525
E value
                  1.0e-53
Match length
                  122
% identity
                  88
NCBI Description (AC006266) putative glucosyltransferase [Arabidopsis
                  thaliana]
                  234497
Seq. No.
                  LIB3272-036-P1-K1-D5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2270994
BLAST score
                  331
E value
                  5.0e-33
Match length
                  113
% identity
NCBI Description (AF004809) Ca+2-binding EF hand protein [Glycine max]
```



Method BLASTX NCBI GI g1353059 BLAST score 179 E value 4.0e-13 124 Match length 32 % identity NCBI Description HYPOTHETICAL 27.4 KD PROTEIN IN MER2-BNA1 INTERGENIC REGION >gi 1077874 pir S57042 hypothetical protein YJR024c yeast (Saccharomyces cerevisiae) >gi 1015663 emb CAA89549 (Z49524) ORF YJR024c [Saccharomyces cerevisiae] >gi 1129160 emb CAA60719 (X87297) J1545 [Saccharomyces cerevisiae] 234499 Seq. No. Seq. ID LIB3272-036-P1-K1-D8 Method BLASTX NCBI GI g4115377 BLAST score 344 E value 2.0e-32 Match length 113 52 % identity NCBI Description (AC005967) unknown protein [Arabidopsis thaliana] Seq. No. 234500 LIB3272-036-P1-K1-D9 Seq. ID BLASTX Method NCBI GI q3128231 BLAST score 315 E value 5.0e-29 132 Match length % identity 11 (AC004077) hypothetical protein [Arabidopsis thaliana] NCBI Description >gi 3337370 (AC004481) hypothetical protein [Arabidopsis thaliana] 234501 Seq. No. Seq. ID LIB3272-036-P1-K1-E1 Method BLASTX NCBI GI g2388585 BLAST score 208 E value 2.0e-16 68 Match length % identity NCBI Description (AC000098) Similar to Caenorhabditis unknown protein T03F1.1 (gb U88169). [Arabidopsis thaliana] Seq. No. 234502 LIB3272-036-P1-K1-E10 Seq. ID Method BLASTX NCBI GI g1173218 BLAST score 585 1.0e-60 E value

115 Match length % identity 98

NCBI Description 40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)

cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Match length

% identity

118

81



```
Seq. No.
                  234503
Seq. ID
                  LIB3272-036-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g3763932
BLAST score
                  219
E value
                  9.0e-18
Match length
                  68
% identity
                  62
                 (AC004450) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  234504
Seq. No.
Seq. ID
                  LIB3272-036-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2651310
BLAST score
                  239
E value
                  4.0e-20
Match length
                  129
% identity
                  35
                  (ACO02336) putative PTR2-B peptide transporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  234505
                  LIB3272-036-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204313
BLAST score
                  160
E value
                  7.0e-11
                  79
Match length
% identity
                  42
                  (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  234506
Seq. ID
                  LIB3272-036-P1-K1-E7
                  BLASTX
Method
NCBI GI
                  g461498
BLAST score
                  536
E value
                  6.0e-55
Match length
                  134
                  75
% identity
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
NCBI Description
                  TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                   (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC
                  2.6.1.2) - proso millet >gi 296204 emb CAA49199 (X69421)
                  alanine aminotransferase [Panicum miliaceum]
                  234507
Seq. No.
Seq. ID
                  LIB3272-036-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3386621
BLAST score
                  507
E value
                  1.0e-51
```

NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                   234508
Seq. ID
                   LIB3272-036-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2499945
BLAST score
                   493
E value
                   6.0e-50
Match length
                   135
% identity
                   67
NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
                   PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                   DECARBOXYLASE >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) /
                   orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                   Arabidopsis thaliana >gi 443818 emb CAA50686 (X71842)
                   pyrE-F [Arabidopsis thaliana]
                   234509
Seq. No.
Seq. ID
                   LIB3272-036-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q1351303
BLAST score
                   280
E value
                   6.0e-25
Match length
                   115
                   55
% identity
NCBI Description
                 INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE PRECURSOR (IGPS)
                   >gi 619732 (U18770) indole-3-glycerol phosphate synthase
                   [Arabidopsis thaliana]
Seq. No.
                   234510
Seq. ID
                   LIB3272-036-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   343
E value
                   3.0e-32
Match length
                   108
% identity
                   64
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                   >gi 1072464 pir A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                   234511
Seq. ID
                   LIB3272-036-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g4455246
BLAST score
                   299
E value
                   3.0e-27
                   77
Match length
% identity
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
```

Seq. ID LIB3272-036-P1-K1-F5

Method BLASTX
NCBI GI g2462929
BLAST score 519
E value 6.0e-53

Seq. ID Method



```
Match length
                    136
 % identity
                    71
NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]
 Seq. No.
                    234513
 Seq. ID
                    LIB3272-036-P1-K1-F6
                    BLASTX
 Method
                    g3158474
 NCBI GI
 BLAST score
                    513
                    3.0e-52
 E value
 Match length
                    110
 % identity
                    90
 NCBI Description (AF067184) aquaporin 1 [Samanea saman]
 Seq. No.
                    234514
 Seq. ID
                    LIB3272-036-P1-K1-F7
 Method
                    BLASTX
 NCBI GI
                    g2827528
                    160
 BLAST score
                    7.0e-11
 E value
 Match length
                    116
 % identity
                    32
 NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]
 Seq. No.
                    234515
 Seq. ID
                    LIB3272-036-P1-K1-F8
 Method
                    BLASTX
 NCBI GI
                    g2662343
 BLAST score
                    586
 E value
                    8.0e-61
                    111
 Match length
 % identity
                    100
 NCBI Description (D63581) EF-1 alpha [Oryza sativa]
                    234516
 Seq. No.
 Seq. ID
                    LIB3272-036-P1-K1-G1
 Method
                    BLASTX
 NCBI GI
                    g3264767
 BLAST score
                    170
 E value
                    3.0e-12
 Match length
                    73
 % identity
                    49
 NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
 Seq. No.
                    234517
                    LIB3272-036-P1-K1-G11
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1669601
 BLAST score
                    577
 E value
                    9.0e-60
                    130
 Match length
 % identity
                    80
"NCBI Description (D88747) AR401 [Arabidopsis thaliana]
                    234518
 Seq. No.
```

33899

LIB3272-036-P1-K1-G12

BLASTX



NCBI GI g266972 BLAST score 204 E value 5.0e-16 54 Match length 65 % identity 40S RIBOSOMAL PROTEIN S29 >gi\_631884\_pir\_\_S30298 ribosomal NCBI Description protein S29 - rat >gi\_1362934\_pir\_\_S55919 ribosomal protein S29 - human >gi\_57133\_emb\_CAA41778\_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi\_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi\_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi 1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi 1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi 1096945 prf 2113200H ribosomal protein S29 [Homo sapiens] >gi  $4\overline{50}67\overline{17}$  ref NP 001023.1 pRPS29 ribosomal protein S29

Seq. No. 234519 Seq. ID LIB3272-036-P1-K1-G3

Method BLASTX
NCBI GI g4249382
BLAST score 457
E value 9.0e-46
Match length 121

% identity 69
NCBI Description (AC005966) Strong similarity to gi\_3337350 F13P17.3

putative permease from Arabidopsis thaliana BAC

gb AC004481. [Arabidopsis thaliana]

Seq. No. 234520

Seq. ID LIB3272-036-P1-K1-G4

Method BLASTX
NCBI GI g1703108
BLAST score 718
E value 3.0e-76
Match length 133
% identity 100

NCBI Description ACTIN 2/7 >gi\_2129525\_pir\_\_S71210 actin 2 - Arabidopsis thaliana >gi\_2129528\_pir\_\_S68107 actin 7 - Arabidopsis

thaliana >gi\_2129528\_pir\_\_S68107 actin 7 - Arabidopsis thaliana >gi\_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi\_1943863 (U27811) actin7 [Arabidopsis

thaliana]

Seq. No. 234521

Seq. ID LIB3272-036-P1-K1-G5

Method BLASTX
NCBI GI g2160166
BLAST score 376
E value 3.0e-36
Match length 136

% identity 56

NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 234522

Seq. ID LIB3272-036-P1-K1-G6

Method BLASTX NCBI GI q543867



```
BLAST score
 E value
                    5.0e-33
                    98
Match length
                    78
  % identity
 NCBI Description ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
                    >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC
                    3.6.1.34) gamma chain precursor - sweet potato
                    >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit
                    [Ipomoea batatas]
                    234523
  Seq. No.
  Seq. ID
                   LIB3272-036-P1-K1-H1
 Method
                   BLASTX
                    q3150404
 NCBI GI
                   99
 BLAST score
                    7.0e-09
 E value
 Match length
                   60
  % identity
                    62
 NCBI Description (AC004165) putative mitochondrial carrier protein
                    [Arabidopsis thaliana]
 Seq. No.
                    234524
                    LIB3272-036-P1-K1-H2
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3334320
 BLAST score
                    261
 E value
                    5.0e-23
 Match length
                    63
                    87
  % identity
 NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                   ribosome-associated protein p40 [Glycine max]
  Seq. No.
                    234525
  Seq. ID
                   LIB3272-036-P1-K1-H3
 Method
                   BLASTX
 NCBI GI
                    g267082
 BLAST score
                   603
 E value
                    8.0e-63
 Match length
                    116
  % identity
                    94
  NCBI Description TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8
                    chain - Arabidopsis thaliana >gi 166908 (M84705) beta-8
                    tubulin [Arabidopsis thaliana]
  Seq. No.
                    234526
  Seq. ID
                   LIB3272-036-P1-K1-H4
                   BLASTX
 Method
 NCBI GI
                    q3643602
  BLAST score
                    152
 E value
                    5.0e-10
 Match length
                    69
```

% identity

Seq. ID LIB3272-036-P1-K1-H6

51

33901

NCBI Description (AC005395) putative tonoplast intrinsic protein

[Arabidopsis thaliana]



```
BLASTX
Method
NCBI GI
                  g3269284
                  275
BLAST score
E value
                  3.0e-24
                  104
Match length
                  59
% identity
NCBI Description (AL030978) histone H2A- like protein [Arabidopsis thaliana]
Seq. No.
                  234528
Seq. ID
                  LIB3272-037-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q3319355
                  280
BLAST score
E value
                  2.0e-25
Match length
                  66
% identity
                  83
NCBI Description (AF077407) similar to chaperonin containing TCP-1 complex
                  gamma chain [Arabidopsis thaliana]
Seq. No.
                  234529
                  LIB3272-037-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2213583
                  200
BLAST score
E value
                  1.0e-28
Match length
                  98
                  72
% identity
NCBI Description (AC000348) T7N9.3 [Arabidopsis thaliana]
Seq. No.
                  234530
Seq. ID
                  LIB3272-037-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g464707
BLAST score
                  585
E value
                  1.0e-60
                  119
Match length
                  96
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S18 >qi 480908 pir S37496 ribosomal
                  protein S18.A - Arabidopsis thaliana
                  >gi 405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi 434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
                  [Arabidopsis thaliana] >gi_434906 emb_CAA82275_ (Z28962)
                  S18 ribosomal protein [Arabidopsis thaliana]
                  >gi 2505871 emb CAA72909 (Y12227) ribosomal protein S18A
                  [Arabidopsis thaliana] >gi 3287678 (AC003979) Match to
                  ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
                  thaliana. ESTs gb T21121, gb Z17755, gb R64776 and
                  gb R30430 come from this gene. [Arabidopsis thaliana]
                  >gi 4538910 emb CAB39647.1 (AL049482) S18.A ribosomal
```

Seq. No. 234531 Seq. ID LIB3272-037-P1-K1-A3

Method BLASTX

NCBI GI g416758

protein [Arabidopsis thaliana]



```
BLAST score
E value
                  2.0e-33
Match length
                  117
                  59
% identity
NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130)
                  carboxypeptidase Y-like protein [Arabidopsis thaliana]
                  >gi_445120_prf 1908426A carboxypeptidase Y [Arabidopsis
                  thaliana]
                  234532
Seq. No.
Seq. ID
                  LIB3272-037-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q541978
BLAST score
                  383
                  5.0e-37
E value
Match length
                  74
% identity
                  100
NCBI Description guanine nucleotide regulatory protein - fava bean
                  >gi_303734_dbj_BAA02118 (D12550) GTP-binding protein
                  [Pisum satīvum] >gi_452359_emb_CAA82707_ (Z29590) guanine
                  nucleotide regulatory protein [Vicia faba]
                  >gi 738942 prf 2001457K GTP-binding protein [Pisum
                  sativum] >gi 1098293_prf__2115367A small GTP-binding
                  protein [Vicia faba]
Seq. No.
                  234533
Seq. ID
                  LIB3272-037-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q1777386
BLAST score
                  235
E value
                  1.0e-19
Match length
                  127
% identity
                  41
NCBI Description (U39301) caffeic acid O-methyltransferase [Pinus taeda]
Seq. No.
                  234534
Seq. ID
                  LIB3272-037-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3023522
BLAST score
                  406
E value
                  1.0e-39
Match length
                  137
% identity
                  54
NCBI Description
                 COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
                  (P102) >gi 2454309 (AF002705) beta prime COP [Rattus
```

norvegicus]

Seq. No. 234535

Seq. ID LIB3272-037-P1-K1-A9

Method BLASTX NCBI GI g4220481 BLAST score 456 E value 1.0e-45 Match length 137 % identity 61

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                  234536
Seq. ID
                  LIB3272-037-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g3063396
BLAST score
                  527
                  7.0e-54
E value
Match length
                  117
% identity
                  85
NCBI Description (AB012947) vcCyP [Vicia faba]
Seq. No.
                  234537
Seq. ID
                  LIB3272-037-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g3450889
BLAST score
                  358
E value
                  3.0e - 34
Match length
                  102
% identity
                  74
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
Seq. No.
                  234538
Seq. ID
                  LIB3272-037-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g462195
BLAST score
                  442
                  6.0e-44
E value
Match length
                  92
% identity
                  93
NCBI Description
                 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
Seq. No.
                  234539
Seq. ID
                  LIB3272-037-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q730456
BLAST score
                  305
E value
                  1.0e-41
Match length
                  118
% identity
                  69
NCBI Description 40S RIBOSOMAL PROTEIN S19
Seq. No.
                  234540
Seq. ID
                  LIB3272-037-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g266945
BLAST score
                  558
E value
                  2.0e-57
Match length
                  127
% identity
                  87
NCBI Description
                 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA)
                  >gi_100065 pir S19978 ribosomal protein L9 - garden pea
```

33904

[Pisum sativum]

>gi\_20727\_emb\_CAA46273\_ (X65155) GA [Pisum sativum]
>gi 1279645 emb CAA65987 (X97322) ribosomal protein L9

Match length

% identity

100



```
Seq. No.
                     234541
Seq. ID
                     LIB3272-037-P1-K1-B4
  Method
                     BLASTX
  NCBI GI
                     g1586940
  BLAST score
                     358
  E value
                     4.0e-34
  Match length
                     100
  % identity
                     67
  NCBI Description Ser/Thr kinase [Lycopersicon esculentum]
                     234542
  Seq. No.
  Seq. ID
                     LIB3272-037-P1-K1-B7
  Method
                     BLASTX
  NCBI GI
                     g120669
  BLAST score
                     428
  E value
                     3.0e-42
  Match length
                     94
  % identity
                     86
  NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                     >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                     >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                     3-phosphate dehydrogenase [Magnolia liliiflora]
  Seq. No.
                     234543
  Seq. ID
                     LIB3272-037-P1-K1-B9
  Method
                     BLASTX
  NCBI GI
                     g2507421
  BLAST score
                     519
  E value
                     6.0e-53
  Match length
                     109
  % identity
                     91
  NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277
                     (U81042) translation initiation factor [Arabidopsis
                     thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680)
                     translation initiation factor [Arabidopsis thaliana]
  Seq. No.
                     234544
  Seq. ID
                     LIB3272-037-P1-K1-C1
  Method
                     BLASTX
  NCBI GI
                     g3668089
  BLAST score
                     234
  E value
                     2.0e-19
  Match length
                     83
  % identity
                     51
  NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     234545
  Seq. ID
                     LIB3272-037-P1-K1-C10
  Method
                     BLASTX
  NCBI GI
                     g3851636
  BLAST score
                     424
  E value
                     6.0e-42
```

NCBI Description (AF098519) unknown [Avicennia marina] >gi 4128206



## (AF056316) 40S ribosome protein S7 [Avicennia marina]

```
Seq. No.
                  234546
                  LIB3272-037-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  g1170747
NCBI GI
BLAST score
                  329
E value
                  9.0e-31
Match length
                  67
% identity
                  100
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                   (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi_167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
                  234547
Seq. No.
Seq. ID
                  LIB3272-037-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g2145358
BLAST score
                  376
E value
                  3.0e-36
Match length
                  107
                  71
% identity
NCBI Description (Y10922) HD-Zip protein [Arabidopsis thaliana]
Seq. No.
                  234548
Seq. ID
                  LIB3272-037-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g2369714
BLAST score
                  248
E value
                  2.0e-21
                  98
Match length
% identity
                  60
NCBI Description (297178) elongation factor 2 [Beta vulgaris]
                  234549
Seq. No.
Seq. ID
                  LIB3272-037-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g3860247
BLAST score
                  522
E value
                  3.0e-53
Match length
                  107
% identity
                  87
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                  234550
Seq. ID
                  LIB3272-037-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q4510363
BLAST score
                  501
E value
                  8.0e-51
Match length
                  109
% identity
                  87
NCBI Description
                  (AC007017) putative DNA-binding protein [Arabidopsis
```

Seq. No. 234551

thaliana]

Seq. ID



```
LIB3272-037-P1-K1-C9
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3249084
 BLAST score
                   266
 E value
                   2.0e-23
 Match length
                   103
 % identity
                   18
 NCBI Description (AC004473) Similar to red-1 (related to thioredoxin) gene
                    gb X92750 from Mus musculus. ESTs gb AA712687 and
                   gb Z37223 come from this gene [Arabidopsis thaliana]
 Seq. No.
                   234552
 Seq. ID
                   LIB3272-037-P1-K1-D11
 Method
                   BLASTX
 NCBI GI
                   g629670
 BLAST score
                   288
 E value
                   7.0e-26
 Match length
                   95
 % identity
                    61
 NCBI Description hypothetical protein - tomato
                   234553
 Seq. No.
 Seq. ID
                   LIB3272-037-P1-K1-D2
 Method
                   BLASTX
 NCBI GI
                   g231504
 BLAST score
                   668
 E value
                   2.0e-70
 Match length
                   137
 % identity
                    96
 NCBI Description ACTIN 100 >gi_100420_pir__S20092 actin - potato (fragment)
                   >gi 1345579 emb CAA39276 (X55746) actin [Solanum
                   tuberosum]
                   234554
 Seq. No.
 Seq. ID
                   LIB3272-037-P1-K1-D6
 Method
                   BLASTX
 NCBI GI
                   g3281853
 BLAST score
                   162
 E value
                   4.0e-11
 Match length
                   33
 % identity
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
 Seq. No.
                   234555
 Seq. ID
                   LIB3272-037-P1-K1-D7
 Method
                   BLASTX
NCBI GI
                   q3023847
 BLAST score
                   329
 E value
                   7.0e-31
 Match length
                   83
 % identity
                   80
 NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta
                   subunit-like [Medicago sativa]
```

33907

234556

LIB3272-037-P1-K1-D9



```
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   493
E value
                   6.0e-50
Match length
                   113
                   82
% identity
NCBI Description
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
                   234557
Seq. No.
Seq. ID
                   LIB3272-037-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g2078350
BLAST score
                   604
E value
                   6.0e-63
                   138
Match length
% identity
                   86
NCBI Description (U95923) transaldolase [Solanum tuberosum]
                   234558
Seq. No.
Seq. ID
                   LIB3272-037-P1-K1-E11
                   BLASTX
Method
NCBI GI
                   g3158376
BLAST score
                   473
E value
                   1.0e-47
Match length
                   125
                   76
% identity
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                   234559
Seq. ID
                   LIB3272-037-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g4104457
BLAST score
                   430
E value
                   1.0e-42
Match length
                   106
                   71
% identity
NCBI Description (AF036172) 2-oxoglutarate/malate translocator [Zea mays]
Seq. No.
                   234560
Seq. ID
                   LIB3272-037-P1-K1-E3
Method
                   BLASTX
                   g1914685
NCBI GI
BLAST score
                   347
E value
                   6.0e-33
Match length
                   93
% identity
                   73
NCBI Description (Y12014) RAD23 protein, isoform II [Daucus carota]
Seq. No.
                   234561
```

Seq. ID LIB3272-037-P1-K1-E4

Method BLASTX
NCBI GI g4128133
BLAST score 218
E value 1.0e-17



Match length 91 % identity 49

NCBI Description (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No. 234562

Seq. ID LIB3272-037-P1-K1-E6

Method BLASTX
NCBI GI g629483
BLAST score 315
E value 5.0e-29
Match length 122
% identity 53

NCBI Description gene 1-Sc3 protein - European white birch

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula] >gi\_1584322\_prf\_\_2122374C allergen Bet v 1-Sc3 [Betula

pendula]

Seq. No. 234563

Seq. ID LIB3272-037-P1-K1-E8

Method BLASTX
NCBI GI g417060
BLAST score 521
E value 3.0e-53
Match length 102
% identity 93

NCBI Description GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA

LIGASE) (GS) >gi\_170637 (M94765) glutamine synthetase [Vigna aconitifolia] >gi\_1094850\_prf\_\_2106409A Gln

synthetase [Vigna aconitifolia]

Seq. No. 234564

Seq. ID LIB3272-037-P1-K1-E9

Method BLASTX
NCBI GI g3264767
BLAST score 310
E value 1.0e-28
Match length 118
% identity 53

NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No. 234565

Seq. ID LIB3272-037-P1-K1-F10

Method BLASTX
NCBI GI g1076511
BLAST score 594
E value 9.0e-62
Match length 138
% identity 79

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - kidney bean

>gi 758250 emb CAA59799 (X85804) H(+)-transporting ATPase

[Phaseolus vulgaris]

Seq. No. 234566

Seq. ID LIB3272-037-P1-K1-F11

Method BLASTX
NCBI GI g1173218
BLAST score 531



```
2.0e-54
E value
Match length
                  112
% identity
                  94
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                  234567
Seq. ID
                  LIB3272-037-P1-K1-F12
Method
                  BLASTX
                  g2497702
NCBI GI
BLAST score
                  191
E value
                  2.0e-14
Match length
                  129
% identity
                  36
NCBI Description
                  OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR
                  >gi_2121019_pir__I40710 outer membrane lipoprotein -
                  Citrobacter freundii >gi 717136 (U21727) lipocalin
                  precursor [Citrobacter freundii]
                  234568
Seq. No.
Seq. ID
                  LIB3272-037-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g3759184
BLAST score
                  268
E value
                  1.0e-23
Match length
                  95
                  59
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                  234569
Seq. ID
                  LIB3272-037-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                  616
E value
                  3.0e-64
Match length
                  118
                  100
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  234570
Seq. ID
                  LIB3272-037-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q3901014
BLAST score
                  235
E value
                  1.0e-19
Match length
                  55
                  76
% identity
NCBI Description
                  (AJ130886) metallothionein-like protein class II [Fagus
                  sylvatica]
```

Seq. ID LIB3272-037-P1-K1-F6

Method BLASTX NCBI GI q2792297 BLAST score 261 E value 1.0e-22

Match length 77 % identity 58

NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No.

234572

Seq. ID Method LIB3272-037-P1-K1-F7

Method BLASTX
NCBI GI g3831471
BLAST score 338
E value 9.0e-32
Match length 96
% identity 61

NCBI Description (AC005700) hypothetical protein [Arabidopsis thaliana]

Seq. No.

234573

Seq. ID LIB3272-037-P1-K1-F9

Method BLASTX
NCBI GI g629483
BLAST score 291
E value 3.0e-26
Match length 111
% identity 54

NCBI Description gene 1-Sc3 protein - European white birch

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula]
>gi\_1584322\_prf\_\_2122374C allergen Bet v 1-Sc3 [Betula

pendula]

Seq. No.

234574

Seq. ID LIB3272-037-P1-K1-G10

Method BLASTX
NCBI GI g1856971
BLAST score 423
E value 1.0e-41
Match length 93
% identity 86

NCBI Description (D26058) This gene is specifically expressed at the S phase

during the cell cycle in the synchronous culture of

periwinkle cells. [Catharanthus roseus]

Seq. No. 234575

Seq. ID LIB3272-037-P1-K1-G11

Method BLASTX
NCBI GI g1086757
BLAST score 331
E value 6.0e-31
Match length 139
% identity 50

NCBI Description (U41037) coded for by C. elegans cDNA yk41a1.3; coded for

by C. elegans cDNA yk128e3.3; coded for by C. elegans cDNA yk37c8.3; coded for by C. elegans cDNA CEESB01F; coded for by C. elegans cDNA CEESG45F; coded for by C. elegans cDNA

CEESG45

Seq. No. 234576

Seq. ID LIB3272-037-P1-K1-G12

Method BLASTX NCBI GI g1170747



```
BLAST score
                  329
E value
                  1.0e-30
                  79
Match length
                  82
% identity
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                  (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi 167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  234577
Seq. ID
                  LIB3272-037-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g559684
BLAST score
                  596
E value
                  5.0e-62
Match length
                  131
% identity
                  89
NCBI Description (L36097) aquaporin [Mesembryanthemum crystallinum]
Seq. No.
                  234578
Seq. ID
                  LIB3272-037-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g3158474
BLAST score
                  456
E value
                  1.0e-45
Match length
                  111
% identity
                  81
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
                  234579
Seq. No.
                  LIB3272-037-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3395436
BLAST score
                  241
E value
                  2.0e-20
Match length
                  97
% identity
                  46
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                  234580
Seq. ID
                  LIB3272-037-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q2129770
BLAST score
                  246
E value
                  6.0e-21
                  70
Match length
% identity
NCBI Description
                  xyloglucan endotransglycosylase-related protein XTR-2 -
                  Arabidopsis thaliana >gi 1244756 (U43487) xyloglucan
                  endotransglycosylase-related protein [Arabidopsis thaliana]
                  >gi 2154611 dbj BAA20290 (D63510) endoxyloglucan
                  transferase related protein [Arabidopsis thaliana]
```

Seq. ID LIB3272-037-P1-K1-G8

Method BLASTX NCBI GI q2500047



BLAST score 464 E value 2.0e-46 Match length 102 % identity 82

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi\_534916\_emb\_CAA85362\_ (Z36894) soluble inorganic pyrophosphatase [Solanum

tuberosum]

Seq. No. 234582

Seq. ID LIB3272-037-P1-K1-G9

Method BLASTX
NCBI GI g3341679
BLAST score 308
E value 3.0e-28
Match length 91

% identity 67

NCBI Description (AC003672) dynamin-like protein phragmoplastin 12

[Arabidopsis thaliana]

Seq. No. 234583

Seq. ID LIB3272-037-P1-K1-H10

Method BLASTX
NCBI GI g1170747
BLAST score 352
E value 2.0e-33
Match length 83
% identity 83

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345

(M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi\_167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 234584

Seq. ID LIB3272-037-P1-K1-H3

Method BLASTX
NCBI GI g549063
BLAST score 498
E value 2.0e-50
Match length 116
% identity 81

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 234585

Seq. ID LIB3272-037-P1-K1-H5

Method BLASTX
NCBI GI g2894599
BLAST score 563
E value 4.0e-58
Match length 122
% identity 81

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 234586

Seq. ID

Method

NCBI GI



```
LIB3272-037-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4467153
BLAST score
                   287
E value
                   8.0e-26
Match length
                   67
                   76
% identity
NCBI Description
                  (AL035540) putative thaumatin-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   234587
Seq. ID
                   LIB3272-038-P1-K1-A11
Method
                  BLASTX
NCBI GI
                   g167367
BLAST score
                   468
E value
                   5.0e-47
Match length
                  120
                   76
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   234588
Seq. ID
                  LIB3272-038-P1-K1-A12
Method
                  BLASTX
NCBI GI
                   g3024020
BLAST score
                   576
E value
                   1.0e-59
Match length
                   122
% identity
                   89
NCBI Description
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
                   >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation
                  factor 5A3 [Solanum tuberosum]
Seq. No.
                  234589
Seq. ID
                  LIB3272-038-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1420887
BLAST score
                  140
E value
                   9.0e-09
                  69
Match length
% identity
                   41
NCBI Description
                  (U34334) non-specific lipid transfer-like protein
                   [Phaseolus vulgaris]
                  234590
Seq. No.
Seq. ID
                  LIB3272-038-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g1657948
BLAST score
                  287
E value
                  9.0e-26
Match length
                  112
% identity
                  54
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
                  234591
Seq. No.
```

LIB3272-038-P1-K1-A6

BLASTX

g417103



BLAST score E value 4.0e-49Match length 107 % identity 98

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460) histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2 [Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulantum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350\_dbj BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 234592

Seq. ID LIB3272-038-P1-K1-A8

Method BLASTX NCBI GI g1173209 BLAST score 227 E value 2.0e-19 Match length 48 92 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal

protein S16 protein - upland cotton

>gi\_439654\_emb\_CAA53567\_ (X75954) RS16 protein, 40S subunit

[Gossypium hirsutum]

Seq. No. 234593

Seq. ID LIB3272-038-P1-K1-B11

Method BLASTX NCBI GI g1709498 BLAST score 495 E value 4.0e-50 Match length 107 % identity 83

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

>gi 1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis

thaliana  $>gi_887390$ \_emb\_CAA61411\_ (X89008) osmotin

[Arabidopsis thaliana]

Seq. No. 234594

Seq. ID LIB3272-038-P1-K1-B5

Method BLASTX NCBI GI q4406768 BLAST score 240 E value 3.0e-20 Match length 103



```
% identity
NCBI Description
                  (AC006836) putative flavonol sulfotransferase [Arabidopsis
                  thaliana]
Seq. No.
                  234595
Seq. ID
                  LIB3272-038-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q1370186
BLAST score
                  665
E value
                  4.0e-70
Match length
                  129
                  97
% identity
NCBI Description (Z73942) RAB7C [Lotus japonicus]
                  234596
Seq. No.
Seq. ID
                  LIB3272-038-P1-K1-B9
Method
                  BLASTX
                  q2507421
NCBI GI
BLAST score
                  303
E value
                  1.0e-27
Match length
                  67
% identity
                  85
NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >qi 1800277
                  (U81042) translation initiation factor [Arabidopsis
                  thaliana] >gi 4490709 emb CAB38843.1 (AL035680)
                  translation initiation factor [Arabidopsis thaliana]
                  234597
Seq. No.
                  LIB3272-038-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g543905
BLAST score
                  460
E value
                  5.0e-46
Match length
                  110
% identity
                  81
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
                  brassinosteroid-regulated protein [Glycine max]
Seq. No.
                  234598
Seq. ID
                  LIB3272-038-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g3393062
BLAST score
                  368
E value
                  3.0e-35
Match length
                  133
% identity
                  53
NCBI Description (Y17386) putative In2.1 protein [Triticum aestivum]
Seq. No.
                  234599
Seq. ID
                  LIB3272-038-P1-K1-C2
Method
                  BLASTX
```

NCBI GI q3063396 BLAST score 486 E value 3.0e-49 Match length 104 % identity 88

NCBI Description (AB012947) vcCyP [Vicia faba]

33916

```
Seq. No.
                  234600
Seq. ID
                  LIB3272-038-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g3033400
BLAST score
                  522
E value
                  3.0e-53
Match length
                  123
% identity
NCBI Description (AC004238) putative Ser/Thr protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  234601
Seq. ID
                  LIB3272-038-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3510256
BLAST score
                  187
E value
                  5.0e-14
                  101
Match length
% identity
                  44
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.
                  234602
Seq. ID
                  LIB3272-038-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q1709498
BLAST score
                  341
E value
                  3.0e-32
Match length
                  84
                  75
% identity
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                  >gi_1362001 pir S57524 osmotin precursor - Arabidopsis
                  thaliana >gi_887390 emb CAA61411 (X89008) osmotin
                  [Arabidopsis thaliana]
Seq. No.
                  234603
                LIB3272-038-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3337366
BLAST score
                  368
E value
                  3.0e-35
Match length
                  135
% identity
NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]
Seq. No.
                  234604
Seq. ID
                  LIB3272-038-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2500399
```

Method BLASTX
NCBI GI g2500399
BLAST score 475
E value 8.0e-48
Match length 109
% identity 90

NCBI Description 40S RIBOSOMAL PROTEIN S3 >gi\_1836060\_bbs\_179561 (S83098)

ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls,

embryos, Peptide, 253 aa] [Ambystoma mexicanum]



```
Seq. No.
                   234605
Seq. ID
                  LIB3272-038-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g3986750
BLAST score
                  748
                  8.0e-80
E value
Match length
                  138
% identity
                  99
NCBI Description
                  (AF107464) serine/threonine protein phosphatase type 2A
                   [Hevea brasiliensis]
                  234606
Seq. No.
Seq. ID
                  LIB3272-038-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g2827888
BLAST score
                  291
E value
                  3.0e-26
Match length
                  108
% identity
                  59
                  (AF016621) ATP-dependent Clp protease proteolytic subunit
NCBI Description
                  [Arabidopsis thaliana]
                  234607
Seq. No.
Seq. ID
                  LIB3272-038-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q3337366
BLAST score
                  154
E value
                  9.0e-11
Match length
                  55
% identity
                  31
NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]
Seq. No.
                  234608
Seq. ID
                  LIB3272-038-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g4220534
BLAST score
                  342
E value
                  4.0e-33
Match length
                  115
% identity
                  62
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  234609
Seq. ID
                  LIB3272-038-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g4539327
BLAST score
                  606
E value
                  4.0e-63
Match length
                  138
% identity
NCBI Description (AL035679) putative proton pump [Arabidopsis thaliana]
```

Seq. ID LIB3272-038-P1-K1-E12

Method BLASTX NCBI GI g119350 BLAST score 560



E value 9.0e-58 Match length 121 90

NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)

(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi\_81608\_pir\_\_JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi\_16271\_emb\_CAA41114\_ (X58107) enolase

[Arabidopsis thaliana]

Seq. No. 234611

Seq. ID LIB3272-038-P1-K1-E2

Method BLASTX
NCBI GI g125606
BLAST score 457
E value 9.0e-46
Match length 99
% identity 88

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463 pir S12248

pyruvate kinase (EC 2.7.1.40) - potato

>gi\_22576\_emb\_CAA37727\_ (X53688) pyruvate kinase [Solanum

tuberosum]

Seq. No. 234612

Seq. ID LIB3272-038-P1-K1-E4

Method BLASTX
NCBI GI g2388575
BLAST score 211
E value 8.0e-17
Match length 116
% identity 39

NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3272-038-P1-K1-E5

234613

Method BLASTX
NCBI GI g136636
BLAST score 560
E value 9.0e-58
Match length 106
% identity 96

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi\_1076424\_pir\_\_S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi\_442594\_pdb\_1AAK\_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi\_2981894\_pdb\_2AAK\_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi\_431260 -(L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]

Seq. No. 234614

Seq. ID LIB3272-038-P1-K1-E9

Method BLASTX
NCBI GI g117988
BLAST score 265
E value 3.0e-23
Match length 74



```
% identity
NCBI Description
                   CYTOCHROME C >gi_65503_pir__CCCN cytochrome c - sea-island
                   cotton
Seq. No.
                   234615
Seq. ID
                   LIB3272-038-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g3094012
BLAST score
                   367
E value
                   4.0e-35
Match length
                   75
% identity
                   87
NCBI Description (AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
Seq. No.
                   234616
Seq. ID
                   LIB3272-038-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g481236
BLAST score
                   169
E value
                   5.0e-12
Match length
                   50
% identity
                   74
NCBI Description
                  hypothetical protein - Madagascar periwinkle
                   >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide
                   [Catharanthus roseus]
Seq. No.
                   234617
Seq. ID
                  LIB3272-038-P1-K1-F12
Method
                  BLASTX
NCBI GI
                   g2213595
BLAST score
                   143
E value
                   1.0e-18
Match length
                  133
% identity
                   44
NCBI Description
                  (AC000348) T7N9.15 [Arabidopsis thaliana]
Seq. No.
                  234618
Seq. ID
                  LIB3272-038-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g3493172
BLAST score
                  515
E value
                  1.0e-52
Match length
                  111
% identity
                  91
NCBI Description
                  (U89609) fiber annexin [Gossypium hirsutum]
Seq. No.
                  234619
Seq. ID
                  LIB3272-038-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g1220196
```

BLAST score 584 E value 1.0e-60 Match length 127 % identity 87

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No. 234620

33920



```
Seq. ID
                   LIB3272-038-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g4406780
BLAST score
                   414
E value
                   1.0e-40
Match length
                   103
% identity
                   75
NCBI Description
                  (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
                   234621
Seq. No.
Seq. ID
                   LIB3272-038-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g2827552
BLAST score
                   459
E value
                   6.0e-46
Match length
                   128
% identity
                   51
NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]
Seq. No.
                   234622
Seq. ID
                   LIB3272-038-P1-K1-G11
Method
                   BLASTX
NCBI GI
                  _g119350
BLAST score
                   387
E value
                   1.0e-37
Match length
                   86
% identity
                   90
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                   thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                   [Arabidopsis thaliana]
Seq. No.
                   234623
Seq. ID
                   LIB3272-038-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g1922278
BLAST score
                   227
E value
                   3.0e-19
Match length
                   48
% identity
NCBI Description (Z86091) TCTP protein [Fragaria x ananassa]
Seq. No.
                   234624
Seq. ID
                   LIB3272-038-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g924951
BLAST score
                   156
E value
                   2.0e-10
Match length
                   47
% identity
NCBI Description
                  (U30324) class I chitinase [Theobroma cacao]
```

Seq. ID LIB3272-038-P1-K1-G3

Method BLASTX



```
NCBI GI
                   q2911859
BLAST score
                   223
E value
                   9.0e-19
Match length
                   56
% identity
                   71
                   (AF047659) contains similarity to N-terminal
NCBI Description
                   acetyltransferase complex subunit Ard1p [Caenorhabditis
                   elegans]
Seq. No.
                   234626
Seq. ID
                   LIB3272-038-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   q1710587
BLAST score
                   436
E value
                   2.0e-44
Match length
                   125
% identity
                   76
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO >gi_1196897 (L46848) acidic
                   ribosomal protein PO [Glycine max]
Seq. No.
                   234627
Seq. ID
                   LIB3272-038-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g1709498
BLAST score
                   589
E value
                   3.0e-61
Match length
                   127
% identity
                   81
                   OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
NCBI Description
                   >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
                   234628
Seq. No.
Seq. ID
                   LIB3272-038-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g1699370
BLAST score
                   284
E value
                   2.0e-25
Match length
                   114
% identity
                   51
NCBI Description (S82620) prolidase=peptidase D/imidopeptidase {EC 3.4.13.9}
                   [mice, liver, Peptide, 493 aa] [Mus sp.]
Seq. No.
                   234629
Seq. ID
                   LIB3272-038-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q3885334
BLAST score
                   162
E value
                   1.0e-11
Match length
                   32
% identity
NCBI Description (AC005623) putative argonaute protein [Arabidopsis
                   thaliana]
```

Seq. ID LIB3272-038-P1-K1-H9



Method BLASTX NCBI GI g2982452 BLAST score 218 E value 1.0e-17 Match length 138 % identity 46

NCBI Description (AL022223) receptor protein kinase-like protein

[Arabidopsis thaliana]

Seq. No. 234631

Seq. ID LIB3272-039-P1-K1-A10

BLASTX Method NCBI GI q2498490 BLAST score 251 E value 1.0e-21 86 Match length 56 % identity

NCBI Description VIRAL INTEGRATION SITE PROTEIN INT-6 >gi 1854579 (L35556)

Int-6 [Mus musculus] >gi\_2114363 (U62962) similar to mouse
Int-6 [Homo sapiens] >gi\_2351382 (U54562) eIF3-p48 [Homo

sapiens] >gi\_2688818 (U85947) Int-6 [Homo sapiens]
>gi\_2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens] >gi 4503521\_ref\_NP\_001559.1\_pEIF3S6\_ murine

mammary tumor integration site 6 (oncogene homolog)

Seq. No. 234632

Seq. ID LIB3272-039-P1-K1-A11

Method BLASTX NCBI GI g2499946 BLAST score 303 E value 7.0e-28 Match length 101 % identity 57

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE

DECARBOXYLASE >gi 747980 (U22260) UMP synthase [Nicotiana

tabacum]

Seq. No. 234633

Seq. ID LIB3272-039-P1-K1-A12

Method BLASTX NCBI GI g3600058 BLAST score 278 E value 4.0e-25 Match length 60 % identity 95

NCBI Description (AF080120) similar to vacuolar ATPases [Arabidopsis

thaliana]

Seq. No. 234634

LIB3272-039-P1-K1-A2 Seq. ID

Method BLASTX NCBI GI q168324 BLAST score 285 E value 1.0e-25 Match length 99 % identity 69



(M92094) aspartate aminotransferase P1 [Lupinus NCBI Description angustifolius]

234635 Seq. No.

Seq. ID LIB3272-039-P1-K1-A7

Method BLASTX NCBI GI q3068713 BLAST score 137 E value 9.0e-09 Match length 36 % identity

NCBI Description (AF049236) unknown [Arabidopsis thaliana]

Seq. No. 234636

Seq. ID LIB3272-039-P1-K1-B11

Method BLASTX NCBI GI g1709498 BLAST score 496 E value 2.0e-50 Match length 122 % identity 75

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

>gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis thaliana >gi\_887390\_emb\_CAA61411\_ (X89008) osmotin

[Arabidopsis thaliana]

Seq. No. 234637

LIB3272-039-P1-K1-B12 Seq. ID

Method BLASTX NCBI GI g1086252 BLAST score 421 1.0e-41 E value Match length 114 % identity 68

NCBI Description sucrose cleavage protein - Potato >gi\_707001\_bbs\_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]

[Solanum tuberosum]

Seq. No. 234638

Seq. ID LIB3272-039-P1-K1-B3

BLASTX Method NCBI GI g2129772 BLAST score 326 E value 2.0e-30 96 Match length 68 % identity

NCBI Description xyloglucan endotransglycosylase-related protein XTR-7 -

Arabidopsis thaliana >gi 1244760 (U43489) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

234639 Seq. No.

Seq. ID LIB3272-039-P1-K1-B4

Method BLASTX NCBI GI g1947137 BLAST score 342 E value 3.0e-32



```
Match length
                     123
                     50
% identity
NCBI Description
                    (AF000264) similar to the ATP-binding transport protein
                     family (ABC transporters). [Caenorhabditis elegans]
Seq. No.
                     234640
Seq. ID
                     LIB3272-039-P1-K1-B5
Method
                     BLASTX
NCBI GI
                     g1351411
BLAST score
                     382
E value
                     6.0e - 37
Match length
                     98
                     72
% identity
NCBI Description
                     VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) (PROTEINASE B)
                     >gi_1076553_pir__S49175 cysteine proteinase precursor -
spring vetch >gi_2129906_pir__S68984 cysteine proteinase
precursor - spring vetch >gi_510358_emb_CAA84383_ (Z34899)
                     cysteine proteinase [Vicia sativa]
Seq. No.
                     234641
Seq. ID
                     LIB3272-039-P1-K1-B6
Method
                     BLASTX
NCBI GI
                     g2791834
BLAST score
                     399
E value
                     1.0e-51
Match length
                     109
% identity
                     95
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.
                     234642
                     LIB3272-039-P1-K1-B9
Seq. ID
Method
                     BLASTX
NCBI GI
                     g1370194
BLAST score
                     447
                     8.0e-45
E value
Match length
                     92
                     97
% identity
NCBL Description (Z73946) RAB8C [Lotus japonicus]
Seq. No.
                     234643
Seq. ID
                     LIB3272-039-P1-K1-C1
Method
                     BLASTX
NCBI GI
                     g3980393
BLAST score
                     369
E value
                     2.0e-35
Match length
                     102
% identity
NCBI Description
                    (AC004561) putative glutathione S-transferase [Arabidopsis
                     thaliana]
Seq. No.
                     234644
```

Seq. ID LIB3272-039-P1-K1-C12

Method BLASTX NCBI GI g2984709 BLAST score 416 E value 6.0e-41Match length 83

% identity

57



```
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                   234645
Seq. ID
                   LIB3272-039-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g117188
BLAST score
                   261
E value
                   6.0e-23
Match length
                   99
                   47
% identity
NCBI Description CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2)
                   >gi 81423 pir A35867 cytochrome P450 71A1 - avocado
Seq. No.
                   234646
Seq. ID
                   LIB3272-039-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g167367
BLAST score
                   571
E value
                   3.0e-59
Match length
                   106
% identity
                   98
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   234647
Seq. ID
                   LIB3272-039-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g2262159
BLAST score
                   399
E value
                   4.0e-39
Match length
                   93
                   78
% identity
NCBI Description (AC002329) predicted protein similar to S.pombe protein
                   C5H10.03 [Arabidopsis thaliana]
Seq. No.
                   234648
Seq. ID
                   LIB3272-039-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g2129944
BLAST score
                   333
E value
                   9.0e-32
Match length
                   72
% identity
                   85
NCBI Description
                  RNA-binding protein RZ-1 - wood tobacco
                   >gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1
[Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_ (D28861)
                   RNA binding protein, RZ-1 [Nicotiana sylvestris]
Seq. No.
                   234649
Seq. ID
                   LIB3272-039-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g2738949
BLAST score
                   291
E value
                   2.0e-26
Match length
                   104
```

33926

NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x

NCBI Description

thaliana]



## ananassa]

```
Seq. No.
                   234650
Seq. ID
                   LIB3272-039-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g4206789
BLAST score
                   251
E value
                   1.0e-21
Match length
                   66
% identity
                   71
NCBI Description
                   (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis
                   thaliana]
Seq. No.
                   234651
Seq. ID
                   LIB3272-039-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g4105772
BLAST score
                   425
E value
                   5.0e-42
Match length
                   111
% identity
                   43
NCBI Description (AF049917) PGP9B [Petunia x hybrida]
Seq. No.
                   234652
Seq. ID
                   LIB3272-039-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g133249
BLAST score
                   160
E value
                   5.0e-11
Match length
                   47
                   38
% identity
                  CHLOROPLAST 33 KD RIBONUCLEOPROTEIN PRECURSOR
NCBI Description
                   >gi_100390_pir__S12111 ribonucleoprotein, 33K, precursor -
                   common tobacco >gi 20005 emb CAA37879 (X53932) 33 kDa ribonucleoprotein precursor [Nicotiana tabacum]
Seq. No.
                   234653
Seq. ID
                   LIB3272-039-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g3367578
BLAST score
                   298
E value
                   3.0e-27
Match length
                   84
% identity
                   68
NCBI Description
                   (AL031135) protein kinase - like protein [Arabidopsis
                   thaliana]
Seq. No.
                   234654
Seq. ID
                   LIB3272-039-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q3297827
BLAST score
                   253
E value
                   8.0e-22
Match length
                   85
% identity
```

33927

(AL031032) putative protein (fragment) [Arabidopsis

E value

Match length

NCBI Description

% identity

5.0e-21

115



```
Seq. No.
                   234655
Seq. ID
                  LIB3272-039-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q3549691
BLAST score
                  163
E value
                   3.0e-11
Match length
                  33
% identity
                  85
NCBI Description (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
Seq. No.
                  234656
Seq. ID
                  LIB3272-039-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q120669
BLAST score
                  420
E value
                  1.0e-41
Match length
                  85
% identity
                  91
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                  234657
Seq. ID
                  LIB3272-039-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g1709498
BLAST score
                  400
E value
                  4.0e-39
Match length
                  99
                  74
% identity
NCBI Description
                  OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                  >gi_1362001 pir S57524 osmotin precursor - Arabidopsis
                  thaliana >gi 887390 emb CAA61411 (X89008) osmotin
                  [Arabidopsis thaliana]
Seq. No.
                  234658
Seq. ID
                  LIB3272-039-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g3158376
BLAST score
                  393
E value
                  3.0e-38
Match length
                  109
% identity
                  73
NCBI Description (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                  234659
Seq. ID
                  LIB3272-039-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g2160166
BLAST score
                  246
```

33928

(AC000132) No definition line found [Arabidopsis thaliana]

Seq. ID

234665

LIB3272-039-P1-K1-E7



```
Seq. No.
                   234660
Seq. ID
                  LIB3272-039-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4098128
BLAST score
                   467
E value
                   5.0e-47
Match length
                  102
% identity
                  89
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
Seq. No.
                   234661
Seq. ID
                  LIB3272-039-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g481236
BLAST score
                  299
E value
                   4.0e-27
Match length
                  72
% identity
                  82
                  hypothetical protein - Madagascar periwinkle
NCBI Description
                  >gi_407410_emb_CAA81526 (Z26880) 14 kDa polypeptide
                   [Catharanthus roseus]
Seq. No.
                  234662
Seq. ID
                  LIB3272-039-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g115492
BLAST score
                  558
E value
                  1.0e-57
Match length
                  110
% identity
                  54
NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                  calmodulin-related protein [Petunia hybrida]
Seq. No.
                  234663
Seq. ID
                  LIB3272-039-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q4572679
BLAST score
                  182
E value
                  8.0e-14
Match length
                  45
% identity
                  73
NCBI Description
                  (AC006954) RSZp22 splicing factor; contains RNA recognition
                  motif [Arabidopsis thaliana]
Seq. No.
                  234664
Seq. ID
                  LIB3272-039-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g508304
BLAST score
                  208
E value
                  1.0e-16
Match length
                  50
% identity
NCBI Description
                 (L22305) corC [Medicago sativa]
```

33929



Method BLASTX
NCBI GI g542157
BLAST score 462
E value 2.0e-46
Match length 100
% identity 86
NCBI Description ribosome

NCBI Description ribosomal 5S RNA-binding protein - Rice

Seq. No. 234666

Seq. ID LIB3272-039-P1-K1-E9

Method BLASTX
NCBI GI g4191778
BLAST score 273
E value 3.0e-24
Match length 76
% identity 74

NCBI Description (AC005917) putative nucleosome assembly protein I

[Arabidopsis thaliana]

Seq. No. 234667

Seq. ID LIB3272-039-P1-K1-F1

Method BLASTX
NCBI GI g1173187
BLAST score 393
E value 2.0e-38
Match length 79
% identity 94

NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi\_1362041\_pir\_\_S56673

ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi 643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

Seq. No. 234668

Seq. ID LIB3272-039-P1-K1-F10

Method BLASTX
NCBI GI g3176687
BLAST score 495
E value 4.0e-50
Match length 134
% identity 67

NCBI Description (AC003671) Strong similarity to trehalose-6-phosphate

synthase homolog from A. thaliana chromosome 4 contig gb\_Z97344. ESTs gb\_H37594, gb\_R65023, gb\_H37578 and gb\_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No. 234669

Seq. ID LIB3272-039-P1-K1-F11

Method BLASTX
NCBI GI g2662343
BLAST score 614
E value 4.0e-64
Match length 120
% identity 97

NCBI Description (D63581) EF-1 alpha [Oryza sativa]

Seq. No. 234670

Seq. ID LIB3272-039-P1-K1-F12



```
Method
                  BLASTX
NCBI GI
                  q730463
BLAST score
                  322
E value
                  7.0e-30
Match length
                  105
% identity
                  59
                  60S RIBOSOMAL PROTEIN L37B (YL37) (RP47)
NCBI Description
                  >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast
                  (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal
                  protein L37 [Saccharomyces cerevisiae]
                  >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c
                  [Saccharomyces cerevisiae]
                - 234671
Seq. No.
Seq. ID
                  LIB3272-039-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q548852
BLAST score
                  301
E value
                  1.0e-27
Match length
                  71
                  80
% identity
                 40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal
NCBI Description
                  protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
Seq. No.
                  234672
Seq. ID
                  LIB3272-039-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g2979544
BLAST score
                  162
E value
                  2.0e-11
Match length
                  92
% identity
                  40
NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
Seq. No.
                  234673
Seq. ID
                  LIB3272-039-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q120669
BLAST score
                  445
E value
                  1.0e-44
Match length
                  93
% identity
                  88
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 66014 pir DEJMG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                  >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                  3-phosphate dehydrogenase [Magnolia liliiflora]
                  234674
Seq. No.
Seq. ID
                  LIB3272-039-P1-K1-G3
Method
                  BLASTX
```

Method BLASTX
NCBI GI g549063
BLAST score 316
E value 3.0e-29
Match length 81
% identity 74



NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626) 21kd polypeptide [Oryza sativa] 234675 Seq. No. Seq. ID LIB3272-039-P1-K1-G4

Method BLASTX NCBI GI g3123745 BLAST score 189 E value 2.0e-14 61 Match length % identity

NCBI Description (AB013447) aluminum-induced [Brassica napus]

234676 Seq. No.

Seq. ID LIB3272-039-P1-K1-G5

Method BLASTX NCBI GI g1352821 BLAST score 562 E value 5.0e-58 Match length 106 100 % identity

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_279581\_pir\_\_RKCNSU ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - upland cotton >gi 450505 emb CAA38026 (X54091) ribulose bisphosphate carboxylase [Gossypium hirsutum]

Seq. No. 234677

Seq. ID LIB3272-039-P1-K1-G6

Method BLASTX NCBI GI g3063396 BLAST score 533 E value 1.0e-54 Match length 118 85 % identity

NCBI Description (AB012947) vcCyP [Vicia faba]

234678 Seq. No.

Seq. ID LIB3272-039-P1-K1-G7

BLASTX Method NCBI GI g832876 BLAST score 457 1.0e-47 E value 118 Match length % identity 85

NCBI Description (L41345) ascorbate free radical reductase [Solanum

lycopersicum] >gi 1097368 prf 2113407A ascorbate free

radical reductase [Lycopersicon esculentum]

Seq. No. 234679

Seq. ID LIB3272-039-P1-K1-G8

Method BLASTX · · · g3033400 NCBI GI BLAST score 214 E value 3.0e-17



```
Match length
                  85
% identity
NCBI Description
                  (AC004238) putative Ser/Thr protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  234680
Seq. ID
                  LIB3272-039-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g3785983
BLAST score
                  140
E value
                  1.0e-08
```

Match length 52
% identity 46
NCRL Proprietion (ACCOSECO) have

NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No. 234681

Seq. ID LIB3272-039-P1-K1-H1

Method BLASTX
NCBI GI g1170747
BLAST score 296
E value 7.0e-27
Match length 72
% identity 82

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi\_167345

(M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi\_167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 234682

Seq. ID LIB3272-039-P1-K1-H10

Method BLASTX
NCBI GI g231574
BLAST score 356
E value 8.0e-34
Match length 143
% identity 55

NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)

>gi\_81837\_pir\_\_S22523 asparaginase (EC 3.5.1.1) - tree

lupine (fragment) >gi\_19137\_emb\_CAA36824 (X52588)

asparaginase [Lupinus arboreus]

Seq. No. 234683

Seq. ID LIB3272-039-P1-K1-H7

Method BLASTX
NCBI GI g1169382
BLAST score 549
E value 2.0e-56
Match length 128
% identity 78

NCBI Description DNAJ PROTEIN HOMOLOG 2 >gi 542196 pir S42031 LDJ2 protein

- leek >gi\_454303\_emb\_CAA5 $\overline{4}$ 720\_ ( $\overline{X}$ 776 $\overline{32}$ ) LDJ2 [Allium

porrum]

Seq. No. 234684

Seq. ID LIB3272-040-P1-K1-A10

Method BLASTX NCBI GI g3941289



```
BLAST score 285
E value 1.0e-25
Match length 113
% identity 50
```

NCBI Description (AF018093) similarity to SCAMP37 [Pisum sativum]

Seq. No. 234685

Seq. ID LIB3272-040-P1-K1-A3

Method BLASTX
NCBI GI g544424
BLAST score 387
E value 2.0e-37
Match length 87
% identity 82

NCBI Description GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi\_419755\_pir\_ S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana

>gi\_16301\_emb\_CAA78711\_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi\_166837 (L00648) RNA-binding

protein [Arabidopsis thaliana]

>gi\_4567224\_gb\_AAD23639.1\_AC007119\_5 (AC007119)

glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No. 234686

Seq. ID LIB3272-040-P1-K1-A6

Method BLASTX
NCBI GI g1246403
BLAST score 245
E value 7.0e-21
Match length 87
% identity 57

NCBI Description (X94698) TINY [Arabidopsis thaliana] >gi\_3406035 (AC005405)

TINY [Arabidopsis thaliana]

Seq. No. 234687

Seq. ID LIB3272-040-P1-K1-A8

Method BLASTX
NCBI GI g1703375
BLAST score 527
E value 6.0e-54
Match length 108
% identity 94

NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi\_965483 dbj BAA08259 (D45420)

DcARF1 [Daucus carota]

Seq. No. 234688

Seq. ID LIB3272-040-P1-K1-A9

Method BLASTX
NCBI GI g2499946
BLAST score 424
E value 7.0e-42
Match length 127
% identity 66

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE

DECARBOXYLASE >gi\_747980 (U22260) UMP synthase [Nicotiana

tabacum]



```
Seq. No.
                  234689
Seq. ID
                  LIB3272-040-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g4105772
BLAST score
                  502
E value
                  5.0e-51
Match length
                  110
% identity
                  46
NCBI Description (AF049917) PGP9B [Petunia x hybrida]
Seq. No.
                  234690
Seq. ID
                  LIB3272-040-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q1711492
BLAST score
                  222
E value
                  2.0e-18
Match length
                  71
% identity
                  62
NCBI Description ARGININE DECARBOXYLASE (ARGDC) (ADC) >gi 478412 pir JQ2341
                  arginine decarboxylase (EC 4.1.1.19) - tomato >gi 295350
                  (L16582) arginine decarboxylase [Lycopersicon esculentum]
Seq. No. Seq. ID
                  234691
                  LIB3272-040-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q730583
BLAST score
                  181
E value
                  2.0e-13
Match length
                  62
% identity
                  66
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P2 >gi 551267 emb CAA55047
                  (X78213) 60s acidic ribosomal protein P2 [Parthenium
                  argentatum]
Seq. No.
                  234692
Seq. ID
                  LIB3272-040-P1-K1-B7
                 BLASTX
Method
NCBI GI
                  q4204575
BLAST score
                  290
E value
                  4.0e-26
Match length
                  86
% identity
                  70
NCBI Description (AF098510) cytochrome b5 DIF-F [Petunia x hybrida]
Seq. No.
                  234693
Seq. ID
                  LIB3272-040-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3033391
BLAST score
                  192
E value
                  1.0e-14
Match length
                  76
% identity
                  49
NCBI Description
                  (AC004238) putative amino acid transporter [Arabidopsis
```

33935

thaliana]

LIB3272-040-P1-K1-C10

234694

Seq. No.

Seq. ID



70

% identity

NCBI Description

```
Method
                       BLASTX
    NCBI GI
                       g119350
    BLAST score
                       428
    E value
                       2.0e-42
Match length
                       101
                       85
    % identity
    NCBI Description
                       ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                       (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                       thaliana >gi 16271 emb CAA41114 (X58107) enolase
                       [Arabidopsis thaliana]
                       234695
    Seq. No.
    Seq. ID
                       LIB3272-040-P1-K1-C12
    Method
                       BLASTX
    NCBI GI
                       g2494275
    BLAST score
                       237
    E value
                       6.0e-20
    Match length
                       62
    % identity
                       66
    NCBI Description ELONGATION FACTOR P (EF-P) >gi 1399829 (U59235) elongation
                       factor P [Synechococcus PCC794\overline{2}]
    Seq. No.
                       234696
    Seq. ID
                       LIB3272-040-P1-K1-C2
    Method
                       BLASTX
    NCBI GI
                       q4220521
    BLAST score
                       354
    E value
                       1.0e-33
    Match length
                       81
    % identity
                       81
    NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
    Seq. No.
                       234697
    Seq. ID
                       LIB3272-040-P1-K1-C5
    Method
                       BLASTX
    NCBI GI
                       g2494144
    BLAST score
                       304
    E value
                       9.0e-28
    Match length
                       118
    % identity
                       11
    NCBI Description
                      (AC002329) predicted leucine-rich protein [Arabidopsis
                       thaliana]
    Seq. No.
                       234698
    Seq. ID
                       LIB3272-040-P1-K1-C7
    Method
                       BLASTX
    NCBI GI
                       g1709498
    BLAST score
                       417
    E value
                       4.0e-41
    Match length
                       113
```

>gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis
thaliana >gi\_887390 emb\_CAA61411 (X89008) osmotin

OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

[Arabidopsis thaliana]



```
Seq. No.
                   234699
                   LIB3272-040-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3540185
BLAST score
                   389
                   9.0e-38
E value
Match length
                   129
                   57
% identity
                   (AC004122) Highly Similar to branched-chain amino acid
NCBI Description
                   aminotransferase [Arabidopsis thaliana]
                   234700
Seq. No.
                   LIB3272-040-P1-K1-C9
Seq. ID
Method
                   BLASTX
                   g549063
NCBI GI
BLAST score
                   338
                   9.0e-32
E value
                   104
Match length
                   63
% identity
NCBI Description
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
                   234701
Seq. No.
Seq. ID
                   LIB3272-040-P1-K1-D1
                   BLASTX
Method
                   g4371280
NCBI GI
BLAST score
                   311
                   1.0e-28
E value
Match length
                   106
                    60
% identity
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   234702
                   LIB3272-040-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3738304
BLAST score
                   257
                    2.0e-22
E value
Match length
                   75
% identity
                    67
NCBI Description (AC005309) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    234703
Seq. ID
                   LIB3272-040-P1-K1-D4
Method
                   BLASTX
                   g3236476
NCBI GI
                   238
BLAST score
E value
                    4.0e-20
                   71
Match length
                    59
% identity
                   (AF071195) 26S protease regulatory subunit [Gossypium
NCBI Description
```

Seq. ID LIB3272-040-P1-K1-D8

hirsutum]



```
BLASTX
Method
NCBI GI
                   q1928981
                   525
BLAST score
E value
                   1.0e-53
Match length
                   117
% identity
                   91
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   234705
Seq. No.
                   LIB3272-040-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3860277
                   397
BLAST score
E value
                   5.0e-42
Match length
                   129
                   74
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                   thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
                   234706
Seq. No.
                   LIB3272-040-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4102723
BLAST score
                   567
                   1.0e-58
E value
Match length
                   120
                   70
% identity
                  (AF015784) TATA-box binding protein [Phaseolus vulgaris]
NCBI Description
                   234707
Seq. No.
Seq. ID
                   LIB3272-040-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g1173043
BLAST score
                   318
E value
                   2.0e-29
Match length
                   68
% identity
                   91
                   60S RIBOSOMAL PROTEIN L38 >gi 479441 pir S33899 ribosomal
NCBI Description
                   protein L38 - tomato (cv. Moneymaker)
                   >gi_313027_emb_CAA49599_ (X69979) ribosomal protein L38
                   [Lycopersicon esculentum]
Seq. No.
                   234708
Seq. ID
                   LIB3272-040-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q3063454
BLAST score
                   140
E value
                   1.0e-08
                   101
Match length
% identity
                   37
NCBI Description (AC003981) F22013.16 [Arabidopsis thaliana]
```

Seq. No. 234709

Seq. ID LIB3272-040-P1-K1-E4

Method BLASTX



```
NCBI GI
                  g3859597
BLAST score
                   252
E value
                   1.0e-21
Match length
                   117
% identity
NCBI Description
                  (AF104919) No definition line found [Arabidopsis thaliana]
Seq. No.
                  234710
Seq. ID
                  LIB3272-040-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q232029
BLAST score
                  367
                  3.0e - 35
E value
Match length
                  82
% identity
                  88
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi 100154 pir S21989 translation elongation factor eEF-1
                  alpha chain - carrot >gi 18339 emb CAA42843 (X60302)
                  elongation factor 1A [Daucus carota]
Seq. No.
                  234711
Seq. ID
                  LIB3272-040-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g2613143
BLAST score
                  266
E value
                  2.0e-41
Match length
                  125
% identity
                   71
NCBI Description
                  (AF030548) tubulin [Oryza sativa]
Seq. No.
                  234712
Seq. ID
                  LIB3272-040-P1-K1-F10
Method
                  BLASTX
                  q132944
                  502
                  5.0e-51
```

NCBI GI BLAST score E value Match length 102 % identity 91

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi\_81658\_pir\_\_JQ0772 ribosomal

protein L3 (ARP2) - Arabidopsis thaliana >qi 806279 (M32655) ribosomal protein [Arabidopsis thaliana]

Seq. No. 234713

Seq. ID LIB3272-040-P1-K1-F4

Method BLASTX NCBI GI g1173055 BLAST score 538 E value 3.0e-55 Match length 111 96 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L11 (L5) >gi 541961 pir S42497

> ribosomal protein L11.e - alfalfa >gi 1076504 pir S51819 RL5 ribosomal protein - alfalfa >gi 463252 emb CAA55090

(X78284) RL5 ribosomal protein [Medicago sativa]

Seq. No. 234714

Seq. ID LIB3272-040-P1-K1-F5

```
Method
                   BLASTX
NCBI GI
                   g4102723
BLAST score
                   579
E value
                   5.0e-60
Match length
                  120
                  57
% identity
NCBI Description (AF015784) TATA-box binding protein [Phaseolus vulgaris]
Seq. No.
                   234715
Seq. ID
                  LIB3272-040-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3334115
BLAST score
                  455
E value
                  2.0e-45
Match length
                  111
% identity
                  84
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                  hirsutum]
Seq. No.
                  234716
Seq. ID
                  LIB3272-040-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g3152591
BLAST score
                  140
E value
                  4.0e-09
Match length
                  66
% identity
                  41
NCBI Description
                  (AC002986) Similar to hypothetical protein gb_Z97336 from
                  A. thaliana. This gene is probably cut off. [Arabidopsis
                  thaliana]
Seq. No.
                  234717
Seq. ID
                  LIB3272-040-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2245064
BLAST score
                  218
E value
                  1.0e-17
                  76
Match length
                  59
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  234718
Seq. ID
                  LIB3272-040-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g729669
BLAST score
                  153
E value
                  3.0e-10
Match length
                  62
% identity
                  50
```

Seq. No. 234719

Seq. ID LIB3272-040-P1-K1-H1

Method BLASTX

pea >gi\_498896 (U10041) histone H2A homolog [Pisum sativum]

NCBI Description HISTONE H2A >gi\_2118992\_pir\_\_S60474 histone H2A - garden

```
NCBI GI
                  g1362086
BLAST score
                  515
E value
                  2.0e-52
                  106
Match length
                  92
% identity
                  5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi 2129919 pir S65957
                  5-methyltetrahydropteroyltriglutamate--homocysteine
                  S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  \geqgi_886471_emb_CAA58474_ (X83499) methionine synthase
                  [Catharanthus roseus]
                  234720
Seq. No.
Seq. ID
                  LIB3272-040-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1362008
BLAST score
                  165
E value
                  6.0e-12
Match length
                  49
                  14
% identity
NCBI Description ubiquitin-like protein 12 - Arabidopsis thaliana
Seq. No.
                  234721
Seq. ID
                  LIB3272-040-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2832783
BLAST score
                  233
E value
                  8.0e-20
                  67
Match length
% identity
                  67
NCBI Description (AJ225806) potassium channel beta subunit [Egeria densa]
Seq. No.
                  234722
                  LIB3272-041-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4557062
BLAST score
                  335
E value
                  2.0e-31
Match length
                  144
% identity
                  53
NCBI Description (AC007045) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  234723
Seq. ID
                  LIB3272-041-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3421109
BLAST score
                  584
E value
                  1.0e-60
Match length
                  122
                  90
```

% identity

NCBI Description (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis thaliana]

Seq. No. 234724

Seq. ID LIB3272-041-P1-K1-B10

Method BLASTX

```
300 50
```

```
NCBI GI
                    g1729860
BLAST score
                    185
E value
                    4.0e-14
Match length
                    93
% identity
                    47
NCBI Description
                    26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
                    PROTEIN HOMOLOG 1) (TBP-1) (MG(2+)-DEPENDENT ATPASE 1)
                    (LEMA-1) >gi_1362099_pir__S56672 probable 26S proteinase chain MA-1 - tomato >gi_732815_emb_CAA52445_ (X74426)
                    Mg-dependent ATPase 1 [Lycopersicon esculentum]
Seq. No.
                    234725
Seq. ID
                    LIB3272-041-P1-K1-B4
Method
                    BLASTX
NCBI GI
                    q1871185
BLAST score
                    229
E value
                    6.0e-19
Match length
                    99
% identity
                    47
NCBI Description (U90439) seven in absentia isolog [Arabidopsis thaliana]
Seq. No.
                    234726
Seq. ID
                    LIB3272-041-P1-K1-B6
Method
                    BLASTX
NCBI GI
                    g4538897
BLAST score
                    303
E value
                    9.0e-28
Match length
                    82
% identity
                    70
NCBI Description (ALO49482) AX110P-like protein [Arabidopsis thaliana]
Seq. No.
                    234727
Seq. ID
                    LIB3272-041-P1-K1-B9
Method
                    BLASTX
NCBI GI
                    g2827082
BLAST score
                    626
E value
                    2.0e-65
Match length
                    140
% identity
                    84
NCBI Description
                   (AF020272) malate dehydrogenase [Medicago sativa]
Seq. No.
                    234728
Seq. ID
                    LIB3272-041-P1-K1-C5
Method
                    BLASTX
NCBI GI
                    g416649
BLAST score
                    166
E value
                    7.0e-12
Match length
                    89
% identity
                    39
                   PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN
NCBI Description
                    PGNT1/PCNT110) >gi_100303_pir__S16267 auxin-induced protein (clone pGNT1) - common tobacco >gi_19789_emb_CAA39709_
```

Seq. No. 234729

[Nicotiana tabacum]

(X56268) auxin-induced protein [Nicotiana tabacum] >gi\_19795\_emb\_CAA39705\_ (X56264) auxin-induced protein



```
Seq. ID
                  LIB3272-041-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3421094
BLAST score
                   442
E value
                   4.0e-44
                  95
Match length
% identity
                  89
NCBI Description
                  (AF043527) 20S proteasome subunit PAF2 [Arabidopsis
                  thaliana]
Seq. No.
                  234730
Seq. ID
                  LIB3272-041-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q4033351
BLAST score
                  165
E value
                  2.0e-13
Match length
                  109
% identity
                  47
NCBI Description
                 (AJ223497) phosphoenolpyruvate carboxylase [Brassica
                  juncea]
Seq. No.
                  234731
Seq. ID
                  LIB3272-041-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q4538929
BLAST score
                  205
E value
                  3.0e-16
Match length
                  112
                  27
% identity
NCBI Description
                 (AL049483) putative nucleic acid binding protein
                  [Arabidopsis thaliana]
Seq. No.
                  234732
Seq. ID
                  LIB3272-041-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q505482
BLAST score
                  329
E value
                  7.0e - 31
Match length
                  92
                  77
% identity
NCBI Description
                 (X64349) 33 kDa polypeptide of water-oxidizing complex of
                  photosystem II [Nicotiana tabacum]
Seq. No.
                  234733
Seq. ID
                  LIB3272-041-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g1172555
BLAST score
                  472
E value
                  2.0e-47
Match length
                  104
                  87
% identity
NCBI Description 34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
                 · (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                  (POM 34) >gi_629720_pir__S46936 34K porin - potato
```

33943

porin [Solanum tuberosum]

>gi\_1076682\_pir\_ A55364\_porin (clone pPOM-34) - potato
mitochondrion >gi\_516166\_emb\_CAA56599 (X80386) 34 kDA

```
234734
```

```
Seq. No.
Seq. ID
                   LIB3272-041-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g4105772
BLAST score
                   346
E value
                   1.0e-32
Match length
                   74
% identity
                   42
NCBI Description
                  (AF049917) PGP9B [Petunia x hybrida]
Seq. No.
                   234735
                   LIB3272-041-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3158474
BLAST score
                   366
E value
                   3.0e-35
Match length
                   89
                   83
% identity
NCBI Description
                  (AF067184) aquaporin 1 [Samanea saman]
Seq. No.
                   234736
Seq. ID
                   LIB3272-041-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g4510345
BLAST score
                   230
E value
                   5.0e-19
Match length
                   44
% identity
                   89
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                   234737
Seq. ID
                   LIB3272-041-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   q3901014
BLAST score
                   226
E value
                   1.0e-18
Match length
                   55
% identity
                   75
NCBI Description
                  (AJ130886) metallothionein-like protein class II [Fagus
                   sylvatica]
Seq. No.
                   234738
Seq. ID
                  LIB3272-041-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g3861068
BLAST score
                  176
E value
                   1.0e-12
Match length
                   60
% identity
                   50
NCBI Description
                  (AJ235272) unknown [Rickettsia prowazekii]
Seq. No.
                  234739
Seq. ID
                  LIB3272-041-P1-K1-E9
```

Method BLASTX NCBI GI g629483 BLAST score 298



E value 5.0e-27 Match length 111 56 % identity

gene 1-Sc3 protein - European white birch NCBI Description

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula] >gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula

pendula]

234740 Seq. No.

LIB3272-041-P1-K1-F2 Seq. ID

Method BLASTX NCBI GI g3023841 BLAST score 221 6.0e-18 E value Match length 54 76 % identity

GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT NCBI Description

>qi 1695179 emb CAA70704 (Y09513) G protein beta subunit

[Nicotiana plumbaginifolia]

Seq. No. 234741

LIB3272-041-P1-K1-F4 Seq. ID

Method BLASTX NCBI GI g4371282 BLAST score 521 E value 3.0e-53 Match length 117 85 % identity

NCBI Description (AC006260) putative 60S ribosomal protein L12 [Arabidopsis

thaliana]

234742 Seq. No.

LIB3272-041-P1-K1-F6 Seq. ID

Method BLASTX NCBI GI q232031 BLAST score 219 E value 8.0e-18 67 Match length % identity 60

NCBI Description

ELONGATION FACTOR 1 BETA' >gi\_322851\_pir\_\_S29224
translation elongation factor eEF-1 beta' chain - rice >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta'

[Oryza satīva]

Seq. No. 234743

Seq. ID LIB3272-041-P1-K1-F8

Method BLASTX NCBI GI g3023841 BLAST score 162 E value 4.0e-11 Match length 54 % identity 59

GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT NCBI Description

>gi 1695179 emb CAA70704 (Y09513) G protein beta subunit

[Nicotiana plumbaginifolia]

234744 Seq. No.

E value

3.0e-37



```
LIB3272-041-P1-K1-F9
   Seq. ID
                     BLASTX
   Method
   NCBI GI
                     g2924520
   BLAST score
                     547
                     3.0e-56
   E value
   Match length
                     123
   % identity
                     86
   NCBI Description
                      (AL022023) plasma membrane intrinsic protein (SIMIP)
                      [Arabidopsis thaliana]
                     234745
   Seq. No.
                     LIB3272-041-P1-K1-G11
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     q2961085
   BLAST score
                     110
                     3.0e-09
   E value
   Match length
                     96
   % identity
                      44
   NCBI Description (AF037228) transcription factor [Arabidopsis thaliana]
   Seq. No.
                     234746
   Seq. ID
                     LIB3272-041-P1-K1-G2
   Method
                     BLASTX
   NCBI GI
                      g3608140
   BLAST score
                     159
                      1.0e-10
   E value
                     87
   Match length
   % identity
                      41
   NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]
                      234747
   Seq. No.
   Seq. ID
                     LIB3272-041-P1-K1-G3
   Method
                     BLASTX
   NCBI GI
                      g3608485
   BLAST score
                      502
   E value
                      5.0e-51
                      101
   Match length
% identity
                      93
   NCBI Description (AF088915) proteasome beta subunit [Petunia x hybrida]
   Seq. No.
                      234748
   Seq. ID
                      LIB3272-041-P1-K1-H1
                      BLASTX
   Method
   NCBI GI
                      g3024583
   BLAST score
                      184
                      7.0e-14
   E value
   Match length
                      96
                      48
   % identity
   NCBI Description RT14 PROTEIN HOMOLOG >gi 2347196 (AC002338) RT14 protein
                      isolog [Arabidopsis thaliana]
                      234749
   Seq. No.
                      LIB3272-041-P1-K1-H2
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      q2984709
   BLAST score
                      385
```

, in



Match length 80 % identity 90

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. Seq. ID

234750 BLASTX

Method

LIB3272-041-P1-K1-H3

NCBI GI BLAST score E value

g3023858 431 1.0e-42

Match length 93 % identity 86

NCBI Description

GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >qi 1256608 (U44850) G protein beta subunit

[Glycine max]

Seq. No. Seq. ID

234751

LIB3272-041-P1-K1-H7

Method BLASTX NCBI GI g4115949 BLAST score 195 E value 3.0e-15 Match length 63 % identity 65

NCBI Description (AF118223) contains similarity to adenosine deaminases

[Arabidopsis thaliana]

Seq. No.

234752

Seq. ID

LIB3272-041-P1-K1-H8

Method BLASTX NCBI GI g1408471 BLAST score 447 2.0e-44 E value Match length 102 % identity 78

NCBI Description

(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi 3851707 (AF102173) actin depolymerizing

factor 1 [Arabidopsis thaliana]

Seq. No. 234753

Seq. ID LIB3272-042-P1-K1-A11

Method BLASTX NCBI GI g2702376 BLAST score 219 E value 9.0e-18 Match length 89 % identity 46

(AF038605) Similar to acyl-CoA dehydrogenase; coded for by NCBI Description

C. elegans cDNA yk58h2.3; coded for by C. elegans cDNA yk466c12.3; coded for by C. elegans cDNA yk258d6.3; coded for by C. elegans cDNA yk158e10.3; coded for by C. elegans

cDNA yk427... >gi 4455127 gb AAD21088 (AF127558) isovaleryl-CoA dehydrogenase precursor [Caenorhabditis

elegans]

Seq. No. 234754

Seq. ID LIB3272-042-P1-K1-A12



```
Method
                    BLASTX
NCBI GI
                    q1813329
BLAST score
                    284
E value
                    2.0e-25
                    60
Match length
                    87
 % identity
                   (AB000637) HMG-1 [Canavalia gladiata]
NCBI Description
Seq. No.
                    234755
                    LIB3272-042-P1-K1-A2
Seq. ID
Method
                    BLASTX
NCBI GI
                    q462195
BLAST score
                    292
                    2.0e-26
E value
Match length
                    82
                    72
% identity
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                    >gi 100682_pir__S21636 GOS2 protein - rice
                    >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                    >gi_3789950 (AF094774) translation initiation factor [Oryza
                    sativa]
                    234756
 Seq. No.
 Seq. ID
                    LIB3272-042-P1-K1-A3
Method
                    BLASTX
NCBI GI
                    g3980393
                    375
BLAST score
                    5.0e-36
E value
Match length
                    122
 % identity
                    58
NCBI Description
                   (AC004561) putative glutathione S-transferase [Arabidopsis
                    thaliana]
                    234757
 Seq. No.
 Seq. ID
                    LIB3272-042-P1-K1-A5
 Method
                    BLASTX
 NCBI GI
                    g2702376
 BLAST score
                    213
                    4.0e-17
 E value
 Match length
                    88
 % identity
                    45
                    (AF038605) Similar to acyl-CoA dehydrogenase; coded for by
 NCBI Description
                    C. elegans cDNA yk58h2.3; coded for by C. elegans cDNA
                    yk466c12.3; coded for by C. elegans cDNA yk258d6.3; coded
                    for by C. elegans cDNA yk158e10.3; coded for by C. elegans
                    cDNA yk427... >gi_4455127_gb_AAD21088_ (AF127558) isovaleryl-CoA dehydrogenase precursor [Caenorhabditis
                    elegans]
                    234758
 Seq. No.
 Seq. ID
                    LIB3272-042-P1-K1-A6
                    BLASTX
 Method
 NCBI GI
                    g4406372
 BLAST score
                    439
```

E value Match length 119 % identity 70

1.0e-43



```
NCBI Description
                  (AF109156) thiosulfate sulfurtransferase [Datisca
                   glomerata]
                   234759
Seq. No.
                  LIB3272-042-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3738257
BLAST score
                   310
E value
                   1.0e-28
                   69
Match length
% identity
                   88
                  (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                  nigra]
Seq. No.
                   234760
Seq. ID
                  LIB3272-042-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                   473
                   2.0e-47
E value
                  117
Match length
% identity
                   79
NCBI Description
                  (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  234761
Seq. ID
                  LIB3272-042-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g3249066
                   343
BLAST score
E value
                  2.0e-32
Match length
                  119
                   64
% identity
                  (AC004473) Similar to S. cerevisiae SIK1P protein
NCBI Description
                   gb 984964. ESTs gb F15433 and gb AA395158 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  234762
                  LIB3272-042-P1-K1-B11
Seq. ID
Method
                  BLASTX
                   q3881978
NCBI GI
BLAST score
                   307
                   3.0e-28
E value
Match length
                  97
% identity
                   36
NCBI Description
                  (Y11348) annexin-like protein [Medicago sativa]
Seq. No.
                  234763
Seq. ID
                  LIB3272-042-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q4220518
BLAST score
                  159
                  5.0e-11
E value
Match length
                  86
% identity
                  45
```

Seq. No. 234764

NCBI Description

(AL035356) hypothetical protein [Arabidopsis thaliana]

BLAST score

E value

405

1.0e-39



```
Seq. ID
                  LIB3272-042-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g1545805
BLAST score
                  136
E value
                  1.0e-08
Match length
                  37
                  76
% identity
NCBI Description (D64052) cytochrome P450 like TBP [Nicotiana tabacum]
Seq. No.
                  234765
Seq. ID
                  LIB3272-042-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q3643602
BLAST score
                  222
E value
                  3.0e-18
Match length
                  93
% identity
                  54
NCBI Description (AC005395) putative tonoplast intrinsic protein
                  [Arabidopsis thaliana]
Seq. No.
                  234766
Seq. ID
                  LIB3272-042-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g2792297
BLAST score
                  261
E value
                  1.0e-22
                  77
Match length
% identity
                  58
NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]
Seq. No.
                  234767
Seq. ID
                  LIB3272-042-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g3914435
BLAST score
                  454
E value
                  2.0e-45
Match length
                  111
                  78
% identity
NCBI Description PROFILIN 1 >qi 3021375 emb CAA11756 (AJ223982) profilin
                  [Glycine max]
Seq. No.
                  234768
Seq. ID
                  LIB3272-042-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g4512688
BLAST score
                  243
E value
                  1.0e-20
Match length
                  112
                  50
% identity
NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  234769
Seq. ID
                  LIB3272-042-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q1350720
```

E value

Match length

% identity

1.0e-60

118

99



```
Match length
                   99
                   77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
Seq. No.
                   234770
Seq. ID
                   LIB3272-042-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g267082
BLAST score
                   578
E value
                   7.0e-60
Match length
                   111
% identity
                   94
NCBI Description
                  TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8
                   chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8
                  tubulin [Arabidopsis thaliana]
Seq. No.
                   234771
Seq. ID
                  LIB3272-042-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g3860274
BLAST score
                   152
E value
                   4.0e-10
Match length
                   32
% identity
                   81
NCBI Description
                   (AC005824) unknown protein [Arabidopsis thaliana]
                  >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger
                  protein [Arabidopsis thaliana]
Seq. No.
                  234772
Seq. ID
                  LIB3272-042-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g3037047
BLAST score
                  491
E value
                  1.0e-49
Match length
                  114
                  75
% identity
                   (AF053354) 1-aminocyclopropane-1-carboxylic acid oxidase
NCBI Description
                   [Phaseolus vulgaris]
Seq. No.
                  234773
Seq. ID
                  LIB3272-042-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1669585
BLAST score
                  147
E value
                  8.0e-12
Match length
                  60
% identity
NCBI Description (D88649) cytosolic ascorbate peroxidase [Cucumis sativus]
Seq. No.
                  234774
Seq. ID
                  LIB3272-042-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1263291
BLAST score
                  406
```



```
NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]
                  234775
Seq. No.
Seq. ID
                  LIB3272-042-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1928981
BLAST score
                  557
E value
                  2.0e-57
Match length
                  125
                  89
% identity
NCBI Description
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
                  oleracea var. botrytis]
Seq. No.
                  234776
Seq. ID
                  LIB3272-042-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g70644
BLAST score
                  611
E value
                  1.0e-63
Match length
                  126
% identity
                  19
NCBI Description ubiquitin precursor - common sunflower (fragment)
Seq. No.
                  234777
Seq. ID
                  LIB3272-042-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q2467088
BLAST score
                  193
E value
                  8.0e-15
Match length
                  118
% identity
                  44
NCBI Description (AJ001911) putative Ckc2 [Arabidopsis thaliana]
Seq. No.
                  234778
Seq. ID
                  LIB3272-042-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q4539390
BLAST score
                  511
E value
                  5.0e-52
Match length
                  112
                  88
% identity
NCBI Description
                  (AL035526) shaggy-like protein kinase etha (EC 2.7.1.-)
                  [Arabidopsis thaliana]
Seq. No.
                  234779
Seq. ID
                  LIB3272-042-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q4126473
BLAST score
                  536
E value
                  5.0e-55
Match length
                  123
                  89
% identity
                  (AB014884) adenylyl cyclase associated protein [Gossypium
NCBI Description
                  hirsutum]
```

234780

LIB3272-042-P1-K1-D5

Seq. No.

Seq. ID



```
BLASTX
Method
NCBI GI
                  a2264382
                  152
BLAST score
E value
                  6.0e-10
Match length
                  114
                  38
% identity
NCBI Description
                  (AC002354) putative tetracycline transporter-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  234781
                  LIB3272-042-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1173187
                  231
BLAST score
E value
                  3.0e-19
Match length
                  109
                  49
% identity
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi_643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
                  234782
Seq. No.
                  LIB3272-042-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g126894
BLAST score
                  474
E value
                  1.0e-47
Match length
                  113
% identity
                  85
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >gi 319832 pir DEPUGW malate dehydrogenase (EC 1.1.1.37)
                  precursor, glyoxysomal - watermelon >gi_167284 (M33148)
                  glyoxysomal malate dehydrogenase precursor (EC 1.1.1.37)
                  [Citrullus vulgaris]
Seq. No.
                  234783
Seq. ID
                  LIB3272-042-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q3913633
BLAST score
                  332
E value
                  5.0e-31
Match length
                  83
                  80
% identity
NCBI Description
                  HYPOTHETICAL PROTEIN F8A5.25 >gi 2462742 (AC002292) Unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  234784
Seq. ID
                  LIB3272-042-P1-K1-E5
```

Method BLASTX NCBI GI g3158474 BLAST score 539 E value 3.0e-55Match length 114 % identity 91

NCBI Description (AF067184) aquaporin 1 [Samanea saman]

% identity



```
234785
Seq. No.
                  LIB3272-042-P1-K1-E8
Seq. ID
Method
                  BLASTX
                  g2130073
NCBI GI
BLAST score
                  520
                  5.0e-53
E value
                  120
Match length
                  86
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                  aldolase C-1 [Oryza sativa]
                  234786
Seq. No.
                  LIB3272-042-P1-K1-F1
Seq. ID
                  BLASTX
Method
                  g3334320
NCBI GI
                  551
BLAST score
                  1.0e-56
E value
                  117
Match length
                  94
% identity
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                  ribosome-associated protein p40 [Glycine max]
                  234787
Seq. No.
                  LIB3272-042-P1-K1-F10
Seq. ID
Method
                  BLASTX
                  g3334147
NCBI GI
                  588
BLAST score
                  5.0e-61
E value
                  134
Match length
                   86
% identity
NCBI Description ENDOCHITINASE 1 PRECURSOR >gi_1469788 (U60197) class I
                  chitinase [Gossypium hirsutum]
Seq. No.
                   234788
Seq. ID
                  LIB3272-042-P1-K1-F11
Method
                  BLASTX
NCBI GI
                   q2262159
BLAST score
                   530
                   3.0e-54
E value
Match length
                   131
                   76
% identity
                  (AC002329) predicted protein similar to S.pombe protein
NCBI Description
                   C5H10.03 [Arabidopsis thaliana]
Seq. No.
                   234789
Seq. ID
                   LIB3272-042-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g1345132
BLAST score
                   197
E value
                   2.0e-15
                   97
Match length
```

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]

>gi\_1389566\_dbj\_BAA11869\_ (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi\_3075386 (AC004484) receptor



## protein kinase, ERECTA [Arabidopsis thaliana]

```
Seq. No.
                  234790
Seq. ID
                  LIB3272-042-P1-K1-F2
Method
                  BLASTX
                  q3738327
NCBI GI '
                  352
BLAST score
                  2.0e-33
E value
Match length
                  141
% identity
                   50
                   (AC005170) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                  thaliana]
                  234791
Seq. No.
                  LIB3272-042-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q487046
BLAST score
                  227
                  1.0e-18
E value
                  103
Match length
                   46
% identity
                  photosystem I chain II precursor - wood tobacco
NCBI Description
                   >gi_407769_dbj_BAA02871_ (D13718) PSI-D1 precursor
                   [Nicotiana sylvestris]
                   234792
Seq. No.
                  LIB3272-042-P1-K1-F5
Seq. ID
Method
                  BLASTX
                   q266579
NCBI GI
                   237
BLAST score
E value
                   5.0e-20
Match length
                   75
                   61
% identity
                  METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi 169713 (L02306)
NCBI Description
                   metallothionein [Ricinus communis]
Seq. No.
                   234793
                   LIB3272-042-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q170507
BLAST score
                   130
E value
                   6.0e-14
Match length
                   70
% identity
                   59
                  (M59251) ORF [Lycopersicon esculentum] >gi 1172167 (U44386)
NCBI Description
                   heat shock protein [Solanum lycopersicum]
Seq. No.
                   234794
                   LIB3272-042-P1-K1-G1
Seq. ID
                   BLASTX
Method
                   q3319882
NCBI GI
                   716
BLAST score
                   5.0e-76
E value
                   141
Match length
                   96
% identity
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
```

33955

arietinum]

Match length

% identity

118 ·-29



```
234795
Seq. No.
                  LIB3272-042-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2879867
BLAST score
                  393
                  3.0e-38
E value
Match length
                  106
                  71
% identity
                   (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
NCBI Description
                  pombe]
                  234796
Seq. No.
                  LIB3272-042-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1169476
                  377
BLAST score
E value
                   3.0e-36
                  137
Match length
                   61
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                  ADHESION PROTEIN 1) (PVN1) >gi_439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
Seq. No.
                   234797
                  LIB3272-042-P1-K1-G4
Seq. ID
Method
                   BLASTX
                   q3687237
NCBI GI
                   154
BLAST score
E value
                   3.0e-10
Match length
                   34
                   74
% identity
                   (AC005169) putative Cys3His zinc-finger protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   234798
Seq. ID
                   LIB3272-042-P1-K1-G5
                   BLASTX
Method
NCBI GI
                   g3122060
BLAST score
                   235
E value
                   5.0e-20
Match length
                   55
                   85
% identity
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi 2598657 emb CAA10847 (AJ222579) elongation factor
                   1-alpha (EF1-a) [Vicia faba]
Seq. No.
                   234799
                   LIB3272-042-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3337366
BLAST score
                   337
E value
                   1.0e-31
```

NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]



72

% identity

NCBI Description

```
234800
Seq. No.
                  LIB3272-042-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3165581
BLAST score
                  142
                  1.0e-08
E value
                  111
Match length
                   34
% identity
                  (AF067942) similar to lysosomal acid lipases (SW:P38571)
NCBI Description
                   [Caenorhabditis elegans]
                   234801
Seq. No.
                  LIB3272-042-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  g3914685
NCBI GI
BLAST score
                   180
                   2.0e-13
E value
                   94
Match length
                   31
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal
                  protein L17 [Zea mays]
Seq. No.
                   234802
                   LIB3272-042-P1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3914430
BLAST score
                   283
                   4.0e-33
E value
Match length
                   106
                   74
% identity
                  PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
NCBI Description
                   CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                   >gi_2285800_dbj_BAA21650_ (D78172) 26S proteasome beta
                   subunit [Spinacia oleracea]
Seq. No.
                   234803
Seq. ID
                   LIB3272-042-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q3980391
BLAST score
                   180
                   8.0e-19
E value
Match length
                   81
% identity
                   62
                   (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   234804
                   LIB3272-043-P1-K1-A11
Seq. ID
Method
                   BLASTX
                   q1658197
NCBI GI
                   339
BLAST score
E value
                   3.0e-32
Match length
                   86
```

(U74631) calreticulin [Ricinus communis]

(U74630) calreticulin [Ricinus communis] >gi\_1763297

% identity

87



```
234805
Seq. No.
                   LIB3272-043-P1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1332579
BLAST score
                   458
                   5.0e-55
E value
                   117
Match length
                   10
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                   234806
Seq. No.
                   LIB3272-043-P1-K1-A4
Seq. ID
                   BLASTX
Method
                   q3603456
NCBI GI
BLAST score
                   442
E value
                   5.0e-44
                   99
Match length
                   28
% identity
NCBI Description (AF088848) polyubiquitin [Capsicum chinense]
                   234807
Seq. No.
                   LIB3272-043-P1-K1-A9
Seq. ID
                   BLASTX
Method
                   g585165
NCBI GI
BLAST score
                   168
                   8.0e-13
E value
Match length
                   64
                   61
% identity
                   GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM
NCBI Description
                   (G6PD) >gi_2129985_pir__S60287 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - potato
                   >gi_471345_emb_CAA52442_ (X74421) glucose-6-phosphate
                   1-dehydrogenase [Solanum tuberosum]
                   234808
Seq. No.
Seq. ID
                   LIB3272-043-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   q586339
BLAST score
                   207
                   2.0e-16
E value
Match length
                   71
% identity
                   PEROXISOMAL-COENZYME A SYNTHETASE >gi_626794_pir__S46098
NCBI Description
                   probable AMP-binding protein - yeast (Saccharomyces
                   cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c
                   [Saccharomyces cerevisiae]
Seq. No.
                   234809
Seq. ID
                   LIB3272-043-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g3043428
BLAST score
                   435
E value
                   4.0e-43
Match length
                   93
```

NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

% identity

NCBI Description



```
Seq. No.
                    234810
Seq. ID
                    LIB3272-043-P1-K1-B2
Method
                    BLASTX
NCBI GI
                    q464621
BLAST score
                    322
E value
                    7.0e-30
Match length
                    112
                    58
% identity
                    60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374 pir S28586
NCBI Description
                    ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                    [Mesembryanthemum crystallinum]
                    234811
Seq. No.
Seq. ID
                    LIB3272-043-P1-K1-B6
Method
                    BLASTX
NCBI GI
                    g3043428
BLAST score
                    465
E value
                    1.0e-46
Match length
                    99
% identity
                    88
                    (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
NCBI Description
                    234812
Seq. No.
                    LIB3272-043-P1-K1-B7
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4539423
BLAST score
                    556
                    2.0e-57
E value
Match length
                    115
% identity
                    94
NCBI Description
                    (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
                    [Arabidopsis thaliana]
Seq. No.
                    234813
Seq. ID
                    LIB3272-043-P1-K1-B9
Method
                    BLASTX
NCBI GI
                    g3513727
BLAST score
                    284
E value
                    2.0e-25
Match length
                    62
% identity
                    90
                    (AF080118) contains similarity to TPR domains (Pfam:
NCBI Description
                    TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                    kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative
                    protein [Arabidopsis thaliana]
                    234814
Seq. No.
Seq. ID
                    LIB3272-043-P1-K1-C1
                    BLASTX
Method
                    g2564066
NCBI GI
BLAST score
                    487
E value
                    3.0e-49
Match length
                    116
                    79
```

(D45900) LEDI-3 protein [Lithospermum erythrorhizon]

Method

BLASTX



```
234815
Seq. No.
                  LIB3272-043-P1-K1-C10
Seq. ID
                  BLASTX
Method
                  q2244904
NCBI GI
                  219
BLAST score
                  8.0e-18
E value
                  70
Match length
                  67
% identity
                  (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
NCBI Description
                   [Arabidopsis thaliana]
                  234816
Seq. No.
                  LIB3272-043-P1-K1-C3
Seq. ID
                  BLASTX
Method
                  g430947
NCBI GI
                  440
BLAST score
                  1.0e-43
E value
                  109
Match length
                  80
% identity
                   (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   234817
Seq. No.
                  LIB3272-043-P1-K1-C5
Seq. ID
                  BLASTX
Method
                   g1082054
NCBI GI
                   287
BLAST score
                   8.0e-26
E value
                   122
Match length
                   48
% identity
                  (Z49859) copper transporter protein [Arabidopsis thaliana]
NCBI Description
                   234818
Seq. No.
                   LIB3272-043-P1-K1-C6
Seq. ID
                   BLASTX
Method
                   g4559358
NCBI GI
BLAST score
                   186
                   6.0e-14
E value
                   58
Match length
                   57
% identity
                   (AC006585) putative steroid binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   234819
Seq. No.
                   LIB3272-043-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3702323
BLAST score
                   364
                   1.0e-61
E value
                   132
Match length
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                   234820
                   LIB3272-043-P1-K1-D1
Seq. ID
```

```
g2879867
NCBI GI
                   403
BLAST score
                   2.0e-39
E value
                   114
Match length
                   68
% identity
                   (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
NCBI Description
                   pombe]
                   234821
Seq. No.
                   LIB3272-043-P1-K1-D10
Seq. ID
                   BLASTX
Method
```

NCBI GI g115492
BLAST score 579
E value 5.0e-60
Match length 113
% identity 53

NCBI Description CALMODULIN-RELATED PROTEIN >gi\_169205 (M80831) calmodulin-related protein [Petunia hybrida]

 Seq. No.
 234822

 Seq. ID
 LIB3272-043-P1-K1-D4

 Method
 BLASTX

 NCBI GI
 g1617036

 BLAST score
 201

BLAST score 201 E value 7.0e-16 Match length 50 % identity 68

NCBI Description (Y08624) Ted2 [Vigna unguiculata]

Seq. No. 234823

Seq. ID LIB3272-043-P1-K1-D5

Method BLASTX
NCBI GI g1816660
BLAST score 205
E value 3.0e-16
Match length 94
% identity 43

NCBI Description (U86521) NhRAD6 [Nectria haematococca]

Seq. No. 234824

Seq. ID LIB3272-043-P1-K1-D8

Method BLASTX
NCBI GI g1922278
BLAST score 251
E value 8.0e-22
Match length 50
% identity 92

NCBI Description (Z86091) TCTP protein [Fragaria x ananassa]

Seq. No. 234825

Seq. ID LIB3272-043-P1-K1-D9

Method BLASTX
NCBI GI g2979555
BLAST score 225
E value 2.0e-18
Match length 113
% identity 46



```
NCBI Description (AC003680) unknown protein [Arabidopsis thaliana]
                  234826
Seq. No.
                  LIB3272-043-P1-K1-E11
Seq. ID
Method
                  BLASTX
                  q4056469
NCBI GI
                  596
BLAST score
                  5.0e-62
E value
                  116
Match length
                  100
% identity
                  (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
NCBI Description
                  factor from Arabidopsis thaliana. ESTs gb_Z25826,
                  gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
                  gb AA712956, gb T46403, gb T46050, gb AI100391 and
                  gb Z25043 come from t
Seq. No.
                  234827
                  LIB3272-043-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3063396
BLAST score
                  408
                  5.0e-40
E value
                  98
Match length
% identity
                  79
                  (AB012947) vcCyP [Vicia faba]
NCBI Description
                   234828
Seq. No.
                  LIB3272-043-P1-K1-E2
Seq. ID
Method
                   BLASTX
                   g3252868
NCBI GI
                   278
BLAST score
                   1.0e-24
E value
                   76
Match length
                   67
% identity
                  (AF033536) putative zinc transporter [Arabidopsis thaliana]
NCBI Description
                   234829
Seq. No.
                   LIB3272-043-P1-K1-E3
Seq. ID
Method
                   BLASTX
                   g4098128
NCBI GI
BLAST score
                   425
                   5.0e-42
E value
                   98
Match length
                   86
% identity
                  (U73588) sucrose synthase [Gossypium hirsutum]
NCBI Description
                   234830
Seq. No.
                   LIB3272-043-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3063396
                   527
BLAST score
                   6.0e-54
E value
Match length
                   117
% identity
                  (AB012947) vcCyP [Vicia faba]
NCBI Description
```

33962

234831

Seq. No.



LIB3272-043-P1-K1-E7 Seq. ID BLASTX Method g1170747 NCBI GI BLAST score 309 2.0e-28 E value 74 Match length 82 % identity LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi\_167345 NCBI Description (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi\_167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum] 234832 Seq. No. LIB3272-043-P1-K1-E8 Seq. ID Method BLASTX g508304 NCBI GI 278 BLAST score 1.0e-24 E value 67 Match length 78 % identity NCBI Description (L22305) corC [Medicago sativa] Seq. No. 234833 LIB3272-043-P1-K1-E9 Seq. ID Method BLASTX NCBI GI q2160166 304 BLAST score E value 9.0e-28 132 Match length 48 % identity (AC000132) No definition line found [Arabidopsis thaliana] NCBI Description 234834 Seq. No. LIB3272-043-P1-K1-F1 Seq. ID Method BLASTX NCBI GI g3851001 BLAST score 411 E value 2.0e-40 Match length 111 75 % identity (AF069909) pyruvate dehydrogenase E1 beta subunit isoform 2 NCBI Description [Zea mays] 234835 Seq. No. LIB3272-043-P1-K1-F11 Seq. ID Method BLASTX NCBI GI g3450889 271 BLAST score 5.0e-24E value 81 Match length 70 % identity NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No. 234836

Seq. ID LIB3272-043-P1-K1-F12

Method BLASTX NCBI GI g4455364



```
308
BLAST score
                  3.0e-28
E value
                  131
Match length
                  40
% identity
                   (AL035524) senescence-associated protein-like [Arabidopsis
NCBI Description
                  thaliana]
                  234837
Seq. No.
                  LIB3272-043-P1-K1-F2
Seq. ID
                  BLASTX
Method
                  g3150415
NCBI GI
                   409
BLAST score
                   4.0e-40
E value
                   92
Match length
                   31
% identity
                   (AC004165) sec13-related protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3420046 (AC004680) sec13-related protein [Arabidopsis
                   thaliana]
                   234838
Seq. No.
                   LIB3272-043-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   g3643609
NCBI GI
BLAST score
                   393
                   3.0e-38
E value
                   129
Match length
                   60
% identity
                   (AC005395) putative Cys3His zinc finger protein
NCBI Description
                   [Arabidopsis thaliana]
                   234839
Seq. No.
                   LIB3272-043-P1-K1-F9
Seq. ID
                   BLASTX
Method
                   g4572671
NCBI GI
                   378
BLAST score
                   2.0e-36
E value
                   130
Match length
                   55
% identity
                   (AC006954) putative cyclic nucleotide regulated ion channel
NCBI Description
                   [Arabidopsis thaliana]
                   234840
Seq. No.
                   LIB3272-043-P1-K1-G1
Seq. ID
                   BLASTX
Method
                   g2160166
NCBI GI
                   334
BLAST score
                   2.0e-31
E value
                   113
Match length
                   60
 % identity
                  (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   234841
 Seq. No.
                   LIB3272-043-P1-K1-G10
 Seq. ID
                   BLASTX
Method
                   g577503
 NCBI GI
```

33964

411

2.0e-40

BLAST score

E value



```
103
Match length
                  °78
% identity
NCBI Description (L37790) cationic peroxidase [Stylosanthes humilis]
                  234842
Seq. No.
                  LIB3272-043-P1-K1-G2
Seq. ID
                  BLASTX
Method
                  g1173218
NCBI GI
                  177
BLAST score
                  4.0e-13
E value
                  86
Match length
                  49
% identity
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
NCBI Description
                  protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  234843
Seq. No.
                  LIB3272-043-P1-K1-G3
Seq. ID
                  BLASTX
Method
                  g1220196
NCBI GI
                   476
BLAST score
                   5.0e-48
E value
                   97
Match length
                   94
% identity
                  (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]
NCBI Description
                   234844
Seq. No.
                  LIB3272-043-P1-K1-G4
Seq. ID
                   BLASTX
Method
                   g3023847
NCBI GI
                   169
BLAST score
                   2.0e-12
E value
                   42
Match length
                   76
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                   PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta
                   subunit-like [Medicago sativa]
                   234845
Seq. No.
                   LIB3272-043-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q548852
                   277
BLAST score
                   1.0e-24
E value
                   82
Match length
                   67
% identity
                  40S RIBOSOMAL PROTEIN S21 >gi_481227_pir S38357 ribosomal
NCBI Description
                   protein S21 - rice >gi 303839 dbj_BAA02158 (D12633) 40S
                   subunit ribosomal protein [Oryza sativa]
                   234846
Seq. No.
                   LIB3272-043-P1-K1-G7
Seq. ID
Method
                   BLASTX
                   g3868758
NCBI GI
                   344
BLAST score
```

33965

1.0e-32

85

E value Match length



```
% identity
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                  234847
Seq. No.
                  LIB3272-043-P1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q729335
                  182
BLAST score
                  1.0e-13
E value
Match length
                  70
                  54
% identity
                  SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN
NCBI Description
                  PRECURSOR (IP) >gi 508849 (L27705) succinate dehydrogenase
                  iron-protein subunit [Drosophila melanogaster]
Seq. No.
                  234848
                  LIB3272-043-P1-K1-H10
Seq. ID
Method
                  BLASTX
                  q2894534
NCBI GI
                   338
BLAST score
                  7.0e-32
E value
                  96
Match length
% identity
                   73
                  (AJ224327) aquaporin [Oryza sativa]
NCBI Description
                   234849
Seq. No.
                  LIB3272-043-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1657948
                   197
BLAST score
                   2.0e-15
E value
                   57
Match length
                   68
% identity
                  (U73466) MipC [Mesembryanthemum crystallinum]
NCBI Description
                   234850
Seq. No.
                   LIB3272-043-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2398807
BLAST score
                   197
                   2.0e-15
E value
                   52
Match length
% identity
                   67
                  (Z99091) succinate dehydrogenase [Schizosaccharomyces
NCBI Description
                   pombe]
Seq. No.
                   234851
Seq. ID
                   LIB3272-043-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q481236
BLAST score
                   165
                   1.0e-11
E value
Match length
                   87
% identity
                   hypothetical protein - Madagascar periwinkle
NCBI Description
                   >gi_407410_emb_CAA81526_ (Z26880) 14 kDa polypeptide
                   [Catharanthus roseus]
```

```
Seq. No.
                    234852
Seq. ID
                    LIB3272-044-P1-K1-A1
Method
                    BLASTX
NCBI GI
                    g2160166
                    207
BLAST score
E value
                    1.0e-16
Match length
                    105
                    51
% identity
                    (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    234853
                    LIB3272-044-P1-K1-A10
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1107526
BLAST score
                    348
E value
                    6.0e-33
Match length
                    100
                    66
% identity
NCBI Description
                    (X87931) SIEP1L protein [Beta vulgaris]
                    234854
Seq. No.
                    LIB3272-044-P1-K1-A3
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2129753
BLAST score
                    201
E value
                    1.0e-15
Match length
                    55
                    75
% identity
                    threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                    thaliana (fragment) >gi_1448917 (L41666) threonine synthase
                     [Arabidopsis thaliana]
                    234855
Seq. No.
                    LIB3272-044-P1-K1-A5
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1702983
BLAST score
                     356
E value
                     7.0e - 34
Match length
                    111
                     59
% identity
                    AUXIN-REPRESSED 12.5 KD PROTEIN >gi 99855 pir S11850
NCBI Description
                    hypothetical protein - garden strawberry >gi_22573_emb_CAA36676_ (X52429) 12.5 kDa protein [Fragaria x ananassa] >gi_927034 (L44142) auxin-repressed protein
                     [Fragaria ananassa]
Seq. No.
                     234856
Seq. ID
                    LIB3272-044-P1-K1-A6
Method
                    BLASTX
NCBI GI
                     g1419088
BLAST score
                     686
```

NCBI Description (Z71395) calreticulin [Nicotiana plumbaginifolia]

1.0e-72

133 96

E value Match length

% identity

NCBI GI

E value

BLAST score

g232190

9.0e-47



```
234857
Seq. No.
                  LIB3272-044-P1-K1-A9
Seq. ID
Method
                  BLASTX
                  q3766535
NCBI GI
                  494
BLAST score
                  4.0e-50
E value
                  102
Match length
                   95
% identity
                  (Y11687) 14-3-3 protein [Solanum tuberosum]
NCBI Description
                  234858
Seq. No.
                  LIB3272-044-P1-K1-B1
Seq. ID
                  BLASTX
Method
                  q4371297
NCBI GI
BLAST score
                   615
                   3.0e-64
E value
Match length
                  123
                   97
% identity
                  (AC006260) phenylalanine ammonia-lyase 1, 3' partial
NCBI Description
                   [Arabidopsis thaliana]
                   234859
Seq. No.
                  LIB3272-044-P1-K1-B11
Seq. ID
                   BLASTX
Method
                   g1107526
NCBI GI
                   385
BLAST score
                   2.0e-37
E value
Match length
                   120
% identity
                   65
                  (X87931) SIEP1L protein [Beta vulgaris]
NCBI Description
                   234860
Seq. No.
                   LIB3272-044-P1-K1-B12
Seq. ID
                   BLASTX
Method
                   g2642158
NCBI GI
                   282
BLAST score
E value
                   3.0e-25
                   98
Match length
                   57
% identity
NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   234861
                   LIB3272-044-P1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3395441
                   192
BLAST score
E. value
                   1.0e-14
Match length
                   54
% identity
                   67
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
                   234862
Seq. No.
Seq. ID
                   LIB3272-044-P1-K1-B7
                   BLASTX
Method
```



```
Match length
                    119
% identity
                    GLUTATHIONE PEROXIDASE HOMOLOG 6P229 >gi 100291 pir S20501
NCBL Description
                    glutathione peroxidase homolog - wood tobacco
                    >gi 19739 emb CAA42780 (X60219) homologous to animal
                    glutathione peroxidases [Nicotiana sylvestris]
                    234863
Seq. No.
                    LIB3272-044-P1-K1-B9
Seq. ID
Method
                    BLASTX
NCBI GI
                    q730645
BLAST score
                    455
                    2.0e-45
E value
                    116
Match length
                    80
% identity
                    40S RIBOSOMAL PROTEIN S15 >gi_629556_pir S43412 ribosomal
NCBI Description
                    protein S15 - Arabidopsis thaliana >gi_313152 emb_CAA80679_
                    (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                    >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                     gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis
                    thaliana]
                     234864
Seq. No.
Seq. ID
                    LIB3272-044-P1-K1-C1
                    BLASTX
Method
                     q3850582
NCBI GI
                     305
BLAST score
                     7.0e-28
E value
Match length
                    99
                     67
% identity
NCBI Description (AC005278) F15K9.14 [Arabidopsis thaliana]
                     234865
Seq. No.
Seq. ID
                     LIB3272-044-P1-K1-C10
Method
                     BLASTX
NCBI GI
                     q2245118
BLAST score
                     149
                     1.0e-09
E value
Match length
                     120
                     36
 % identity
                    (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                     234866
 Seq. No.
                     LIB3272-044-P1-K1-C11
 Seq. ID
 Method
                     BLASTX
                     q729470
 NCBI GI
                     415
 BLAST score
                     7.0e-41
 E value
                     104
 Match length
                     76
 % identity
                    MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
 NCBI Description
                     (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
```

>gi\_542089\_pir\_\_JQ2272 formate dehydrogenase (EC 1.2.1.2)
precursor, mitochondrial - potato >gi\_297798\_emb\_CAA79702\_
(Z21493) mitochondrial formate dehydrogenase precursor



## [Solanum tuberosum]

```
234867
Seq. No.
                  LIB3272-044-P1-K1-C2
Seq. ID
Method
                  BLASTX
                  q2982268
NCBI GI
                  348
BLAST score
                  6.0e-33
E value
                  75
Match length
% identity
                  91
                  (AF051217) probable 40S ribosomal protein S15 [Picea
NCBI Description
                  mariana]
                  234868
Seq. No.
Seq. ID
                  LIB3272-044-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q3212869
BLAST score
                  449
                  9.0e-45
E value
Match length
                  118
% identity
                   69
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                  234869
Seq. No.
                  LIB3272-044-P1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q481236
                   265
BLAST score
                   3.0e-23
E value
                   64
Match length
% identity
                   81
                  hypothetical protein - Madagascar periwinkle
NCBI Description
                   >gi 407410_emb_CAA81526__ (Z26880) 14 kDa polypeptide
                   [Catharanthus roseus]
Seq. No.
                   234870
Seq. ID
                   LIB3272-044-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   q2677830
BLAST score
                   525
E value
                   1.0e-53
Match length
                   112
                   93
% identity
NCBI Description (U93168) ribosomal protein L12 [Prunus armeniaca]
                   234871
Seq. No.
Seq. ID
                   LIB3272-044-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g4263712
BLAST score
                   302
                   1.0e-27
E value
                   80
Match length
                   70
% identity
                  (AC006223) putative ribosomal protein S12 [Arabidopsis
NCBI Description
                   thaliana]
```

33970

234872

Seq. No.

% identity

NCBI Description



```
LIB3272-044-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  g3395427
NCBI GI
BLAST score
                  219
                  7.0e-18
E value
                  109
Match length
                  49
% identity
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                  234873
Seq. No.
                  LIB3272-044-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1169383
BLAST score
                  146
                  2.0e-09
E value
                  54
Match length
                  57
% identity
NCBI Description DNAJ PROTEIN HOMOLOG ATJ >gi 535588 (L36113) putative
                  [Arabidopsis thaliana] >gi_1582356 prf__2118338A AtJ2
                  protein [Arabidopsis thaliana]
Seq. No.
                  234874
                  LIB3272-044-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  g3335355
NCBI GI
BLAST score
                  579
E value
                  5.0e-60
Match length
                  118
                  27
% identity
                  (AC004512) Match to polyubiquitin DNA gb_L05401 from A.
NCBI Description
                  thaliana. Contains insertion of mitochondrial NADH
                  dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene
                  with an expressed insert. EST gb_AA586248 comes from this
                  region. [Arabi
                  234875
Seq. No.
Seq. ID
                  LIB3272-044-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g1709128
BLAST score
                  219
                  2.0e-27
E value
Match length
                  92
                  70
% identity
                  GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-2
NCBI Description
                  >gi_481019_pir__S37643 protein kinase MSK-2 (EC 2.7.1.-) -
                  alfalfa >gi 313146 emb CAA48473 (X68410) protein kinase
                   [Medicago sativa]
Seq. No.
                  234876
                  LIB3272-044-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  409
E value
                   4.0e-40
Match length
                  94
```

(AF027174) cellulose synthase catalytic subunit

Method

NCBI GI

BLASTX

g3122785



## [Arabidopsis thaliana]

```
234877
Seq. No.
                  LIB3272-044-P1-K1-D9
Seq. ID
Method
                  BLASTX
                  g1166450
NCBI GI
                  297
BLAST score
                  6.0e-27
E value
                  65
Match length
% identity
                  82
NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]
                  234878
Seq. No.
                  LIB3272-044-P1-K1-E11
Seq. ID
                  BLASTX
Method
                  g2760320
NCBI GI
                  301
BLAST score
                  1.0e-27
E value
                  94
Match length
                  67
% identity
NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]
                  234879
Seq. No.
                  LIB3272-044-P1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g167367
BLAST score
                  313
                  4.0e-29
E value
                  80
Match length
                  81
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                  234880
Seq. No.
                  LIB3272-044-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3132675
BLAST score
                  585
E value
                  9.0e-61
                  117
Match length
                  93
% identity
NCBI Description (AF061740) asparagine synthetase [Elaeagnus umbellata]
Seq. No.
                  234881
                  LIB3272-044-P1-K1-E5
Seq. ID
Method
                  BLASTX
                  g2462761
NCBI GI
BLAST score
                  184
E value
                   3.0e-16
Match length
                  70
% identity
                   60
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  234882
Seq. No.
                  LIB3272-044-P1-K1-E7
Seq. ID
```



```
BLAST score 267
E value 1.0e-23
Match length 79
% identity 73
```

NCBI Description 40S RIBOSOMAL PROTEIN S14 >gi\_2565340 (AF026079) ribosomal

protein S14 [Lupinus luteus]

Seq. No. 234883

Seq. ID LIB3272-044-P1-K1-E8

Method BLASTX
NCBI GI g549063
BLAST score 163
E value 5.0e-17
Match length 70
% identity 71

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi\_303835\_dbj BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 234884

Seq. ID LIB3272-044-P1-K1-E9

Method BLASTX
NCBI GI g2462753
BLAST score 150
E value 8.0e-10
Match length 34
% identity 79

NCBI Description (AC002292) putative polygalacturonase [Arabidopsis

thaliana]

Seq. No. 234885

Seq. ID LIB3272-044-P1-K1-F1

Method BLASTX
NCBI GI g2995384
BLAST score 233
E value 1.0e-19
Match length 87
% identity 62

NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No. 234886

Seq. ID LIB3272-044-P1-K1-F11

Method BLASTX
NCBI GI g266567
BLAST score 202
E value 8.0e-16
Match length 62
% identity 58

NCBI Description MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR

(ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi\_421956\_pir\_\_S23558 mitochondrial processing peptidase

(EC 3.4.99.41) alpha chain precursor - potato

>gi\_21493\_emb\_CAA46990\_ (X66284) mitochondrial processing

peptidase [Solanum tuberosum]

Seq. No. 234887



LIB3272-044-P1-K1-F12 Seq. ID Method BLASTX NCBI GI q1724102 475 BLAST score E value 7.0e-48 95 Match length 96 % identity (U79766) S-adenosyl-L-homocystein hydrolase; SAH NCBI Description [Mesembryanthemum crystallinum] 234888 Seq. No. Seq. ID LIB3272-044-P1-K1-F2 Method BLASTX g2160166 NCBI GI BLAST score 211 6.0e-17 E value 118 Match length % identity 50 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana] 234889 Seq. No. LIB3272-044-P1-K1-F6 Seq. ID BLASTX Method g2895866 NCBI GI BLAST score 253 8.0e-22 E value Match length 89 % identity 60 (AF045770) methylmalonate semi-aldehyde dehydrogenase NCBI Description [Oryza sativa] Seq. No. 234890 LIB3272-044-P1-K1-G1 Seq. ID Method BLASTX NCBI GI q1170747 BLAST score 296 E value 7.0e-27 72 Match length 82 % identity LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >qi 167345 NCBI Description (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi\_167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum] 234891 Seq. No. Seq. ID LIB3272-044-P1-K1-G10 Method BLASTX NCBI GI g3377517 BLAST score 243 E value 1.0e-20 Match length 98 % identity

NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No. 234892

Seq. ID LIB3272-044-P1-K1-G12

Method BLASTX



g549063 NCBI GI BLAST score 512 4.0e-52 E value 117 Match length % identity 83 NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626) 21kd polypeptide [Oryza sativa] 234893 Seq. No. Seq. ID LIB3272-044-P1-K1-G5 BLASTX g2811025 277

Method NCBI GI BLAST score E value 1.0e-24 94 Match length 62 % identity

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi 1944181 dbj BAA19607\_

(AB002695) aspartic endopeptidase [Cucurbita pepo]

234894 Seq. No.

LIB3272-044-P1-K1-G8 Seq. ID

Method BLASTX NCBI GI q4432840 192 BLAST score E value 1.0e-14Match length 82 51 % identity

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 234895

LIB3272-044-P1-K1-G9 Seq. ID

Method BLASTX NCBI GI q1710585 BLAST score 362 E value 1.0e-34Match length 84 % identity 85

NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN PO >qi 1143507 emb CAA63786

(X93587) PO ribosomal protein [Lupinus luteus]

Seq. No. 234896

Seq. ID LIB3272-044-P1-K1-H11

Method BLASTX NCBI GI g1666228 BLAST score 263 E value 2.0e-34 Match length 91 77 % identity

NCBI Description (U76190) actin [Pisum sativum] >gi 1666230 (U76191) actin

[Pisum sativum] >gi 1724137 (U8 $104\overline{6}$ ) actin [Pisum sativum]

>gi 1724139 (U81047) actin [Pisum sativum]

Seq. No. 234897

Seq. ID LIB3272-044-P1-K1-H12

Method BLASTX



```
g629483
NCBI GI
                   280
BLAST score
                   5.0e-25
E value
                   101
Match length
                   55
% identity
                   gene 1-Sc3 protein - European white birch
NCBI Description
                   >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                   >gi_158432\overline{2} pr\overline{f} 212237\overline{4}C allergen Bet v 1-Sc3 [Betula
                   pendula]
                   234898
Seq. No.
                   LIB3272-044-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4454026
BLAST score
                   318
E value
                   2.0e-29
                   94
Match length
                   67
% identity
NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]
                   234899
Seq. No.
                   LIB3272-044-P1-K1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2648032
BLAST score
                   335
                   2.0e-31
E value
Match length
                   99
% identity
                   61
NCBI Description (AJ001374) alpha-glucosidase [Solanum tuberosum]
                   234900
Seq. No.
                   LIB3272-044-P1-K1-H7
Seq. ID
Method
                   BLASTX
                   q4249390
NCBI GI
                   292
BLAST score
E value
                   2.0e-26
Match length
                   108
% identity
                   49
                   (AC005966) Similar to gb AF039182 probable aldo-keto
NCBI Description
                   reductase from Fragaria x ananassa. This gene may be cut
                   off. EST gb U74151 comes from this gene. [Arabidopsis
                   thaliana]
                   234901
Seq. No.
Seq. ID
                   LIB3272-045-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g1076660
BLAST score
                   192
E value
                   7.0e-15
Match length
                   37
% identity
                   95
```

NCBI Description D13F(MYBST1) protein - potato >gi\_786426\_bbs\_159122 (S74753) MybSt1=Myb-related transcriptional activator

{DNA-binding domain repeats} [Solanum tuberosum=potatoes,

leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No. 234902



Seq. ID LIB3272-045-P1-K1-A11 Method BLASTX NCBI GI g2160182 BLAST score 170 E value 4.0e-12 117 Match length 39 % identity (AC000132) ESTs qb ATTS1236, qb T43334, qb N97019, qb\_AA395203 NCBI Description come from this gene. [Arabidopsis thaliana] 234903 Seq. No. LIB3272-045-P1-K1-A6 Seq. ID Method BLASTX g1173234 NCBI GI BLAST score 327 2.0e-30 E value Match length 72 89 % identity 40S RIBOSOMAL PROTEIN S25 >qi 481909 pir S40089 ribosomal NCBI Description protein S25 - tomato >gi 435679 emb CAA54132 (X76714) ribosomal protein S25 [Lycopersicon esculentum] >gi 1584836 prf\_\_2123431A ribosomal protein S25 [Lycopersicon esculentum] 234904 Seq. No. LIB3272-045-P1-K1-A8 Seq. ID BLASTX Method g2341034 NCBI GI BLAST score 508 7.0e-52 E value Match length 103 97 % identity NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana] 234905 Seq. No. LIB3272-045-P1-K1-B10 Seq. ID Method BLASTX g2970051 NCBI GI BLAST score 445 3.0e-44E value Match length 109 78 % identity NCBI Description (AB012110) ARG10 [Vigna radiata] 234906 Seq. No. LIB3272-045-P1-K1-B11 Seq. ID BLASTX Method NCBI GI g4539417 290 BLAST score 4.0e-26 E value 67 Match length 76 % identity NCBI Description (AL049171) putative protein [Arabidopsis thaliana]

Seq. No. 234907

Seq. ID LIB3272-045-P1-K1-B12

Method BLASTX

Match length

% identity

91

43



```
g3320120
NCBI GI
BLAST score
                   176
                   8.0e-13
E value
Match length
                   117
                   36
% identity
                   (U66669) 3-hydroxyisobutyryl-coenzyme A hydrolase [Homo
NCBI Description
                   sapiens]
                   234908
Seq. No.
                  LIB3272-045-P1-K1-B4
Seq. ID
                  BLASTX
Method
                   g2499804
NCBI GI
BLAST score
                   265
                   4.0e-23
E value
                   107
Match length
% identity
                   50
                  PROTEIN ARGININE N-METHYLTRANSFERASE 1 >gi_1390025 (U60882)
NCBI Description
                   protein arginine N-methyltransferase [Rattus norvegicus]
                   234909
Seq. No.
                   LIB3272-045-P1-K1-B5
Seq. ID
Method
                   BLASTX
                   g1546702
NCBI GI
                   379
BLAST score
                   2.0e-36
E value
Match length
                   119
                   61
% identity
                  (X98809) peroxidase ATP5a [Arabidopsis thaliana]
NCBI Description
                   234910
Seq. No.
                   LIB3272-045-P1-K1-B8
Seq. ID
Method
                   BLASTX
                   g3868758
NCBI GI
BLAST score
                   281
                   2.0e-25
E value
Match length
                   67
% identity
                   78
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                   234911
Seq. No.
                   LIB3272-045-P1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3021344
BLAST score
                   171
E value
                   2.0e-12
Match length
                   68
                   47
% identity
NCBI Description (AJ004959) hypothetical protein [Cicer arietinum]
Seq. No.
                   234912
                   LIB3272-045-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2829871
BLAST score
                   144
                   5.0e-09
E value
```



```
(AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  234913
Seq. No.
                  LIB3272-045-P1-K1-C4
Seq. ID
                  BLASTX
Method
                  q3643602
NCBI GI
BLAST score
                  298
                  5.0e-27
E value
                  111
Match length
                  58
% identity
                  (AC005395) putative tonoplast intrinsic protein
NCBI Description
                  [Arabidopsis thaliana]
                  234914
Seq. No.
                  LIB3272-045-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  q3915031
NCBI GI
BLAST score
                  466
                  5.0e-47
E value
                  89
Match length
                  100
% identity
                  ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
NCBI Description
                  (STEAROYL-ACP DESATURASE) >gi_1217628_emb_CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
                  234915
Seq. No.
Seq. ID
                  LIB3272-045-P1-K1-C8
Method
                  BLASTX
                  q131770
NCBI GI
                  301
BLAST score
                  1.0e-27
E value
Match length
                  82
                  66
% identity
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
NCBI Description
                   (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                   discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                   [Dictyostelium discoideum]
                  234916
Seq. No.
                  LIB3272-045-P1-K1-C9
Seq. ID
                  BLASTX
Method
                  g2194137
NCBI GI
                  165
BLAST score
                   2.0e-11
E value
                  78
Match length
                   58
% identity
                  (AC002062) ESTs gb R29947, gb_H76702 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   234917
Seq. No.
                  LIB3272-045-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1199778
                  207
BLAST score
```

1.0e-16

E value

Seq. No.

Seq. ID

234922

LIB3272-045-P1-K1-D7



```
Match length
                   65
% identity
NCBI Description (D83225) peroxidase [Populus nigra]
                   234918
Seq. No.
                   LIB3272-045-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2662343
BLAST score
                   496
                   2.0e-50
E value
Match length
                   96
% identity
                   98
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   234919
                   LIB3272-045-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q170354
BLAST score
                   632
E value
                   3.0e-66
Match length
                   128
                   22
% identity
NCBI Description (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
Seq. No.
                   234920
Seq. ID
                   LIB3272-045-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   a464986
BLAST score
                   511
                   5.0e-52
E value
Match length
                   94
                   99
% identity
NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating
                   enzyme E2 [Arabidopsis thaliana]
                   >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
Seq. No.
                   234921
Seq. ID
                   LIB3272-045-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g3540199
BLAST score
                   430
E value
                   1.0e-42
                   91
Match length
% identity
                  (AC004260) Putative monosaccharide transport protein
NCBI Description
                   .[Arabidopsis thaliana]
```

33980

Seq. No.

234927



```
Method
                  BLASTX
NCBI GI
                  g421923
BLAST score
                  414
                  1.0e-40
E value
Match length
                  101
                  70
% identity
                  pathogenesis-related protein P23 - tomato (fragment)
NCBI Description
                  >gi 542031_pir__PQ0742 pathogenesis-related protein P23
                  precursor - tomato (fragment) >gi_19315_emb_CAA50059_
                   (X70787) pathogenesis-related protein PR P23 [Lycopersicon
                  esculentum]
                  234923
Seq. No.
                  LIB3272-045-P1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3860323
                  374
BLAST score
                   6.0e-36
E value
                  78
Match length
                   87
% identity
                  (AJ012688) hypothetical protein [Cicer arietinum]
NCBI Description
                   234924
Seq. No.
                  LIB3272-045-P1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3319882
BLAST score
                   367
                   2.0e-35
E value
                   99
Match length
                   71
% identity
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                   arietinum]
                   234925
Seq. No.
                   LIB3272-045-P1-K1-E11
Seq. ID
                   BLASTX
Method
                   g629597
NCBI GI
                   349
BLAST score
                   5.0e-33
E value
                   83
Match length
                   77
% identity
                   proline-rich protein - rape >gi_545029_bbs_142669 (S68113)
NCBI Description
                   proline-rich SAC51 [Brassica napus=oilseed rape, pods,
                   Peptide, 147 aa] [Brassica napus]
                   234926
Seq. No.
                   LIB3272-045-P1-K1-E2
Seq. ID
                   BLASTX
Method
                   g3402279
NCBI GI
BLAST score
                   600
                   2.0e-62
E value
                   127
Match length
% identity
                   (AJ000999) putative beta-subunit of K+ channels [Solanum
NCBI Description
                   tuberosum]
```

33981



```
LIB3272-045-P1-K1-E3
Seq. ID
                  BLASTX
Method
                  g2662343
NCBI GI
                  626
BLAST score
                  2.0e-65
E value
                  120
Match length
                  100
% identity
                 (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  234928
Seq. No.
                  LIB3272-045-P1-K1-E5
Seq. ID
                  BLASTX
Method
                  g3822036
NCBI GI
                  220
BLAST score
                  6.0e-18
E value
                  118
Match length
                   42
% identity
NCBI Description (AF072326) endo-1,3-1,4-beta-D-glucanase [Zea mays]
                   234929
Seq. No.
                  LIB3272-045-P1-K1-E8
Seq. ID
                  BLASTX
Method
                   q1076660
NCBI GI
                   231
BLAST score
                   2.0e-19
E value
                   50
Match length
                   90
% identity
NCBI Description D13F(MYBST1) protein - potato >gi_786426_bbs_159122
                   (S74753) MybSt1=Myb-related transcriptional activator
                   {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                   leaf, Peptide, 342 aa] [Solanum tuberosum]
                   234930
Seq. No.
                   LIB3272-045-P1-K1-F1
Seq. ID
                   BLASTX
Method
                   g3493172
NCBI GI
                   479
BLAST score
                   2.0e-48
E value
                   106
Match length
 % identity
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
                   234931
Seq. No.
                   LIB3272-045-P1-K1-F10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2286153
 BLAST score
                   589
                   4.0e-61
E value
Match length
                   128
                   94
 % identity
 NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                   234932
 Seq. No.
                   LIB3272-045-P1-K1-F12
 Seq. ID
                   BLASTX
 Method
```

33982

g1531672

649

NCBI GI

BLAST score

Method

NCBI GI

BLASTX

g136251

```
E value
                  3.0e-68
                  126
Match length
                  98
% identity
                  (U68461) actin [Striga asiatica]
NCBI Description
                  234933
Seq. No.
                  LIB3272-045-P1-K1-F2
Seq. ID
                  BLASTX
Method
                  g729470
NCBI GI
                  400
BLAST score
                  4.0e-39
E value
Match length
                  102
                  75
% identity
                  MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
NCBI Description
                   (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi_297798_emb_CAA79702_
                   (Z21493) mitochondrial formate dehydrogenase precursor
                   [Solanum tuberosum]
                  234934
Seq. No.
                  LIB3272-045-P1-K1-F3
Seq. ID
Method
                  BLASTX
                  g3080442
NCBI GI
BLAST score
                   317
                   2.0e-29
E value
                  85
Match length
                   67
% identity
                  (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                   234935
Seq. No.
                  LIB3272-045-P1-K1-F5
Seq. ID
                   BLASTX
Method
                   g113116
NCBI GI
                   443
BLAST score
                   5.0e-44
E value
                   143
Match length
                   59
% identity
                  ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)
NCBI Description
                   >gi_111396_pir__A35007 ATP citrate (pro-S)-lyase (EC
                   4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase
                   [Rattus norvegicus]
                   234936
Seq. No.
                   LIB3272-045-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   g2369766
NCBI GI
BLAST score
                   198
                   5.0e-33
E value
Match length
                   115
% identity
                   49
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
Seq. No.
                   234937
                   LIB3272-045-P1-K1-G1
Seq. ID
```

33983



220 BLAST score 6.0e-18E value 80 Match length 59 % identity

TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR NCBI Description

>gi 99767\_pir\_\_A31393 tryptophan synthase (EC 4.2.1.20) beta chain - Arabidopsis thaliana >gi 166892 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]

234938 Seq. No.

LIB3272-045-P1-K1-G12 Seq. ID

Method BLASTX g629483 NCBI GI BLAST score 326 3.0e-30 E value 125 Match length 54 % identity

gene 1-Sc3 protein - European white birch NCBI Description

>gi 534898 emb CAA54696\_ (X77601) 1 Sc-3 [Betula pendula]

>gi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula

pendula]

234939 Seq. No.

LIB3272-045-P1-K1-G5 Seq. ID

Method BLASTX NCBI GI g1220196 BLAST score 547 E value 3.0e-56115 Match length 89 % identity

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

234940 Seq. No.

LIB3272-045-P1-K1-G8 Seq. ID

Method BLASTX NCBI GI g2160166 BLAST score 332 E value 3.0e - 31104 Match length % identity 63

(AC000132) No definition line found [Arabidopsis thaliana] NCBI Description

Seq. No. 234941

LIB3272-045-P1-K1-H1 Seq. ID

Method BLASTX NCBI GI q3659909 BLAST score 543 E value 1.0e-55 Match length 138 % identity

NCBI Description (AF020715) histidyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 234942

LIB3272-045-P1-K1-H10 Seq. ID

Method BLASTX NCBI GI g70642 BLAST score 420



```
E value
                   2.0e-41
Match length
                   90
                   20
% identity
                   ubiquitin precursor - Arabidopsis thaliana
NCBI Description
                   >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382)
                   [Arabidopsis thaliana] >gi 987519 (U33014) polyubiquitin
                   [Arabidopsis thaliana] >gi_226499_prf__1515347A
                   poly-ubiquitin [Arabidopsis thaliana]
                   234943
Seq. No.
                   LIB3272-045-P1-K1-H2
Seq. ID
Method
                   BLASTX
                   g4468979
NCBI GI
                   506
BLAST score
E value
                   2.0e-51
Match length
                   107
% identity
                   86
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]
                   234944
Seq. No.
                   LIB3272-045-P1-K1-H3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3122388
                   402
BLAST score
                   2.0e-39
E value
Match length
                   102
% identity
                   42
NCBI Description WD-40 REPEAT PROTEIN MSI2 >gi_2394231 (AF016847) WD-40
                   repeat protein [Arabidopsis thaliana]
                   234945
Seq. No.
                   LIB3272-045-P1-K1-H5
Seq. ID
Method
                   BLASTX
                   g3378491
NCBI GI
                   293
BLAST score
                   1.0e-26
E value
Match length
                   99
*% identity
                   58
NCBI Description (AJ007578) pRIB5 protein [Ribes nigrum]
                   234946
Seq. No.
                   LIB3272-045-P1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1166450
BLAST score
                   262
                   7.0e-23
E value
                   64
Match length
 % identity
                   78
NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]
```

234947 Seq. No.

LIB3272-045-P1-K1-H7 Seq. ID

Method BLASTX NCBI GI g3122785 BLAST score 457 8.0e-46 E value 99 Match length

NCBI Description



```
% identity
                   92
NCBI Description
                  40S RIBOSOMAL PROTEIN S14 >gi 2565340 (AF026079) ribosomal
                  protein S14 [Lupinus luteus]
                  234948
Seq. No.
                  LIB3272-045-P1-K1-H9
Seq. ID
Method
                  BLASTX
                  g3320120
NCBI GI
                  158
BLAST score
                  9.0e-11
E value
                  98
Match length
% identity
                  34
                  (U66669) 3-hydroxyisobutyryl-coenzyme A hydrolase [Homo
NCBI Description
                  sapiens]
Seq. No.
                  234949
                  LIB3272-046-P1-K1-A11
Seq. ID
Method
                  BLASTX
                   a3721540
NCBI GI
BLAST score
                   295
                   1.0e-26
E value
                  104
Match length
% identity
                   63
                  (D83583) Sulfite Reductase [Nicotiana tabacum]
NCBI Description
                  >gi 3738234 dbj BAA33796 (AB010717) sulfite reductase
                   [Nicotiana tabacum]
Seq. No.
                   234950
Seq. ID
                  LIB3272-046-P1-K1-A12
Method
                  BLASTX
NCBI GI
                   g2388570
BLAST score
                   149
E value
                   2.0e-09
                   110
Match length
% identity
                   36
                  (AC000098) YUP8H12.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   234951
                  LIB3272-046-P1-K1-A2
Seq. ID
                  BLASTX
Method
                   g2191131
NCBI GI
BLAST score
                   188
E value
                   2.0e-14
Match length
                   55
                   67
% identity
NCBI Description (AF007269) A_IG002N01.8 gene product [Arabidopsis thaliana]
                   234952
Seq. No.
                   LIB3272-046-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2924520
BLAST score
                   500
E value
                   1.0e-50
Match length
                   124
% identity
                   79
```

33986

[Arabidopsis thaliana]

(AL022023) plasma membrane intrinsic protein (SIMIP)

Seq. ID Method



```
Seq. No.
                  234953
                  LIB3272-046-P1-K1-A5
Seq. ID
Method
                  BLASTX
                  g1838976
NCBI GI
BLAST score
                  279
                  9.0e-25
E value
Match length
                  147
                  43
% identity
                  (X73635) vsf-1 [Lycopersicon esculentum]
NCBI Description
                  234954
Seq. No.
                  LIB3272-046-P1-K1-A6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3236253
BLAST score
                   658
                   3.0e-69
E value
Match length
                   143
% identity
                   85
                   (AC004684) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   234955
                   LIB3272-046-P1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g433970
BLAST score
                   128
E value
                   9.0e-16
Match length
                   116
% identity
                  (Z28649) polyubiquitin [Acetabularia cliftonii]
NCBI Description
                   234956
Seq. No.
                   LIB3272-046-P1-K1-B10
Seq. ID
                   BLASTX
Method
                   g1545805
NCBI GI
                   157
BLAST score
E value
                   4.0e-11
                   51
Match length
% identity
                   65
NCBI Description (D64052) cytochrome P450 like TBP [Nicotiana tabacum]
                   234957
Seq. No.
                   LIB3272-046-P1-K1-B11
Seq. ID
Method
                   BLASTX
                   g303730
NCBI GI
                   533
BLAST score
                   2.0e-54
E value
                   121
Match length
                   86
% identity
                   (D12540) GTP-binding protein [Pisum sativum]
NCBI Description
                   >gi_738933_prf__2001457A GTP-binding protein [Pisum
                   sativum]
Seq. No.
                   234958
```

33987

LIB3272-046-P1-K1-B12

BLASTX



```
g3024020
NCBI GI
                  627
BLAST score
E value
                  1.0e-65
Match length
                  133
% identity
                  89
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation
                  factor 5A3 [Solanum tuberosum]
Seq. No.
                  234959
Seq. ID
                  LIB3272-046-P1-K1-B4
Method
                  BLASTX
                  q3851636
NCBI GI
BLAST score
                  551
E value
                  7.0e-60
                  146
Match length
                  79
% identity
                  (AF098519) unknown [Avicennia marina] >gi_4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
Seq. No.
                  234960
                  LIB3272-046-P1-K1-B5
Seq. ID
Method
                  BLASTX
                  q3868758
NCBI GI
                   397
BLAST score
E value
                   1.0e-38
                   99
Match length
                   74
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                   234961
                   LIB3272-046-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120669
BLAST score
                   460
E value
                   5.0e-46
                   98
Match length
% identity
                   88
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >qi 66014 pir DEJMG glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi 19566 emb CAA42905 (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
                   234962
Seq. No.
Seq. ID
                   LIB3272-046-P1-K1-C10
Method .
                   BLASTX
NCBI GI
                   g2129871
BLAST score
                   181
E value
                   3.0e-13
Match length
                   82
                   51
% identity
NCBI Description proline-rich protein, 14K - kidney bean >gi_1420885
                   (U34333) proline-rich 14 kDa protein [Phaseolus vulgaris]
```

Seq. No. 234963

Seq. ID LIB3272-046-P1-K1-C11



```
Method
                  BLASTX
NCBI GI
                  g1172811
                  565
BLAST score
                   2.0e-64
E value
                  130
Match length
                  95
% identity
                  60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)
NCBI Description
                  >gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic
                   - rice >gi 575355 emb CAA57339 (X81691) putative tumor
                  suppresser [Oryza sativa]
                  234964
Seq. No.
                  LIB3272-046-P1-K1-C12
Seq. ID
                  BLASTX
Method
NCBI GI
                   g167367
BLAST score
                   573
                   3.0e-59
E value
Match length
                   134
                   85
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                   234965
Seq. No.
                  LIB3272-046-P1-K1-C3
Seq. ID
                  BLASTX
Method
                   g2982259
NCBI GI
BLAST score
                   385
                   2.0e-37
E value
Match length
                   95
                   78
% identity
                  (AF051212) probable 60s ribosomal protein L13a [Picea
NCBI Description
                   mariana]
                   234966
Seq. No.
                   LIB3272-046-P1-K1-C5
Seq. ID
Method
                   BLASTX
                   g3096949
NCBI GI
BLAST score
                   246
E value
                   6.0e-21
                   139
Match length
% identity
                  (Y16328) putative cyclic nucleotide-regulated ion channel
NCBI Description
                   [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic
                   nucleotide-gated cation channel [Arabidopsis thaliana]
                   234967
Seq. No.
                   LIB3272-046-P1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1321627
BLAST score
                   145
                   3.0e-09
E value
                   49
Match length
                   57
% identity
```

(D83656) thylakoid-bound ascorbate peroxidase [Cucurbita NCBI Description

sp.]

234968 Seq. No.

Seq. ID LIB3272-046-P1-K1-C7



```
Method BLASTX
NCBI GI g1170747
BLAST score 322
E value 6.0e-30
Match length 67
% identity 99
NCBI Description LATE EMB
(M88324)
hirsutum
```

LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi\_167345 (M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >qi 167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

 Seq. No.
 234969

 Seq. ID
 LIB3272-046-P1-K1-C9

 Method
 BLASTX

 NCBI GI
 g3450889

 BLAST score
 383

 E value
 3.0e-39

Match length 136 % identity 68

NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

 Seq. No.
 234970

 Seq. ID
 LIB3272-046-P1-K1-D12

 Method
 BLASTX

 NCBI GI
 g1170747

 BLAST score
 403

BLAST score 403 E value 3.0e-39 Match length 92 % identity 85

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi\_167345 (M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi\_167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 234971

Seq. ID LIB3272-046-P1-K1-D4

Method BLASTX
NCBI GI g322867
BLAST score 631
E value 5.0e-66
Match length 146
% identity 82

NCBI Description translation initiation factor eIF-4F isozyme form subunit

p82 - wheat

Seq. No. 234972

Seq. ID LIB3272-046-P1-K1-D5

Method BLASTX
NCBI GI g3953471
BLAST score 410
E value 4.0e-40
Match length 142
% identity 59

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 234973

Seq. ID LIB3272-046-P1-K1-D6

33990



```
Method
                  BLASTX
NCBI GI
                   g2088651
BLAST score
                   276
                   2.0e-24
E value
Match length
                   125
% identity
                   (AF002109) hypersensitivity-related gene 201 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   234974
Seq. No.
                   LIB3272-046-P1-K1-D7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3901014
BLAST score
                   234
                   1.0e-19
E value
                   55
Match length
                   76
% identity
                  (AJ130886) metallothionein-like protein class II [Fagus
NCBI Description
                   sylvatica]
                   234975
Seq. No.
                  LIB3272-046-P1-K1-D8
Seq. ID
                   BLASTX
Method
                   g3915031
NCBI GI
                   453
BLAST score
                   3.0e-45
E value
                   128
Match length
                   70
% identity
NCBI Description
                  ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                   (STEAROYL-ACP DESATURASE) >gi 1217628 emb CAA65232
                   (X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase
                   [Gossypium hirsutum]
Seq. No.
                   234976
Seq. ID
                   LIB3272-046-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g1065515
BLAST score
                   188
E value
                   4.0e-14
Match length
                   79
% identity
                   44
                  (U40420) weak similarity to procollagen alpha chain 1(V)
NCBI Description
                   chain [Caenorhabditis elegans]
Seq. No.
                   234977
                  · LIB3272-046-P1-K1-E10
Seq. ID
Method
                   BLASTX
                   g131754
NCBI GI
BLAST score
                   308
                   4.0e-28
E value
Match length
                   126
% identity
                   46
NCBI Description PPLZ02 PROTEIN >gi_99973_pir__S11881 hypothetical protein
                   (clone pPLZ2) - large-leaved lupine >gi_19507_emb_CAA36069_
```

polyphyllus]

(X51767) put. pPLZ2 product (AA 1-164) [Lupinus

Seq. ID Method

NCBI GI



```
234978
Seq. No.
                  LIB3272-046-P1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g285741
BLAST score
                  378
                  2.0e-36
E value
                  113
Match length
                  65
% identity
                 (D14550) EDGP precursor [Daucus carota]
NCBI Description
                  234979
Seq. No.
                  LIB3272-046-P1-K1-E4
Seq. ID
                  BLASTX
Method
                  g1917019
NCBI GI
                  553
BLAST score
                  5.0e-59
E value
Match length
                  129
% identity
                  85
                 (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
                  234980
Seq. No.
                  LIB3272-046-P1-K1-E6
Seq. ID
                  BLASTX
Method
                  g3023195
NCBI GI
                   442
BLAST score
E value
                   5.0e-44
Match length
                  112
% identity
                   78
NCBI Description 14-3-3-LIKE PROTEIN B (SGF14B) >gi_1575727 (U70534) SGF14B
                   [Glycine max]
                   234981
Seq. No.
                  LIB3272-046-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   g303730
NCBI GI
BLAST score
                   519
E value
                   6.0e-53
Match length
                   118
                   86
% identity
                   (D12540) GTP-binding protein [Pisum sativum]
NCBI Description
                   >gi_738933_prf__2001457A GTP-binding protein [Pisum
                   sativum]
                   234982
Seq. No.
                   LIB3272-046-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q228404
BLAST score
                   560
E value
                   1.0e-57
                   126
Match length
% identity
                   78
NCBI Description alpha amylase [Vigna radiata]
Seq. No.
                   234983
```

33992

LIB3272-046-P1-K1-F1

BLASTX

q122770



BLAST score 582 E value 3.0e-60 Match length 137 % identity 83

NCBI Description HEMOGLOBIN II >gi\_99509\_pir\_\_S13378 hemoglobin II - swamp oak >gi\_18015\_emb\_CAA37898\_ (X53950) hemoglobin [Casuarina

glauca]

Seq. No. 234984

Seq. ID LIB3272-046-P1-K1-F10

Method BLASTX
NCBI GI g3668082
BLAST score 292
E value 3.0e-26
Match length 115
% identity 55

NCBI Description (AC004667) putative DAL1 protein [Arabidopsis thaliana]

Seq. No. 234985

Seq. ID LIB3272-046-P1-K1-F2

Method BLASTX
NCBI GI g3341695
BLAST score 537
E value 5.0e-55
Match length 147
% identity 67

NCBI Description (AC003672) putative thiamin pyrophosphokinase [Arabidopsis

thaliana]

Seq. No. 234986

Seq. ID LIB3272-046-P1-K1-F4

Method BLASTX
NCBI GI g3660467
BLAST score 398
E value 9.0e-39
Match length 103
% identity 78

NCBI Description (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis

thaliana]

Seq. No. 234987

Seq. ID LIB3272-046-P1-K1-F6

Method BLASTX
NCBI GI g1709498
BLAST score 528
E value 5.0e-54
Match length 120
% identity 79

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

>gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis

thaliana >gi\_887390\_emb\_CAA61411\_ (X89008) osmotin

[Arabidopsis thaliana]

Seq. No. 234988

Seq. ID LIB3272-046-P1-K1-F9

Method BLASTX NCBI GI g3550985

```
BLAST score
                   247
E value
                   3.0e-21
                   83
Match length
                   54
% identity
                  (AB010740) OsS5a [Oryza sativa]
NCBI Description
                   234989
Seq. No.
                  LIB3272-046-P1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3980393
BLAST score
                   287
                   1.0e-25
E value
                   89
Match length
                   58
% identity
                   (AC004561) putative glutathione S-transferase [Arabidopsis
NCBI Description
                   thaliana]
                   234990
Seq. No.
                  LIB3272-046-P1-K1-G3
Seq. ID
                  BLASTX
Method
                   g1173218
NCBI GI
BLAST score
                   212
                   4.0e-27
E value
                   78
Match length
                   87
% identity
NCBI Description
                   234991
Seq. No.
```

40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)

cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

LIB3272-046-P1-K1-G6 Seq. ID

Method BLASTX g4158232 NCBI GI BLAST score 612 E value 7.0e-64Match length 129

% identity 88

NCBI Description (Y18626) reversibly glycosylated polypeptide [Triticum

aestivum]

Seq. No. 234992

Seq. ID LIB3272-046-P1-K1-G7

Method BLASTX NCBI GI g119150 BLAST score 242 E value 8.0e-25 Match length 89 % identity 66

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

>gi\_82081\_pir\_\_S10507 translation elongation factor eEF-1 alpha chain - tomato >gi 19273 emb CAA32618 (X14449) EF

1-alpha (AA 1-448) [Lycopersicon esculentum]

>gi 295810 emb CAA37212 (X53043) elongation factor 1-alpha

[Lycopersicon esculentum]

Seq. No. 234993

Seq. ID LIB3272-046-P1-K1-G8



```
Method
                  BLASTX
                  g543905
NCBI GI
BLAST score
                  392
E value
                  5.0e-38
Match length
                  125
                  63
% identity
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
                  brassinosteroid-regulated protein [Glycine max]
                  234994
Seq. No.
                  LIB3272-046-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539335
BLAST score
                  312
                 1.0e-28
E value
Match length
                  144
                  46
% identity
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
                  234995
Seq. No.
Seq. ID
                  LIB3272-046-P1-K1-H11
Method
                  BLASTX
                  g3935152
NCBI GI
                  471
BLAST score
E value
                  3.0e-47
Match length
                  124
% identity
                  69
NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]
                  234996
Seq. No.
                  LIB3272-046-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3551838
BLAST score
                  521
E value
                  3.0e-53
Match length
                  120
% identity
NCBI Description (AF070967) SKP1-like protein [Nicotiana clevelandii]
Seq. No.
                  234997
                  LIB3272-046-P1-K1-H4
Seq. ID
Method
                  BLASTX
                  g1155261
NCBI GI
BLAST score
                  367
E value
                  2.0e-42
Match length
                  113
% identity
NCBI Description
                  (U40217) eukaryotic release factor 1 homolog [Arabidopsis
                  thaliana]
Seq. No.
                  234998
Seq. ID
                  LIB3272-046-P1-K1-H5
Method
                  BLASTX
```

NCBI GI g2529229
BLAST score 441
E value 9.0e-44
Match length 106

```
% identity
                  (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
                  234999
Seq. No.
                  LIB3272-046-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3935152
                  249
BLAST score
                  1.0e-21
E value
                  82
Match length
                  59
% identity
NCBI Description
                 (AC005106) T25N20.16 [Arabidopsis thaliana]
Seq. No.
                  235000
Seq. ID
                  LIB3272-047-P1-K1-A11
Method
                  BLASTX
                  q112697
NCBI GI
BLAST score
                  299
                   3.0e-27
E value
Match length
                  108
% identity
                   61
                  14 KD PROLINE-RICH PROTEIN DC2.15 PRECURSOR
NCBI Description
                  >gi 486809 pir S35714 proline-rich protein, 14K, embryonic
                   - carrot >gi_18316_emb_CAA33476_ (X15436) 14 kD protein (AA
                   1-137) [Daucus carota]
Seq. No.
                   235001
Seq. ID
                  LIB3272-047-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q3702327
BLAST score
                  241
                  2.0e-20
E value
                  119
Match length
% identity
                  51
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                   235002
Seq. No.
                  LIB3272-047-P1-K1-A3
Seq. ID
Method
                  BLASTX
                  g1708462
NCBI GI
                  525
BLAST score
                  1.0e-53
E value
Match length
                  132
                   73
% identity
NCBI Description IAA-AMINO ACID HYDROLASE HOMOLOG 2 PRECURSOR >gi 902791
                   (U23796) ILL2 [Arabidopsis thaliana]
                   235003
Seq. No.
                   LIB3272-047-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3868758
BLAST score
                   423
                   9.0e-42
E value
                   102
Match length
```

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

76

% identity



```
Seq. No.
                   235004
                   LIB3272-047-P1-K1-A7
Seq. ID
Method
                   BLASTX
                   q3395423
NCBI GI
BLAST score
                   300
                   3.0e-27
E value
Match length
                   117
% identity
                   56
                   (AC004683) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >qi 3786023 (AC005499) putative protein kinase [Arabidopsis
                   thaliana]
                   235005
Seq. No.
                   LIB3272-047-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3319882
BLAST score
                   496
                   3.0e-50
E value
Match length
                   101
                   92
% identity
                   (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                   arietinum]
                   235006
Seq. No.
                   LIB3272-047-P1-K1-A9
Seq. ID
                   BLASTX
Method
                   g1709498
NCBI GI
BLAST score
                   506
E value
                   2.0e-51
                   109
Match length
                   83
% identity
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                   >gi 1362001_pir S57524 osmotin precursor - Arabidopsis
                   tha\overline{l}iana >g\overline{l}_88\overline{73}90_emb_CAA61411_ (X89008) osmotin
                   [Arabidopsis thaliana]
                   235007
Seq. No.
                   LIB3272-047-P1-K1-B1
Seq. ID
Method
                   BLASTX
                   g2982331
NCBI GI
BLAST score
                   578
                   6.0e-60
E value
                   118
Match length
                   97
% identity
NCBI Description (AF051251) TAT-binding protein homolog [Picea mariana]
                   235008
Seq. No.
                   LIB3272-047-P1-K1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1737492
                   407
BLAST score
```

6.0e-40E value Match length 103 % identity

(U81318) poly(A)-binding protein [Triticum aestivum] NCBI Description

235009 Seq. No.

Seq. ID Method

```
Seq. ID
                  LIB3272-047-P1-K1-B2
                  BLASTX
Method
NCBI GI
                  q3126967
                  146
BLAST score
                  1.0e-19
E value
Match length
                  83
% identity
                  11
NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]
Seq. No.
                  235010
                  LIB3272-047-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3386621
BLAST score
                  514
                   2.0e-52
E value
Match length
                  109
% identity
                   91
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
                   235011
Seq. No.
                  LIB3272-047-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1352316
BLAST score
                  422
                   1.0e-41
E value
Match length
                  87
                   92
% identity
                  DR1 PROTEIN HOMOLOG >gi 633026 dbj BAA07288 (D38110) Dr1
NCBI Description
                   [Arabidopsis thaliana]
                   235012
Seq. No.
                   LIB3272-047-P1-K1-B6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3334115
BLAST score
                   602
                   9.0e-63
E value
Match length
                   126
% identity
                   49
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi 2463664
                   (AF006489) adenine nucleotide translocator 1 [Gossypium
                   hirsutum]
Seq. No.
                   235013
                   LIB3272-047-P1-K1-B7
Seq. ID
Method
                   BLASTX
                   g2688824
NCBI GI
                   382
BLAST score
E value
                   6.0e-37
Match length
                   103
% identity
                   76
                  (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                   armeniaca]
                   235014
Seq. No.
```

33998

LIB3272-047-P1-K1-B8

BLASTX



g4126401 NCBI GI BLAST score 468 E value 5.0e-47Match length 106 % identity 85 NCBI Description (AB011795) flavanone 3-hydroxylase [Citrus sinensis] 235015 Seq. No. LIB3272-047-P1-K1-B9 Seq. ID Method BLASTX g1350956 504 3.0e-51

NCBI GI BLAST score E value 106 Match length 93 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S20 (S22)

235016 Seq. No.

LIB3272-047-P1-K1-C1 Seq. ID

Method BLASTX NCBI GI g3885340 BLAST score 166 1.0e-23 E value 90 Match length % identity 68

NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 235017

Seq. ID LIB3272-047-P1-K1-C10

Method BLASTX NCBI GI q1170938 BLAST score 495 3.0e-50 E value 99 Match length 92 % identity

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi\_481566\_pir\_\_S38875 methionine adenosyltransferase (EC

2.5.1.6) - tomato >gi\_429106\_emb\_CAA80866\_ (Z24742) S-adenosyl-L-methionine synthetase [Lycopersicon

esculentum]

Seq. No. 235018

LIB3272-047-P1-K1-C11 Seq. ID

Method BLASTX NCBI GI q3868758 BLAST score 418 E value 4.0e-41 Match length 101 % identity 75

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

235019 Seq. No.

Seq. ID LIB3272-047-P1-K1-C12

Method BLASTX NCBI GI q1903364 BLAST score 362

Match length

% identity

89 51





```
E value
                  9.0e-35
                  100
Match length
% identity
                  70
                  (AC000104) EST gb T45093 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  235020
Seq. No.
                  LIB3272-047-P1-K1-C2
Seq. ID
                  BLASTX
Method
                  g4455169
NCBI GI
                  306
BLAST score
                  4.0e-28
E value
Match length
                  116
% identity
                  53
NCBI Description (AL035521) putative aldehyde dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  235021
                  LIB3272-047-P1-K1-C3
Seq. ID
Method
                  BLASTX
                  g1166450
NCBI GI
BLAST score
                  295
E value
                  1.0e-26
Match length
                  63
% identity
                  84
NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]
Seq. No.
                  235022
Seq. ID
                  LIB3272-047-P1-K1-C7
                  BLASTX
Method
NCBI GI
                  g3183207
                  371
BLAST score
E value
                  1.0e-35
                  119
Match length
                  55
% identity
NCBI Description HYPOTHETICAL PROTEIN KIAA0017 >gi_285999_dbj_BAA02805_
                  (D13642) KIAA0017 [Homo sapiens]
                  235023
Seq. No.
                  LIB3272-047-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244979
BLAST score
                  402
                  3.0e - 39
E value
                  118
Match length
% identity
                  (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  235024
Seq. ID
                  LIB3272-047-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g1172995
                  213
BLAST score
                  4.0e-17
E value
```

34000

Match length

```
NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi_1083790_pir__S52084 ribosomal
                    protein L22 - rat >gi_710295_emb_CAA55204_ (X78444) ribosomal protein L22 [Rattus norvegicus]
                    >gi 1093952_prf__2105193A ribosomal protein L22 [Rattus
                    norvegicus]
                    235025
Seq. No.
                    LIB3272-047-P1-K1-D2
Seq. ID
                    BLASTX
Method
                    g549063
NCBI GI
                    336
BLAST score
                    2.0e-31
E value
                    105
Match length
% identity
                    64
                    TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                    >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                    21kd polypeptide [Oryza sativa]
                    235026
Seq. No.
                    LIB3272-047-P1-K1-D3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2286153
BLAST score
                    538
                    3.0e-55
E value
                    109
Match length
                    99
% identity
NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                    235027
Seq. No.
                    LIB3272-047-P1-K1-D4
Seq. ID
                    BLASTX
Method
                    g3738302
NCBI GI
BLAST score
                    351
                    3.0e - 33
E value
                    123
Match length
                    54
% identity
                    (AC005309) tubby-like protein [Arabidopsis thaliana]
NCBI Description
                    >gi_4249398 (AC006072) putative tubby protein [Arabidopsis
                    thaliana]
                     235028
Seq. No.
                    LIB3272-047-P1-K1-D5
Seq. ID
Method
                    BLASTX
                     g231536
NCBI GI
                     314
BLAST score
E value
                     5.0e-29
                    95
```

67 % identity CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) NCBI Description (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi\_99683\_pir\_\_S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana

>gi\_16394\_emb\_CAA45040\_ (X63444) leucine aminopeptidase
[Arabidopsis thaliana] >gi\_4115380 (AC005967) putative

leucine aminopeptidase [Arabidopsis thaliana]



```
235029
 Seq. No.
                   LIB3272-047-P1-K1-D6
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2286153
 BLAST score
                   554
                   4.0e-57
 E value
                   112
 Match length
                   99
 % identity
 NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
                   235030
 Seq. No.
                   LIB3272-047-P1-K1-D7
 Seq. ID
                   BLASTX
 Method
                   g1864017
 NCBI GI
 BLAST score
                   313
                   4.0e-55
 E value
                   123
 Match length
                   89
 % identity
 NCBI Description (D63396) elongation factor-1 alpha [Nicotiana tabacum]
                   235031
 Seq. No.
                   LIB3272-047-P1-K1-D8
 Seq. ID
Method
                   BLASTX
                   g3024020
 NCBI GI
 BLAST score
                   498
                   1.0e-50
E value
 Match length
                   104
                   89
 % identity
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
 NCBI Description
                   >gi_2225881_dbj_BAA20877_ (AB004824) eukaryotic initiation
                   factor 5A3 [Solanum tuberosum]
                   235032
 Seq. No.
                   LIB3272-047-P1-K1-D9
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g4128197
 BLAST score
                   172
                   3.0e-14
 E value
 Match length
                   65
 % identity
                   62
 NCBI Description (U75273) acyl-CoA binding protein [Arabidopsis thaliana]
                   235033
 Seq. No.
                   LIB3272-047-P1-K1-E10
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q1313972
 BLAST score
                   294
 E value
                    1.0e-26
 Match length
                   118
                   53
 % identity
 NCBI Description (Z72428) major allergen Mal d1 [Malus domestica]
 Seq. No.
                    235034
                   LIB3272-047-P1-K1-E11
 Seq. ID
```

Method BLASTX

NCBI GI g2935298 BLAST score 622



```
E value
                  4.0e-65
Match length
                  125
                  98
% identity
NCBI Description
                  (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
                  1 [Gossypium hirsutum]
                  235035
Seq. No.
Seq. ID
                  LIB3272-047-P1-K1-E2
                  BLASTX
Method
                  g2662310
NCBI GI
BLAST score
                  363
                  1.0e-34
E value
Match length
                  113
% identity
                  62
NCBI Description (AB009307) bpw1 [Hordeum vulgare]
Seq. No.
                  235036
                  LIB3272-047-P1-K1-E3
Seq. ID
Method
                  BLASTX
                  q1710401
NCBI GI
BLAST score
                  532
                  2.0e-54
E value
                  114
Match length
                  87
% identity
NCBI Description RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN
                   (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT)
                  >gi_1044912_emb_CAA63194_ (X92443) ribonucleotide reductase
                  R2 [Nicotiana tabacum]
Seq. No.
                   235037
                  LIB3272-047-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2695711
BLAST score
                   395
E value
                   2.0e-38
Match length
                  116
                   60
% identity
NCBI Description (AJ001370) cytochome b5 [Olea europaea]
Seq. No.
                   235038
Seq. ID
                  LIB3272-047-P1-K1-E5
Method
                  BLASTX
NCBI GI
                   g2980770
BLAST score
                   324
E value
                   4.0e-30
Match length
                   126
% identity
                   56
NCBI Description (AL022198) putative protein kinase [Arabidopsis thaliana]
                   235039
Seq. No.
                  LIB3272-047-P1-K1-E7
Seq. ID
Method
                  BLASTX
                  g3445207
NCBI GI
                   160
BLAST score
                   7.0e-11
E value
```

34003

93

42

Match length

% identity



```
NCBI Description (AC004786) unknown protein [Arabidopsis thaliana]
Seq. No.
                  235040
Seq. ID
                  LIB3272-047-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2980793
BLAST score
                  479
E value
                  3.0e-48
Match length
                  123
                  72
% identity
NCBI Description (AL022197) putative protein [Arabidopsis thatiana]
Seq. No.
                  235041
Seq. ID
                  LIB3272-047-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q508304
BLAST score
                  234
E value
                  1.0e-19
Match length
                  56
% identity
                  79
NCBI Description (L22305) corC [Medicago sativa]
Seq. No.
                  235042
Seq. ID
                  LIB3272-047-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3694872
BLAST score
                  415
E value
                  8.0e-41
Match length
                  102
% identity
                  77
                 (AF092547) profilin [Ricinus communis]
NCBI Description
                  235043
Seq. No.
                  LIB3272-047-P1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1531672
BLAST score
                  630
                  4.0e-66
E value
Match length
                  120
% identity
                  97
                 (U68461) actin [Striga asiatica]
NCBI Description
                  235044
Seq. No.
Seq. ID
                  LIB3272-047-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g112972
BLAST score
                  451
E value
                  5.0e-45
Match length
                  128
                  70
% identity
                  ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
NCBI Description
                  >gi 167546 (M92660) aspartate aminotransferase [Daucus
                  carota] >gi_445587 prf_ 1909339A Asp aminotransferase
                   [Daucus carota]
```

Seq. No. 235045

Seq. ID LIB3272-047-P1-K1-F7

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g3421123
BLAST score
                  437
E value
                  2.0e-43
Match length
                  94
                  86
% identity
NCBI Description
                  (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis
                  thalianal
Seq. No.
                  235046
Seq. ID
                  LIB3272-047-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q125887
BLAST score
                  171
E value
                  2.0e-12
Match length
                  93
% identity
                  44
NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                  >gi 82092 pir S04765 LAT52 protein precursor - tomato
                  >gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon
                  esculentum]
Seq. No.
                  235047
Seq. ID
                  LIB3272-047-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g484656
BLAST score
                  569
E value
                  7.0e-59
Match length
                  125
% identity
                  88
NCBI Description
                  monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
                  cucumber >gi 452165 dbj BAA05408 (D26392)
                  monodehydroascorbate reductase [Cucumis sativus]
Seq. No.
                  235048
Seq. ID
                  LIB3272-047-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  416
E value
                  6.0e-41
Match length
                  83
% identity
                  93
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  235049
Seq. No.
Seq. ID
                  LIB3272-047-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g4490705
BLAST score
                  508
E value
                  1.0e-51
Match length
                  113
% identity
NCBI Description
                  (AL035680) ribosomal protein L14-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  235050
```

34005

LIB3272-047-P1-K1-G6



Method BLASTX NCBI GI q1170747 BLAST score 285 1.0e-25 E value Match length 70 81 % identity LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345 NCBI Description (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi\_167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 235051 Seq. ID LIB3272-047-P1-K1-H1

Method BLASTX
NCBI GI g3249066
BLAST score 457
E value 1.0e-45
Match length 123
% identity 74

NCBI Description (AC004473) Similar to S. cerevisiae SIK1P protein

gb\_984964. ESTs gb\_F15433 and gb\_AA395158 come from this

gene. [Arabidopsis thaliana]

Seq. No. 235052

Seq. ID LIB3272-047-P1-K1-H10

Method BLASTX
NCBI GI g3219269
BLAST score 590
E value 2.0e-61
Match length 126
% identity 88

NCBI Description (AB015314) MAP kinase kinase 3 [Arabidopsis thaliana]

Seq. No. 235053

Seq. ID LIB3272-047-P1-K1-H12

Method BLASTX
NCBI GI g4193388
BLAST score 220
E value 3.0e-18
Match length 52

% identity 85
NCBI Description (AF091455) translationally controlled tumor protein [Hevea

brasiliensis]

Seq. No. 235054

Seq. ID LIB3272-047-P1-K1-H4

Method BLASTX
NCBI GI 94530585
BLAST score 357
E value 5.0e-34
Match length 85
% identity 74

NCBI Description (AF130978) B12D protein [Ipomoea batatas]

Seq. No. 235055

Seq. ID LIB3272-047-P1-K1-H5

Method BLASTX

34006



```
NCBI GI
                   q167367
BLAST score
                   461
                   3.0e-46
E value
Match length
                   120
                   75
% identity
                  (L08199) peroxidase [Gossypium hirsutum]
NCBI Description
                  235056
Seq. No.
Seq. ID
                  LIB3272-047-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g1922938
BLAST score
                   189
E value
                   2.0e-14
Match length
                  105
% identity
                   39
NCBI Description
                  (AC000106) Similar to Caenorhabditis hypothetical protein
                  CO7A9.11 (gb Z29094). [Arabidopsis thaliana]
                   235057
Seq. No.
                  LIB3272-047-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1332579
BLAST score
                   420
E value
                   4.0e-45
Match length
                  107
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                   235058
Seq. No.
                  LIB3272-048-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q232031
BLAST score
                   197
                   2.0e-15
E value
Match length
                   77
% identity
                   52
                  ELONGATION FACTOR 1 BETA' >gi_322851_pir__$29224
NCBI Description
                   translation elongation factor eEF-1 beta chain - rice
                   >gi 218161 dbj BAA02253 (D12821) elongation factor 1 beta'
                   [Oryza sativa]
Seq. No.
                   235059
Seq. ID
                   LIB3272-048-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g1353193
BLAST score
                   175
E value
                   9.0e-13
Match length
                   100
% identity
                   45
NCBI Description
                  O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268
                  O-methyltransferase (EC 2.1.1.-) - maize >gi 404070
                   (L14063) O-methyltransferase [Zea mays]
Seq. No.
                   235060
```

Seq. ID LIB3272-048-P1-K1-A12 Method

BLASTX NCBI GI g2499945



BLAST score 434
E value 5.0e-43
Match length 126
% identity 66
NCBI Description URIDINE
PHOSPHOLOGY
DECARBOL

URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE

DECARBOXYLASE >gi\_1076363\_pir\_\_S46440 orotate

phosphoribosyltransferase (EC 2.4.2.10) /

orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi 443818 emb CAA50686 (X71842)

pyrE-F [Arabidopsis thaliana]

Seq. No. 235061

Seq. ID LIB3272-048-P1-K1-A2

Method BLASTX
NCBI GI g2244835
BLAST score 301
E value 1.0e-27
Match length 139
% identity 52

NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]

Seq. No. 235062

Seq. ID LIB3272-048-P1-K1-A6

Method BLASTX
NCBI GI g1345787
BLAST score 543
E value 9.0e-56
Match length 109
% identity 94

NCBI Description CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2)

>gi\_567937\_dbj\_BAA05641\_ (D26594) chalcone synthase

[Camellia sinensis]

Seq. No. 235063

Seq. ID LIB3272-048-P1-K1-A9

Method BLASTX
NCBI GI g2826882
BLAST score 431
E value 1.0e-42
Match length 90
% identity 92

NCBI Description (AJ223634) transcription factor IIA small subunit

[Arabidopsis thaliana]

Seq. No. 235064

Seq. ID LIB3272-048-P1-K1-B10

Method BLASTX
NCBI GI g4415936
BLAST score 146
E value 2.0e-09
Match length 78
% identity 51

NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]

Seq. No. 235065

Seq. ID LIB3272-048-P1-K1-B11



```
Method
                   BLASTX
NCBI GI
                   g3386615
BLAST score
                   496
                   3.0e-50
E value
Match length
                   117
% identity
                   83
NCBI Description
                   (AC004665) putative phosphomannomutase [Arabidopsis
                   thaliana]
                   235066
Seq. No.
                  LIB3272-048-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3063396
BLAST score
                   506
E value
                   2.0e-51
Match length
                  113
% identity
                   84
NCBI Description
                  (AB012947) vcCyP [Vicia faba]
Seq. No.
                   235067
Seq. ID
                  LIB3272-048-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1172555
BLAST score
                   493
E value
                   5.0e - 50
Match length
                  111
                   85
% identity
NCBI Description
                   34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
                   (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   (POM 34) >gi 629720 pir S46936 34K porin - potato
                  >gi 1076682 pir A55364 porin (clone pPOM-34) - potato
                  mitochondrion >gi 516166 emb CAA56599 (X80386) 34 kDA
                  porin [Solanum tuberosum]
Seq. No.
                  235068
                  LIB3272-048-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1256259
BLAST score
                  314
E value
                   4.0e-31
Match length
                  102
% identity
                  72
NCBI Description
                  (U50900) voltage-dependent anion channel protein [Spinacia
                  oleracea]
                  235069
Seq. No.
Seq. ID
                  LIB3272-048-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q4063746
BLAST score
                  505
E value
                  3.0e-51
```

Match length 118 % identity

NCBI Description (AC005851) nodulin-like protein [Arabidopsis thaliana]

235070 Seq. No.

Seq. ID LIB3272-048-P1-K1-C1



```
Method
                  BLASTX
NCBI GI
                  g2129648
BLAST score
                  148
                  1.0e-09
E value
Match length
                  126
% identity
                  43
NCBI Description
                  MYB-related protein 33,3K - Arabidopsis thaliana
                  >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein
                  [Arabidopsis thaliana]
Seq. No.
                  235071
Seq. ID
                  LIB3272-048-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g585272
BLAST score
                  565
E value
                  2.0e-58
Match length
                  122
% identity
                  89
NCBI Description
                  MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR
                  >gi 20835 emb CAA38536 (X54739) HSP70 [Pisum sativum]
Seq. No.
                  235072
Seq. ID
                  LIB3272-048-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q1709498
BLAST score
                  141
                  3.0e-09
E value
Match length
                  36
% identity
                  72
NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR
                  >gi 1362001 pir S57524 osmotin precursor - Arabidopsis
                  thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin
                  [Arabidopsis thaliana]
                  235073
Seq. No.
Seq. ID
                  LIB3272-048-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g1173187
BLAST score
                  443
                  3.0e-44
E value
                  92
Match length
                  91
% identity
NCBI Description
                 40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi 643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
Seq. No.
                  235074
Seq. ID
                  LIB3272-048-P1-K1-C8
Method
                  BLASTX
                  g1703292
NCBI GI
BLAST score
                  303
E value
                  4.0e-28
```

Match length 72 % identity 81

NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER >gi 551219 emb CAA53473

(X75879) amt1 [Arabidopsis thaliana]

Method

BLASTX

```
Seq. No.
                   235075
                   LIB3272-048-P1-K1-D11
Seq. ID
Method
                  BLASTX
                   g4314370
NCBI GI
BLAST score
                   599
E value
                   2.0e-62
                   132
Match length
% identity
                   85
NCBI Description
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
                   235076
Seq. No.
                  LIB3272-048-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2369714
BLAST score
                   651
E value
                   2.0e-68
Match length
                   129
                   94
% identity
NCBI Description
                  (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                   235077
Seq. ID
                  LIB3272-048-P1-K1-D4
                  BLASTX
Method
NCBI GI
                   g629806
BLAST score
                   600
E value
                   2.0e-62
Match length
                   115
                   94
% identity
NCBI Description
                  tubulin beta chain - rice >gi 493725 emb CAA55912 (X79367)
                  beta tubulin [Oryza sativa]
Seq. No.
                   235078
                  LIB3272-048-P1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827559
BLAST score
                   160
E value
                   7.0e-11
Match length
                   42
% identity
                   71
NCBI Description
                   (AL021635) predicted protein [Arabidopsis thaliana]
                   >gi_3292808_emb_CAA19798_ (AL031018) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                   235079
Seq. ID
                  LIB3272-048-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3603456
BLAST score
                  511
E value
                   4.0e-52
Match length
                  105
% identity
                   30
NCBI Description (AF088848) polyubiquitin [Capsicum chinense]
Seq. No.
                   235080
Seq. ID
                  LIB3272-048-P1-K1-D9
```



```
NCBI GI
                  q4539399
BLAST score
                  593
                  1.0e-61
E value
Match length
                  118
% identity
                  97
                   (AL035526) ras-like GTP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  235081
Seq. ID
                  LIB3272-048-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2894599
BLAST score
                  460
                  5.0e-46
E value
Match length
                  104
% identity
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  235082
Seq. ID
                  LIB3272-048-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q1173187
BLAST score
                  102
E value
                  2.0e-09
                  71
Match length
                  56
% identity
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                  strawberry >gi 643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
Seq. No.
                  235083
Seq. ID
                  LIB3272-048-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g3924597
BLAST score
                  167
E value
                  9.0e-12
                  78
Match length
% identity
                  44
NCBI Description
                  (AF069442) putative oxidoreductase [Arabidopsis thaliana]
                  235084
Seq. No.
                  LIB3272-048-P1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1491776
BLAST score
                  245
E value
                  6.0e-21
Match length
                  71
% identity
                  68
                  (M37636) cationic peroxidase [Arachis hypogaea]
NCBI Description
                  235085
Seq. No.
                  LIB3272-048-P1-K1-E6
Seq. ID
```

Method BLASTX g3851636 NCBI GI BLAST score 408 6.0e-40 E value



```
Match length 93
% identity 82
NCBI Description (AF098519) unknown [Avicennia marina] >gi_4128206
(AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No. 235086
Seq. ID LIB3272-048-P1-K1-E9
```

Method BLASTX
NCBI GI g1076660
BLAST score 229
E value 6.0e-19
Match length 47
% identity 89

NCBI Description D13F(MYBST1) protein - potato >gi\_786426\_bbs\_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes,

leaf, Peptide, 342 aa] [Solanum tuberosum]

 Seq. No.
 235087

 Seq. ID
 LIB3272-048-P1-K1-F1

 Method
 BLASTX

 NCBI GI
 g3643609

 BLAST score
 429

 E value
 2.0e-42

E value 2.0e-Match length 133 % identity 65

NCBI Description (AC005395) putative Cys3His zinc finger protein

[Arabidopsis thaliana]

Seq. No. 235088

Seq. ID LIB3272-048-P1-K1-F12

Method BLASTX
NCBI GI g417060
BLAST score 522
E value 2.0e-53
Match length 103
% identity 92

NCBI Description GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA

LIGASE) (GS) >gi\_170637 (M94765) glutamine synthetase [Vigna aconitifolia] >gi\_1094850\_prf\_\_2106409A Gln

synthetase [Vigna aconitifolia]

Seq. No. 235089

Seq. ID LIB3272-048-P1-K1-F2

Method BLASTX
NCBI GI g2388575
BLAST score 166
E value 1.0e-11
Match length 97
% identity 37

NCBI Description (AC000098) YUP8H12.18 [Arabidopsis thaliana]

Seq. No. 235090

Seq. ID LIB3272-048-P1-K1-F6

Method BLASTX NCBI GI g3367522 BLAST score 482



```
E value
                  1.0e-48
Match length
                  135
% identity
NCBI Description
                  (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
                  thaliana]
                  235091
Seq. No.
                  LIB3272-048-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738315
BLAST score
                  274
E value
                  3.0e-24
                  130
Match length
% identity
                  45
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
                  235092
Seq. No.
                  LIB3272-048-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131770
BLAST score
                  386
                  2.0e-37
E value
Match length
                  105
% identity
                  67
                 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
NCBI Description
                  (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3DO24
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                  [Dictyostelium discoideum]
Seq. No.
                  235093
Seq. ID
                  LIB3272-048-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q4210948
BLAST score
                  516
E value
                  1.0e-52
Match length
                  105
% identity
                  92
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
Seq. No.
                  235094
Seq. ID
                  LIB3272-048-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2341034
BLAST score
                  445
E value
                  2.0e-44
                  91
Match length
% identity
NCBI Description (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                  235095
```

Seq. ID LIB3272-048-P1-K1-G2

Method BLASTX NCBI GI g3643609 BLAST score 377 E value 3.0e-36 Match length 134



% identity

NCBI Description (AC005395) putative Cys3His zinc finger protein

[Arabidopsis thaliana]

Seq. No.

235096

Seq. ID Method

LIB3272-048-P1-K1-G3

NCBI GI

BLASTX g464986

BLAST score E value

405 1.0e-39

Match length % identity

78 95

NCBI Description

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi\_421857\_pir\_\_S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana

>gi\_297884\_emb\_CAA78714\_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)

ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No.

235097

Seq. ID

LIB3272-048-P1-K1-G4

Method BLASTX NCBI GI g3024020 627 BLAST score E value 1.0e-65 Match length 125 % identity 94

NCBI Description INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)

>gi 2225881 dbj BAA20877 (AB004824) eukaryotic initiation

factor 5A3 [Solanum tuberosum]

Seq. No.

235098

Seq. ID

LIB3272-048-P1-K1-G7

Method BLASTX NCBI GI g3786016 BLAST score 326 2.0e-30 E value Match length 131 % identity

NCBI Description (AC005499) putative elongation factor [Arabidopsis

thaliana]

Seq. No.

235099

Seq. ID

LIB3272-048-P1-K1-G9

Method BLASTX NCBI GI g3901014 BLAST score 235 E value 1.0e-19 Match length 55

% identity NCBI Description

76 (AJ130886) metallothionein-like protein class II [Fagus

sylvatica]

```
235100
 Seq. No.
 Seq. ID
                    LIB3272-048-P1-K1-H2
 Method
                   BLASTX
 NCBI GI
                    g2244835
 BLAST score
                    239
 E value
                    4.0e-20
 Match length
                    69
 % identity
                    70
 NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]
                   235101
 Seq. No.
 Seq. ID
                   LIB3272-048-P1-K1-H3
 Method
                   BLASTX
 NCBI GI
                   q4432860
 BLAST score
                    326
 E value
                    2.0e-30
 Match length
                   109
                    61
 % identity
 NCBI Description
                   (AC006300) putative glucose-induced repressor protein
                    [Arabidopsis thaliana]
 Seq. No.
                    235102
 Seq. ID
                   LIB3272-048-P1-K1-H4
 Method
                   BLASTX
 NCBI GI
                    q2961372
 BLAST score
                    283
 E value
                    2.0e-32

    Match length

                    77
 % identity
                    88
 NCBI Description
                   (AL022141) putative ribosomal protein L8 [Arabidopsis
                    thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal
                   protein L2 [Arabidopsis thaliana]
 Seq. No.
                    235103
 Seq. ID
                   LIB3272-048-P1-K1-H8
 Method
                   BLASTX
 NCBI GI
                   q1657948
 BLAST score
                   560
 E value
                    9.0e-58
 Match length
                   124
 % identity
                   87
 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
 Seq. No.
                    235104
 Seq. ID
                   LIB3272-049-P1-K1-A1
 Method
                   BLASTX
 NCBI GI
                   g2500376
 BLAST score
                   522
 E value
                   2.0e-53
 Match length
                   108
 % identity
                    94
 NCBI Description 60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb AAD14494
                    (AC005508) 23552 [Arabidopsis thaliana]
```

Seq. No. 235105

Seq. ID LIB3272-049-P1-K1-A10



```
BLASTX
Method
NCBI GI
                  q1170748
                  295
BLAST score
                  1.0e-26
E value
Match length
                  72
                  82
% identity
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-D >gi 167349
                   (M88323) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi_167351 (L01102) late embryogenesis-abundant
                  protein [Gossypium hirsutum]
                  235106
Seq. No.
                  LIB3272-049-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2695711
BLAST score
                  311
                  1.0e-28
E value
                  72
Match length
                  82
% identity
NCBI Description (AJ001370) cytochome b5 [Olea europaea]
Seq. No.
                  235107
                  LIB3272-049-P1-K1-A3
Seq. ID
                  BLASTX
Method
                  g2924518
NCBI GI
BLAST score
                  166
E value
                   1.0e-11
                  100
Match length
                   47
% identity
NCBI Description (AL022023) putative protein [Arabidopsis thaliana]
                  235108
Seq. No.
                  LIB3272-049-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1928981
BLAST score
                   521
E value
                   3.0e-53
Match length
                   113
% identity
                   92
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   235109
Seq. No.
Seq. ID
                   LIB3272-049-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q3337356
BLAST score
                   431
E value
                   1.0e-42
Match length
                   84
% identity
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
```

subunit [Arabidopsis thaliana]

235110 Seq. No.

LIB3272-049-P1-K1-A6 Seq. ID

Method BLASTX NCBI GI g2130149



```
BLAST score
                  658
                  3.0e-69
E value
Match length
                  127
% identity
                  99
                  translation elongation factor eEF-1 alpha chain - maize
NCBI Description
                  (fragment)
                  235111
Seq. No.
                  LIB3272-049-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1519680
BLAST score
                  167
E value
                  1.0e-11
Match length
                  127
% identity
                  31
NCBI Description (U67953) contains similarity to C3HC4-class zinc finger
                  (PS:PS00518) [Caenorhabditis elegans]
                  235112
Seq. No.
                  LIB3272-049-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g169913
BLAST score
                  403
E value
                  2.0e-39
Match length
                  128
% identity
                  59
NCBI Description (M92090) beta-amylase [Glycine max]
Seq. No.
                  235113
                  LIB3272-049-P1-K1-B11
Seq. ID
Method
                  BLASTX
                  q1888485
NCBI GI
BLAST score
                  435
E value
                  4.0e-43
                  98
Match length
                  83
% identity
NCBI Description (Y11749) dihydroflavonol 4-reductase [Vitis vinifera]
Seq. No.
                  235114
                  LIB3272-049-P1-K1-B12
Seq. ID
Method
                  BLASTX
                  g3643609
NCBI GI
BLAST score
                  414
E value
                  1.0e-40
Match length
                  126
                  67
% identity
                  (AC005395) putative Cys3His zinc finger protein
NCBI Description
                  [Arabidopsis thaliana]
                  235115
Seq. No.
                  LIB3272-049-P1-K1-B2
Seq. ID
Method
                  BLASTX
```

Seq. ID LIB3272-0
Method BLASTX
NCBI GI g2829133
BLAST score 148
E value 2.0e-09
Match length 102
% identity 35



NCBI Description (AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis

thaliana] >gi\_4490745\_emb\_CAB38907.1\_ (AL035708) adenosine-5'-phosphosulfate-kinase [Ārabidopsis thaliana]

Seq. No. 235116

Seq. ID LIB3272-049-P1-K1-B3

Method BLASTX
NCBI GI g629483
BLAST score 309
E value 2.0e-28
Match length 115
% identity 56

NCBI Description gene 1-Sc3 protein - European white birch

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula] >gi\_1584322\_prf\_\_2122374C allergen Bet v 1-Sc3 [Betula

pendula]

Seq. No. 235117

Seq. ID LIB3272-049-P1-K1-B6

Method BLASTX
NCBI GI g3928099
BLAST score 272
E value 5.0e-24
Match length 122
% identity 24

NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 235118

Seq. ID LIB3272-049-P1-K1-B9

Method BLASTX
NCBI GI g2462746
BLAST score 503
E value 4.0e-51
Match length 112
% identity 84

NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 235119

Seq. ID LIB3272-049-P1-K1-C10

Method BLASTX
NCBI GI g3860259
BLAST score 212
E value 5.0e-17
Match length 112
% identity 45

NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]

Seq. No. 235120

Seq. ID LIB3272-049-P1-K1-C11

Method BLASTX
NCBI GI g462195
BLAST score 453
E value 3.0e-45
Match length 94
% identity 94

NCBI Description PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)

```
T-T-SERVEN
```

>gi\_100682\_pir\_\_S21636 GOS2 protein - rice
>gi\_20238\_emb\_CAA36190\_ (X51910) GOS2 [Oryza sativa]
>gi\_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No. 235121

Seq. ID LIB3272-049-P1-K1-C2

Method BLASTX
NCBI GI g1170747
BLAST score 318
E value 2.0e-29
Match length 65
% identity 100

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi\_167345

(M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi\_167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 235122

Seq. ID LIB3272-049-P1-K1-C5

Method BLASTX
NCBI GI g3643609
BLAST score 414
E value 1.0e-40
Match length 126
% identity 67

NCBI Description (AC005395) putative Cys3His zinc finger protein

[Arabidopsis thaliana]

Seq. No. 235123

Seq. ID LIB3272-049-P1-K1-C6

Method BLASTX
NCBI GI g2500354
BLAST score 573
E value 2.0e-59
Match length 110
% identity 95

NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi\_1902894\_dbj\_BAA19462\_

(AB001891) QM family protein [Solanum melongena]

Seq. No. 235124

Seq. ID LIB3272-049-P1-K1-C8

Method BLASTX
NCBI GI g2507300
BLAST score 402
E value 3.0e-39
Match length 99
% identity 76

NCBI Description ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD

SUBUNIT) (A1 40 KD SUBUNIT) (RF-C 40 KD SUBUNIT) (RFC40) >gi\_1590811 (M87338) replication factor C, 40-kDa subunit [Homo sapiens] >gi\_2914760 (AF045555) replication factor C subunit 2 [Homo sapiens] >gi\_4506487\_ref\_NP\_002905.1\_pRFC2\_

replication factor C (activator 1) 2 (40kD)

Seq. No. 235125

Seq. ID LIB3272-049-P1-K1-D10



```
Method
                   BLASTX
NCBI GI
                   g3738308
BLAST score
                   373
E value
                   7.0e-36
Match length
                  116
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  235126
Seq. ID
                  LIB3272-049-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g1362103
BLAST score
                  560
E value
                  8.0e-58
Match length
                  126
% identity
                  83
                  ubiquitin conjugating enzyme - tomato
NCBI Description
                  >gi_886679_emb_CAA58111_ (X82938) ubiquitin conjugating
                  enzyme [Lycopersicon esculentum]
Seq. No.
                  235127
Seq. ID
                  LIB3272-049-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q4510430
BLAST score
                  495
E value
                  4.0e-50
Match length
                  102
% identity
                  86
NCBI Description (AC006929) unknown protein, 3' partial [Arabidopsis
                  thaliana]
Seq. No.
                  235128
Seq. ID
                  LIB3272-049-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g1170747
BLAST score
                  309
E value
                  2.0e-28
                  74
Match length
% identity
                  82
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345
                   (M88324) late embryogenesis-abundant protein [Gossypium
                  hirsutum] >gi 167347 (M37697) Lea5-A late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  235129
Seq. ID
                  LIB3272-049-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g1053063
BLAST score
                  600
```

2.0e-62 E value Match length 129 % identity 89

NCBI Description (U38464) small GTP-binding protein [Solanum lycopersicum]

Seq. No. 235130

Seq. ID LIB3272-049-P1-K1-D6

Method BLASTX

E value

Match length

% identity

5.0e-34

NCBI Description RECEPTOR-LIKE PROTEIN, KINASE 5 PRECURSOR

111



```
NCBI GI
                    g4406816
 BLAST score
                    576
 E value
                    1.0e-59
 Match length
                    114
                    93
 % identity
 NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
 Seq. No.
                    235131
 Seq. ID
                    LIB3272-049-P1-K1-D7
 Method
                    BLASTX
 NCBI GI
                    g1488043
 BLAST score
                    255
 E value
                    5.0e-22
                    80
 Match length
 % identity
                    68
 NCBI Description (U63784) PAPS-reductase-like protein [Catharanthus roseus]
 Seq. No.
                    235132
 Seq. ID
                    LIB3272-049-P1-K1-D8
 Method
                    BLASTX
 NCBI GI
                    q167367
 BLAST score
                    514
 E value
                    2.0e-52
Match length
                    119
 % identity
                    85
 NCBI Description (L08199) peroxidase [Gossypium hirsutum]
                    235133
 Seq. No.
 Seq. ID
                   LIB3272-049-P1-K1-D9
 Method
                   BLASTX
 NCBI GI
                    g3738257
 BLAST score
                    505
 E value
                    2.0e-51
 Match length
                    107
 % identity
                    93
 NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
                   nigra]
 Seq. No.
                    235134
 Seq. ID
                    LIB3272-049-P1-K1-E1
 Method
                   BLASTX
 NCBI GI
                   g3158474
 BLAST score
                    608
 E value
                    2.0e-63
 Match length
                   129
 % identity
                    91
 NCBI Description (AF067184) aquaporin 1 [Samanea saman]
 Seq. No.
                    235135
 Seq. ID
                   LIB3272-049-P1-K1-E10
 Method
                   BLASTX
 NCBI GI
                    g1350783
 BLAST score
                   357
```



>gi\_282883\_pir\_\_S27756 receptor-like protein kinase
precursor - Arabidopsis thaliana >gi\_166850 (M84660)
receptor-like protein kinase [Arabidopsis thaliana]
>gi\_2842492\_emb\_CAA16889\_ (AL021749) receptor-like protein
kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. ID LIB3272-049-P1-K1-E11
Method BLASTX
NCBI GI g3169182
BLAST score 313
E value 7.0e-29
Match length 78
% identity 76

Seq. No.

NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No. 235137

Seq. ID LIB3272-049-P1-K1-E12

235136

Method BLASTX
NCBI GI g1173256
BLAST score 535
E value 7.0e-55
Match length 108
% identity 94

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi 629496 pir S45026 ribosomal

protein S4 - upland cotton >gi\_488739 emb\_CAA55882 (X79300) ribosomal protein, small subunit 4e (RS4e)

[Gossypium hirsutum]

Seq. No. 235138

Seq. ID LIB3272-049-P1-K1-E2

Method BLASTX
NCBI GI g3281861
BLAST score 216
E value 2.0e-17
Match length 107
% identity 44

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 235139

Seq. ID LIB3272-049-P1-K1-E4

Method BLASTX
NCBI GI g543905
BLAST score 427
E value 3.0e-42
Match length 103
% identity 82

NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >qi 347459 (L22162)

brassinosteroid-regulated protein [Glycine max]

Seq. No. 235140

Seq. ID LIB3272-049-P1-K1-E5

Method BLASTX
NCBI GI g100525
BLAST score 573
E value 2.0e-59
Match length 115



% identity ubiquitin precursor UbB2 - common sunflower (fragment) NCBI Description >gi 18803 emb CAA40323 (X57003) polyubiquitin protein [Helianthus annuus] 235141 Seq. No. Seq. ID LIB3272-049-P1-K1-E8 Method BLASTX NCBI GI g2288887 BLAST score 426 E value 4.0e-42 Match length 94 85 % identity NCBI Description (Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi 3250736 emb CAA76803 (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi\_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] 235142 Seq. No. Seq. ID LIB3272-049-P1-K1-F5 Method BLASTX NCBI GI q3080442 BLAST score 405 1.0e-39 E value Match length 102 % identity 69 NCBI Description (AL022605) putative protein [Arabidopsis thaliana] 235143 Seq. No. LIB3272-049-P1-K1-F6 Seq. ID Method BLASTX NCBI GI q4006829 BLAST score 163 3.0e-11 E value 91 Match length % identity NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana] 235144 Seq. No. Seq. ID LIB3272-049-P1-K1-F7 Method BLASTX q549060 376 3.0e-36

NCBI GI BLAST score E value Match length 95 % identity 78

NCBI Description T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)

>gi 631656 pir S43058 CCTeta protein eta chain - mouse >gi 468504 emb CAA83274 (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

235145 Seq. No.

Seq. ID LIB3272-049-P1-K1-F8

Method BLASTX NCBI GI q4580460 BLAST score 454

Match length

% identity

100



```
E value
                  2.0e-45
Match length
                  118
% identity
                  (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  235146
Seq. ID
                  LIB3272-049-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1173256
BLAST score
                  567
E value
                  1.0e-58
Match length
                  108
                  100
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S4 > gi 629496 pir S45026 ribosomal
                  protein S4 - upland cotton >gi 488739 emb CAA55882
                  (X79300) ribosomal protein, small subunit 4e (RS4e)
                  [Gossypium hirsutum]
Seq. No.
                  235147
Seq. ID
                  LIB3272-049-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1657948
BLAST score
                  538
E value
                  3.0e-55
Match length
                  117
                  89
% identity
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
                  235148
Seq. No.
                  LIB3272-049-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1495366
BLAST score
                  424
E value
                  7.0e-42
Match length
                  89
% identity
                  83
NCBI Description (Z69370) nitrite transporter [Cucumis sativus]
Seq. No.
                  235149
Seq. ID
                  LIB3272-049-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3549691
BLAST score
                  431
E value
                  1.0e-42
Match length
                  98
% identity
NCBI Description (AJ010501) thaumatin-like protein PR-5b [Cicer arietinum]
Seq. No.
                  235150
Seq. ID
                  LIB3272-049-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g4210948
BLAST score
                  481
E value
                  2.0e-48
```



```
NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]
 Seq. No.
                    235151
 Seq. ID
                   LIB3272-049-P1-K1-H2
 Method
                   BLASTX
 NCBI GI
                   g1166450
 BLAST score
                   302
 E value
                   1.0e-27
 Match length
                   66
 % identity
                   82
 NCBI Description (X95262) Tfm5 [Lycopersicon esculentum]
 Seq. No.
                   235152
 Seq. ID
                   LIB3272-049-P1-K1-H3
 Method
                   BLASTX
 NCBI GI
                   g2160166
 BLAST score
                   265
 E value
                   3.0e-23
 Match length
                   118
 % identity
                   56
 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
 Seq. No.
                   235153
 Seq. ID
                   LIB3272-049-P1-K1-H5
 Method
                   BLASTX
 NCBI GI
                   g4006881
 BLAST score
                   161
 E value
                   5.0e-11
 Match length
                   99
 % identity
                   40
 NCBI Description (299707) putative protein [Arabidopsis thaliana]
 Seq. No.
                   235154
 Seq. ID
                   LIB3272-049-P1-K1-H7
 Method
                   BLASTX
 NCBI GI
                   g4056506
BLAST score
                   230
 E value
                   4.0e-19
 Match length
                   118
 % identity
                   39
 NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]
 Seq. No.
                   235155
 Seq. ID
                   LIB3272-049-P1-K1-H9
 Method
                   BLASTX
 NCBI GI
                   g2914706
 BLAST score
                   144
 E value
                   5.0e-09
 Match length
                   80
 % identity
 NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]
```

Seq. No. 235156

Seq. ID LIB3272-050-P1-K1-A11

Method BLASTX
NCBI GI g1172597
BLAST score 226



```
E value
                   1.0e-18
Match length
                   47
% identity
                   91
                   WOUND-INDUCED BASIC PROTEIN >gi_81888_pir__JS0731 wound-inducible basic protein - kidney bean >gi_169365
NCBI Description
                    (L00625) basic protein [Phaseolus vulgaris]
                   >gi_217989_dbj_BAA02299_ (D12914) 5.8 kb basic protein
                   [Phaseolus vulgaris]
Seq. No.
                   235157
Seq. ID
                   LIB3272-050-P1-K1-A12
                   BLASTX
Method
NCBI GI
                   g3123271
BLAST score
                   453
E value
                   3.0e-45
Match length
                   105
% identity
                   82
NCBI Description 40S RIBOSOMAL PROTEIN S6 >gi 2224751 emb CAA74381 (Y14052)
                   ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                   235158
Seq. ID
                   LIB3272-050-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g1155261
BLAST score
                   523
E value
                   2.0e-53
Match length
                   118
% identity
                   86
NCBI Description (U40217) eukaryotic release factor 1 homolog [Arabidopsis
                   thaliana]
Seq. No.
                   235159
Seq. ID
                   LIB3272-050-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q3687237
BLAST score
                   349
E value
                   4.0e-33
Match length
                   117
% identity
                   62
NCBI Description (AC005169) putative Cys3His zinc-finger protein
                   [Arabidopsis thaliana]
Seq. No.
                   235160
Seq. ID
                   LIB3272-050-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g1928981
BLAST score
                   527
E value
                   6.0e-54
```

Match length 114 % identity 92

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 235161

LIB3272-050-P1-K1-B10 Seq. ID

Method BLASTX NCBI GI q2501578



```
BLAST score
E value
                  2.0e-19
Match length
                  102
% identity
                  53
NCBI Description ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
Seq. No.
                  235162
Seq. ID
                  LIB3272-050-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q3461837
BLAST score
                  316
                  3.0e-29
E value
Match length
                  94
% identity
NCBI Description
                  (AC005315) putative expansin [Arabidopsis thaliana]
                  >gi 3927842 (AC005727) expansin AtEx6 [Arabidopsis
                  thaliana]
Seq. No.
                  235163
Seq. ID
                  LIB3272-050-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1107526
BLAST score
                  408
E value
                  5.0e-40
Match length
                  103
% identity
                  75
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
Seq. No.
                  235164
Seq. ID
                  LIB3272-050-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q1922938
BLAST score
                  218
E value
                  1.0e-17
Match length
                  93
% identity
NCBI Description (AC000106) Similar to Caenorhabditis hypothetical protein
                  CO7A9.11 (gb_Z29094). [Arabidopsis thaliana]
Seq. No.
                  235165
Seq. ID
                  LIB3272-050-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q1220196
BLAST score
                  570
E value
                  5.0e-59
Match length
                  120
% identity
                  89
```

NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum]

Seq. No.

Seq. ID LIB3272-050-P1-K1-B5

235166

Method BLASTX NCBI GI q3122232 BLAST score 260



```
E value
                   1.0e-22
Match length
                  103
                   56
% identity
NCBI Description
```

MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR

>gi\_1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] >gi\_4454008\_emb\_CAA23061\_ (AL035396) Arabidopsis

mitochondrion-localized small heat shock protein

(AtHSP23.6-mito) [Arabidopsis thaliana]

235167 Seq. No. Seq. ID LIB3272-050-P1-K1-B6 Method BLASTX NCBI GI g1172995 235 BLAST score E value 1.0e-19 Match length 94

% identity NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi 1083790 pir S52084 ribosomal

protein L22 - rat >gi\_710295\_emb\_CAA55204\_ (X78444) ribosomal protein L22 [Rattus norvegicus]

>gi 1093952 prf 2105193A ribosomal protein L22 [Rattus

norvegicus]

54

Seq. No. Seq. ID

235168

LIB3272-050-P1-K1-B7

Method BLASTX NCBI GI g125606 BLAST score 431 E value 1.0e-42 Match length 95 85 % identity

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463 pir S12248

pyruvate kinase (EC 2.7.1.40) - potato

>gi\_22576\_emb\_CAA37727\_ (X53688) pyruvate kinase [Solanum

tuberosum]

Seq. No.

235169

Seq. ID LIB3272-050-P1-K1-C1

Method BLASTX NCBI"GI g4530585 BLAST score 357 E value 4.0e-34 Match length 85 % identity

NCBI Description (AF130978) B12D protein [Ipomoea batatas]

Seq. No.

235170

LIB3272-050-P1-K1-C10 Seq. ID

Method BLASTX NCBI GI q1709498 BLAST score 506 E value 2.0e-51 Match length 109 % identity 83

NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

>gi 1362001 pir S57524 osmotin precursor - Arabidopsis thaliana >gi\_887390\_emb\_CAA61411\_ (X89008) osmotin

BLAST score

Match length

E value

399

122

6.0e-39



## [Arabidopsis thaliana]

```
Seq. No.
                  235171
Seq. ID
                  LIB3272-050-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3377797
BLAST score
                  458
E value
                  7.0e-46
Match length
                  118
                  76
% identity
NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
Seq. No.
                  235172
Seq. ID
                  LIB3272-050-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1172977
BLAST score
                  540
E value
                  2.0e-55
Match length
                 127
% identity
                  83
NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic
                  ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                  235173
Seq. ID
                  LIB3272-050-P1-K1-C3
Method
                  BLASTX
                  g1666234
NCBI GI
BLAST score
                 472
E value
                  2.0e-47
Match length
                 88
% identity
                  100
NCBI Description (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin
                  [Pisum sativum]
Seq. No.
                  235174
Seq. ID
                  LIB3272-050-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3024017
BLAST score
                  465
E value
                  1.0e-46
Match length
                  101
% identity
                  92
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
                  (EIF-4C) >gi 2565421 (AF026804) eukaryotic translation
                  initiation factor eIF-1A [Onobrychis viciifolia]
Seq. No.
                  235175
Seq. ID
                  LIB3272-050-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q2677828
```

E value

Match length

% identity

2.0e-52

115

84



```
% identity
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
Seq. No.
                   235176
Seq. ID
                  LIB3272-050-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g125606
BLAST score
                  443
E value
                   4.0e-44
Match length
                   94
% identity
                   88
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463 pir S12248
                   pyruvate kinase (EC 2.7.1.40) - potato
                   >gi 22576 emb CAA37727 (X53688) pyruvate kinase [Solanum
                   tuberosum]
Seq. No.
                   235177
Seq. ID
                  LIB3272-050-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g4559342
BLAST score
                  137
E value
                  9.0e-09
Match length
                  70
% identity
                  49
NCBI Description (AC007087) putative copper methylamine oxidase [Arabidopsis
                  thaliana]
                  235178
Seq. No.
Seq. ID
                  LIB3272-050-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g3694872
BLAST score
                  429
E value
                  2.0e-42
Match length
                  105
% identity
NCBI Description (AF092547) profilin [Ricinus communis]
Seq. No.
                  235179
Seq. ID
                  LIB3272-050-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g3023930
BLAST score
                  254
E value
                  6.0e-22
Match length
                  70
% identity
                   60
NCBI Description HISTONE DEACETYLASE 1 (HD1) >gi 2654077 gb AAB87685
                   (AF032919) histone deacetylase [Strongylocentrotus
                  purpuratus]
Seq. No.
                  235180
Seq. ID
                  LIB3272-050-P1-K1-D7
Method
                  BLASTX
·NCBI GI
                  g3851636
BLAST score
                  515
```



NCBI Description (AF098519) unknown [Avicennia marina] >gi\_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No. 235181

Seq. ID LIB3272-050-P1-K1-D9

Method BLASTX
NCBI GI g3334147
BLAST score 353
E value 1.0e-33
Match length 104
% identity 66

NCBI Description ENDOCHITINASE 1 PRECURSOR >gi 1469788 (U60197) class I

chitinase [Gossypium hirsutum]

Seq. No. 235182

Seq. ID LIB3272-050-P1-K1-E10

Method BLASTX
NCBI GI g2129758
BLAST score 523
E value 2.0e-53
Match length 101
% identity 89

NCBI Description ubiquitin conjugating enzyme E2 protein - Arabidopsis

thaliana >gi\_992704 (U33757) UBC7 [Arabidopsis thaliana]

Seq. No. 235183

Seq. ID LIB3272-050-P1-K1-E11

Method BLASTX
NCBI GI g3024017
BLAST score 449
E value 8.0e-45
Match length 101
% identity 90

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)

(EIF-4C) >gi\_2565421 (AF026804) eukaryotic translation

initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No. 235184

Seq. ID LIB3272-050-P1-K1-E2

Method BLASTX
NCBI GI g2267567
BLAST score 394
E value 2.0e-38
Match length 85
% identity 87

NCBI Description (AF009003) glycine-rich RNA binding protein 1 [Pelargonium

x hortorum] >gi\_2267569 (AF009004) glycine-rich RNA binding

protein 2 [Pelargonium x hortorum]

Seq. No. 235185

Seq. ID LIB3272-050-P1-K1-E4

Method BLASTX
NCBI GI g232031
BLAST score 220
E value 6.0e-18
Match length 67
% identity 60



NCBI Description ELONGATION FACTOR 1 BETA' >gi\_322851\_pir\_\_S29224 translation elongation factor eEF-1 beta' chain - rice >gi\_218161\_dbj\_BAA02253\_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No. 235186

Seq. ID LIB3272-050-P1-K1-E5

Method BLASTX
NCBI GI g3687237
BLAST score 319
E value 1.0e-29
Match length 123
% identity 58

NCBI Description (AC005169) putative Cys3His zinc-finger protein

[Arabidopsis thaliana]

Seq. No. 235187

Seq. ID LIB3272-050-P1-K1-E6

Method BLASTX
NCBI GI g1173187
BLAST score 471
E value 2.0e-47
Match length 109
% identity 83

NCBI Description 40S RIBOSOMAL PROTEIN S23 (S12) >gi\_1362041\_pir\_\_S56673

ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi 643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

Seq. No. 235188

Seq. ID LIB3272-050-P1-K1-E7

Method BLASTX
NCBI GI g1928981
BLAST score 549
E value 2.0e-56
Match length 114
% identity 95

NCBI Description (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica

oleracea var. botrytis]

Seq. No. 235189

Seq. ID LIB3272-050-P1-K1-E9

Method BLASTX
NCBI GI g508304
BLAST score 277
E value 1.0e-24
Match length 66
% identity 79

NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 235190

Seq. ID LIB3272-050-P1-K1-F1

Method BLASTX
NCBI GI g2130073
BLAST score 186
E value 5.0e-14
Match length 78



```
% identity
NCBI Description fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
                   cytosolic - rice >gi 786178 dbj BAA08845 (D50307) aldolase
                   C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301)
                   aldolase C-1 [Oryza sativa]
Seq. No.
                   235191
Seq. ID
                  LIB3272-050-P1-K1-F11
                  {\tt BLASTX}
Method
NCBI GI
                  g4432855
BLAST score
                  143
E value
                   6.0e-09
Match length
                  35
                  86
% identity
NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]
Seq. No.
                   235192
Seq. ID
                  LIB3272-050-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g481236
BLAST score
                  265
E value
                  3.0e-23
Match length
                  64
% identity
                  81
NCBI Description hypothetical protein - Madagascar periwinkle
                  >gi 407410 emb CAA81526 (Z26880) 14 kDa polypeptide
                  [Catharanthus roseus]
Seq. No.
                  235193
Seq. ID
                  LIB3272-050-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3660467
BLAST score
                  266
E value
                  2.0e-23
Match length
                  58
% identity
                  84
                  (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  235194
Seq. ID
                  LIB3272-050-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  q3869088
BLAST score
                  524
                  1.0e-53
E value
Match length
                  100
% identity
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
Seq. No.
                  235195
Seq. ID
                  LIB3272-050-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2088651
BLAST score
                  298
E value
```

34034

4.0e-27

114

50

Match length

% identity



```
NCBI Description (AF002109) hypersensitivity-related gene 201 isolog
                  [Arabidopsis thaliana]
                  235196
Seq. No.
                  LIB3272-050-P1-K1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1351271
BLAST score
                  560
E value
                  8.0e-58
                  127
Match length
% identity
                  83
NCBI Description TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM)
                  >gi 1084309 pir S52032 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - spinach >gi 806312
                  (L36387) triosephosphate isomerase, chloroplast isozyme
                  [Spinacia oleracea]
                  235197
Seq. No.
Seq. ID
                  LIB3272-050-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3337366
BLAST score
                  359
E value
                  3.0e - 34
Match length
                  105
% identity
                  32
NCBI Description (AC004481) unknown protein [Arabidopsis thaliana]
Seq. No.
                  235198
Seq. ID
                  LIB3272-050-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1061040
BLAST score
                  577
                  8.0e-60
E value
Match length
                  113
% identity
                  93
NCBI Description (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
                  >gi 1587694 prf 2207220A sterol C-methyltransferase
                  [Arabidopsis thaliana]
Seq. No.
                  235199
                  LIB3272-050-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g396595
BLAST score
                  155
E value
                  3.0e-10
Match length
                  115
% identity
NCBI Description (Z25485) ACR1-protein [Saccharomyces cerevisiae]
Seq. No.
                  235200
                  LIB3272-050-P1-K1-G2
Seq. ID
Method
                  BLASTX
```

NCBI GI g1708191 BLAST score 514 E value 2.0e-52 Match length 129 % identity 77

% identity

85



NCBI Description HEXOSE CARRIER PROTEIN HEX6 > gi 467319 (L08188) hexose carrier protein [Ricinus communis] 235201 Seq. No. LIB3272-050-P1-K1-G3 Seq. ID BLASTX Method NCBI GI g3868758 BLAST score 430 E value 1.0e-42 Match length 106 75 % identity NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa] Seq. No. 235202 Seq. ID LIB3272-050-P1-K1-G6 BLASTX Method NCBI GI q416758 BLAST score 208 E value 1.0e-16 Match length 83 52 % identity NCBI Description SERINE CARBOXYPEPTIDASE PRECURSOR >gi 166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis thaliana] Seq. No. 235203 Seq. ID LIB3272-050-P1-K1-G7 Method BLASTX NCBI GI g1107526 BLAST score 408 E value 5.0e-40 Match length 103 75 % identity NCBI Description (X87931) SIEP1L protein [Beta vulgaris] 235204 Seq. No. Seq. ID LIB3272-050-P1-K1-H10 Method BLASTX NCBI GI g1166450 BLAST score 246 E value 5.0e-21 Match length 53 % identity 83 NCBI Description (X95262) Tfm5 [Lycopersicon esculentum] 235205 Seq. No. LIB3272-050-P1-K1-H11 Seq. ID Method BLASTX NCBI GI g3914394 BLAST score 537 E value 4.0e-55 Match length 118

.34036

NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi 2118335 pir S60473 phosphoglycerate mutase (EC

Seq. No.

Seq. ID

235211

LIB3272-051-P1-K1-A6



```
5.4.2.1) - common ice plant >gi_602426 (U16021) phosphoglyceromutase [Mesembryanthemum crystallinum]
```

235206 Seq. No. Seq. ID LIB3272-050-P1-K1-H12 Method BLASTX NCBI GI g3869088 492 BLAST score E value 8.0e-50 Match length 94 % identity 100 NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata] 235207 Seq. No. Seq. ID LIB3272-050-P1-K1-H4 Method BLASTX NCBI GI g464981 BLAST score 367 E value 3.0e - 35Match length 68 99 % identity NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum] 235208 Seq. No. Seq. ID LIB3272-050-P1-K1-H5 BLASTX Method NCBI GI g1350680 BLAST score 477 E value 4.0e-48 Match length 112 % identity 80 NCBI Description 60S RIBOSOMAL PROTEIN L1 Seq. No. 235209 Seq. ID LIB3272-050-P1-K1-H8 Method BLASTX g2982432 NCBI GI BLAST score 177 3.0e-13 E value Match length 42 % identity NCBI Description (AL022224) putative protein [Arabidopsis thaliana] 235210 Seq. No. Seq. ID LIB3272-051-P1-K1-A4 Method BLASTX g3158376 NCBI GI BLAST score 488 E value 3.0e-49 Match length 131 % identity NCBI Description (AF035385) unknown [Arabidopsis thaliana]



```
Method
                    BLASTX
 NCBI GI
                    g2493146
 BLAST score
                    424
                    8.0e-42
 E value
                    119
 Match length
                    53
 % identity
 NCBI Description VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >qi 755148
                    (U13669) vacuolar H+-ATPase proteolipid (16 kDa) subunit
                    [Gossypium hirsutum] >gi 4519415 dbj BAA75542.1 (AB024275)
                    vacuolar H+-ATPase c subunit [Citrus unshiu]
                    235212
 Seq. No.
 Seq. ID
                    LIB3272-051-P1-K1-A9
 Method
                    BLASTX
 NCBI GI
                    g1518540
 BLAST score
                    523
 E value
                    2.0e-53
 Match length
                    107
 % identity
                    93
 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
 Seq. No.
                    235213
 Seq. ID
                    LIB3272-051-P1-K1-B1
Method
                    BLASTX
 NCBI GI
                    g4455349
 BLAST score
                    182
 E value
                    2.0e-13
 Match length
                    84
 % identity
                    46
 NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
 Seq. No.
                    235214
 Seq. ID
                   LIB3272-051-P1-K1-B10
                   BLASTX
 Method
 NCBI GI
                    g1107526
 BLAST score
                    447
 E value
                    2.0e-44
 Match length
                   111
 % identity
                    75
 NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
 Seq. No.
                    235215
 Seq. ID
                   LIB3272-051-P1-K1-B11
 Method
                   BLASTX
 NCBI GI
                    q125887
 BLAST score
                   169
 E value
                    6.0e-12
 Match length
                   89
 % identity
                    45
 NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR
                    >gi 82092 pir S04765 LAT52 protein precursor - tomato
```

>gi\_295812\_emb\_CAA33854\_ (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No. 235216

Seq. ID LIB3272-051-P1-K1-B12

Method BLASTX



```
NCBI GI
                  g1703129
BLAST score
                  581
                  3.0e-60
E value
Match length
                  108
% identity
                  99
NCBI Description ACTIN 11 >gi 2129522 pir S68109 actin 11 - Arabidopsis
                  thaliana >gi 1002533 (U27981) actin-11 [Arabidopsis
                  thaliana]
Seq. No.
                  235217
Seq. ID
                  LIB3272-051-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g543905
BLAST score
                  454
E value
                  2.0e-45
Match length
                  112
% identity
                  79
NCBI Description BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi 347459 (L22162)
                  brassinosteroid-regulated protein [Glycine max]
Seq. No.
                  235218
Seq. ID
                  LIB3272-051-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  472
                  2.0e-47
E'value
Match length
                  116
% identity
                  80
NCBI Description (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
Seq. No.
                  235219
Seq. ID
                  LIB3272-051-P1-K1-B7
Method
                  BLASTX
                  q3869088
NCBI GI
BLAST score
                  580
E value
                  4.0e-60
Match length
                  112
% identity
NCBI Description (AB019427) elongation factor-1 alpha [Nicotiana paniculata]
                  235220
Seq. No.
Seq. ID
                  LIB3272-051-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q3386621
BLAST score
                  477
E value
                  5.0e-48
Match length
                  101
% identity
NCBI Description (AC004665) unknown protein [Arabidopsis thaliana]
Seq. No.
                  235221
Seq. ID
                  LIB3272-051-P1-K1-C1
```

5eq. 10 h1652/2-051-F1-K1-01

Method BLASTX
NCBI GI g2160166
BLAST score 190
E value 2.0e-14

E value

Match length

% identity

2.0e-57

135

75



```
Match length
                   109
% identity
                   52
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
                   235222
Seq. No.
                   LIB3272-051-P1-K1-C10
Seq. ID
Method
                   BLASTX
                   g4335751
NCBI GI
BLAST score
                   394
E value
                   3.0e - 38
                   89
Match length
                   80
% identity
NCBI Description (AC006284) putative methyltransferase [Arabidopsis
                   thaliana]
                   235223
Seq. No.
Seq. ID
                   LIB3272-051-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g1706318
                   427
BLAST score
E value
                   3.0e-42
Match length
                   111
                   70
% identity
NCBI Description GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)
                  . >gi_1362098_pir__S56177 probable glutamate decarboxylase -
                   tomato >gi_995555_emb_CAA56812_ (X80840) homology to pyroxidal-5'-phosphate-dependent glutamate decarboxylases;
                   putative start codon [Lycopersicon esculentum]
                   235224
Seq. No.
                   LIB3272-051-P1-K1-C12
Seq. ID
                   BLASTX
Method
                   g1370166
NCBI GI
BLAST score
                   637
                   8.0e-67
E value
                   133
Match length
                   90
% identity
NCBI Description (Z73932) RAB1C [Lotus japonicus]
                   235225
Seq. No.
Seq. ID
                   LIB3272-051-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g508304
BLAST score
                   241
E value
                   2.0e-20
Match length
                   82
% identity
                   57
NCBI Description (L22305) corC [Medicago sativa]
                   235226
Seq. No.
Seq. ID
                   LIB3272-051-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   q4249382
BLAST score
                   558
```



235227

235228

(AC005966) Strong similarity to gi 3337350 F13P17.3 NCBI Description putative permease from Arabidopsis thaliana BAC gb AC004481. [Arabidopsis thaliana]

Seq. ID LIB3272-051-P1-K1-C9 Method BLASTX NCBI GI g3334659 BLAST score 164 2.0e-11 E value

Match length 42 74 % identity

Seq. No.

Seq. No.

NCBI Description (Y10489) putative cytochrome P450 [Glycine max]

LIB3272-051-P1-K1-D1 Seq. ID Method BLASTX NCBI GI g3859606 BLAST score 250 E value 1.0e-21

52 Match length % identity 87

NCBI Description (AF104919) contains similarity to cysteine proteases (Pfam:

PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

235229 Seq. No.

Seq. ID LIB3272-051-P1-K1-D10

BLASTX Method NCBI GI g3694872 BLAST score 492 E value 8.0e-50 Match length 118 % identity 80

NCBI Description (AF092547) profilin [Ricinus communis]

235230 Seq. No.

Seq. ID LIB3272-051-P1-K1-D11

Method BLASTX NCBI GI g3860255 BLAST score 204 E value 5.0e-16 Match length 131 % identity

NCBI Description (AC005824) hypothetical protein [Arabidopsis thaliana]

235231 Seq. No.

LIB3272-051-P1-K1-D12 Seq. ID

Method BLASTX NCBI GI g3953470 BLAST score 142 9.0e-09 E value Match length 43

NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]

Seq. No. 235232

% identity

Seq. ID LIB3272-051-P1-K1-D6



```
Method
                  BLASTX
NCBI GI
                  g3080439
BLAST score
                  488
E value
                  2.0e-49
                  126
Match length
                  75
% identity
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]
Seq. No.
                  235233
Seq. ID
                  LIB3272-051-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q2118220
BLAST score
                  400
E value
                  5.0e-39
Match length
                  115
                  75
% identity
NCBI Description H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                   (clone AVA-P1) - Arabidopsis thaliana >gi 926929 (L44581)
                  vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana] >gi 926933 (L44583) vacuolar H+-pumping ATPase 16
                  kDa proteolipid [Arabidopsis thaliana]
                  >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar
                  H+-transporting ATPase 16K chain [Arabidopsis thaliana]
                  >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting
                  ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
Seq. No.
                  235234
                  LIB3272-051-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1107526
BLAST score
                  425
E value
                  6.0e-42
Match length
                  108
% identity
                  74
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
Seq. No.
                  235235
Seq. ID
                  LIB3272-051-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1350720
BLAST score
                  455
E value
                  2.0e-45
Match length
                  111
                  77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L32
```

Seq. No. 235236

Seq. ID LIB3272-051-P1-K1-E2 Method BLASTX

NCBI GI g2760837 BLAST score 234 E value 2.0e-19 Match length 104 % identity

NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 235237



```
Seq. ID
                    LIB3272-051-P1-K1-E4
 Method
                    BLASTX
 NCBI GI
                    g1351856
 BLAST score
                    594
 E value
                    9.0e-62
 Match length
                    123
 % identity
                    92
 NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
                    (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase
                    [Cucurbita sp.]
 Seq. No.
                    235238
 Seq. ID
                    LIB3272-051-P1-K1-E6
 Method
                    BLASTX
 NCBI GI
                    g3372230
 BLAST score
                    499
 E value
                    1.0e-50
 Match length
                    121
 % identity
                    79
 NCBI Description (AF017074) RNA polymerase I, II and III 16.5 kDa subunit
                    [Arabidopsis thaliana]
 Seq. No.
                    235239
 Seq. ID
                    LIB3272-051-P1-K1-E9
 Method
                    BLASTX
NCBI GI
                    g3927838
 BLAST score
                    293
 E value
                    2.0e-26
 Match length
                   77
                    77
 % identity
 NCBI Description (AC005727) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    235240
 Seq. ID
                   LIB3272-051-P1-K1-F1
 Method
                   BLASTX
 NCBI GI
                    g2586082
 BLAST score
                    141
 E value
                    1.0e-08
                   51
 Match length
 % identity
                    45
 NCBI Description (U72725) retrofit [Oryza longistaminata]
 Seq. No.
                    235241
 Seq. ID
                   LIB3272-051-P1-K1-F11
 Method
                   BLASTX
 NCBI GI
                   q464981
 BLAST score
                    446
 E value
                    2.0e-44
 Match length
                   84
 % identity
                    96
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762)
```

Seq. No. 235242

Seq. ID LIB3272-051-P1-K1-F12

Method BLASTX

ubiquitin carrier protein [Lycopersicon esculentum]



NCBI GI g543715 BLAST score 169 E value 4.0e-12 Match length 37 % identity 89

NCBI Description PROTEIN PHOSPHATASE PP2A REGULATORY SUBUNIT A (PR65) 
>gi\_541969\_pir\_\_S40171 phosphoprotein phosphatase 2A 65K 
regulatory chain - garden pea >gi\_629639\_pir\_\_S43776 
phosphoprotein phosphatase 2A 65kDa regulatory subunit - garden pea (fragment) >gi\_437901\_emb\_CAA81107\_ (Z25888) 
phosphoprotein phosphatase 2A 65kDa regulatory subunit

[Pisum sativum]

Seq. No. 235243

Seq. ID LIB3272-051-P1-K1-F2

Method BLASTX
NCBI GI g3551952
BLAST score 338
E value 9.0e-32
Match length 131
% identity 56

NCBI Description (AF082029) senescence-associated protein 4 [Hemerocallis

hybrid cultivar]

Seq. No. 235244

Seq. ID LIB3272-051-P1-K1-F3

Method BLASTX
NCBI GI g1408471
BLAST score 470
E value 3.0e-47
Match length 105
% identity 80

NCBI Description (U48938) actin depolymerizing factor 1 [Arabidopsis

thaliana] >gi 3851707 (AF102173) actin depolymerizing

factor 1 [Arabidopsis thaliana]

Seq. No. 235245

Seq. ID LIB3272-051-P1-K1-F4

Method BLASTX
NCBI GI g2961372
BLAST score 530
E value 3.0e-54
Match length 106
% identity 92

NCBI Description (AL022141) putative ribosomal protein L8 [Arabidopsis

thaliana] >gi\_3036817\_emb\_CAA18507\_ (AL022373) ribosomal

protein L2 [Arabidopsis thaliana]

Seq. No. 235246

Seq. ID LIB3272-051-P1-K1-F5

Method BLASTX
NCBI GI g3551245
BLAST score 201
E value 1.0e-15
Match length 108
% identity 44

NCBI Description (AB012702) P40-like protein [Daucus carota]

```
Seq. No. 235247
Seq. ID LIB3272-051-P1-K1-F7
Method BLASTX
NCBI GI g3746568
```

BLAST score 461
E value 4.0e-46
Match length 98
% identity 90
NCBI Description (AF061638) branched-chain alpha-keto acid doc

NCBI Description (AF061638) branched-chain alpha-keto acid decarboxylase E1

beta subunit [Arabidopsis thaliana]

Seq. No. 235248

Seq. ID LIB3272-051-P1-K1-G1

Method BLASTX
NCBI GI g4105782
BLAST score 422
E value 1.0e-41
Match length 97
% identity 85

NCBI Description (AF049922) PGP169-12 [Petunia x hybrida]

Seq. No. 235249

Seq. ID LIB3272-051-P1-K1-G10

Method BLASTX
NCBI GI g2499945
BLAST score 373
E value 7.0e-36
Match length 112
% identity 64

NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE

PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE

DECARBOXYLASE >gi\_1076363\_pir\_\_S46440 orotate

phosphoribosyltransferase (EC 2.4.2.10) /

orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi\_443818\_emb\_CAA50686 (X71842)

pyrE-F [Arabidopsis thaliana]

Seq. No. 235250

Seq. ID LIB3272-051-P1-K1-G11

Method BLASTX
NCBI GI g133867
BLAST score 542
E value 1.0e-55
Match length 123
% identity 84

NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi\_82722\_pir\_\_S16577 ribosomal

protein S11 - maize >gi 22470 emb CAA39438 (X55967)

ribosomal protein S11 [Zea mays]

Seq. No. 235251

Seq. ID LIB3272-051-P1-K1-G12

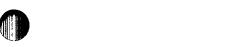
Method BLASTX
NCBI GI g1170747
BLAST score 388
E value 1.0e-37
Match length 78



% identity LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi 167345 NCBI Description (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi 167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum] 235252 Seq. No. Seq. ID LIB3272-051-P1-K1-G3 Method BLASTX NCBI GI q832876 BLAST score 580 E value 4.0e-60 Match length 126 % identity 90 (L41345) ascorbate free radical reductase [Solanum NCBI Description lycopersicum] >gi\_1097368\_prf\_\_2113407A ascorbate free radical reductase [Lycopersicon esculentum] Seq. No. 235253 LIB3272-051-P1-K1-G6 Seq. ID Method BLASTX NCBI GI g2160156 399 BLAST score 6.0e - 39E value Match length 96 74 % identity NCBI Description (AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb Z73100). [Arabidopsis thaliana] Seq. No. 235254 LIB3272-051-P1-K1-G8 Seq. ID BLASTX Method NCBI GI q1166450 BLAST score 321 E value 1.0e-29 71 Match length 82 % identity NCBI Description (X95262) Tfm5 [Lycopersicon esculentum] Seq. No. 235255 Seq. ID LIB3272-051-P1-K1-G9 BLASTX Method NCBI GI g1332579 BLAST score 430 E value 4.0e-63 137 Match length % identity NCBI Description (X98063) polyubiquitin [Pinus sylvestris] 235256 Seq. No. Seq. ID LIB3272-051-P1-K1-H1

BLASTX

Method NCBI GI g4262174 BLAST score 305 E value 7.0e-28 Match length 132 % identity 45



```
(AC005508) 9058 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  235257
                  LIB3272-051-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129675
                  251
BLAST score
E value
                  2.0e-21
Match length
                  97
                  62
% identity
                  probable chlorophyll synthetase G4 - Arabidopsis thaliana
NCBI Description
                  >qi 972938 (U19382) putative chlorophyll synthetase
                   [Arabidopsis thaliana] >gi 3068709 (AF049236) putative
                  chlorophyll synthetase [Arabidopsis thaliana]
Seq. No.
                  235258
                  LIB3272-051-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063396
BLAST score
                  421
E value
                  1.0e-41
Match length
                  98
% identity
                  81
NCBI Description (AB012947) vcCyP [Vicia faba]
Seq. No.
                  235259
Seq. ID
                  LIB3272-051-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3892058
BLAST score
                  154
E value
                  9.0e-11
Match length
                  131
% identity
                  37
NCBI Description (AC002330) putative glutamate-/aspartate-binding peptide
                   [Arabidopsis thaliana]
                  235260
Seq. No.
Seq. ID
                  LIB3272-051-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g4322421
BLAST score
                  532
                  2.0e-54
E value
                  127
Match length
                  76
% identity
NCBI Description (AF085230) cadmium resistance factor 1 [Arabidopsis
                  thaliana]
                  235261
Seq. No.
Seq. ID
                  LIB3272-051-P1-K1-H4
                  BLASTX
Method
NCBI GI
                  q3123271
BLAST score
                  524
E value
                  1.0e-53
Match length
                  115
% identity
                  88
```

NCBI Description 40S RIBOSOMAL PROTEIN S6 >gi\_2224751\_emb\_CAA74381\_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

E value

Match length

% identity

2.0e-09

73

45



```
235262
Seq. No.
                   LIB3272-051-P1-K1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2879867
BLAST score
                   418
E value
                   4.0e-41
Match length
                   115
                   70
% identity
                   (AL021816) 40s ribosomal protein S17 [Schizosaccharomyces
NCBI Description
                   pombe]
Seq. No.
                   235263
Seq. ID
                   LIB3272-051-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g1808656
                   546
BLAST score
E value
                   4.0e-56
Match length
                   136
% identity
                   74
NCBI Description (Y10804) Ubiquitin activating enzyme E1 [Nicotiana tabacum]
Seq. No.
                   235264
                   LIB3272-051-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q417060
BLAST score
                   507
E value
                   1.0e-51
Match length
                   113
% identity
                   86
                   GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA
NCBI Description
                   LIGASE) (GS) >gi 170637 (M94765) glutamine synthetase
                    [Vigna aconitifo\overline{\text{lia}}] >gi_1094850_prf__2106409A Gln
                    synthetase [Vigna aconitifolia]
Seq. No.
                    235265
Seq. ID
                   LIB3272-051-P1-K1-H9
                   BLASTX
Method
NCBI GI
                   g1703108
                   495
BLAST score
E value
                    4.0e-50
                   91
Match length
                    100
% identity
NCBI Description ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis
                   thaliana >gi 2129528 pir S68107 actin 7 - Arabidopsis thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                    thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                    thaliana]
Seq. No.
                    235266
Seq. ID
                   LIB3272-052-P1-K1-A1
                   BLASTX
Method
NCBI GI
                   g4469175
BLAST score
                   144
```

34048

Seq. ID

Method



```
NCBI Description (AJ133470) beta-1,3-glucanase [Hevea brasiliensis]
  Seq. No.
                     235267
                     LIB3272-052-P1-K1-A10
  Seq. ID
  Method
                     BLASTX
                     g3668089
  NCBI GI
  BLAST score
                     131
  E value
                     4.0e-12
                    82
  Match length
  % identity
                     50
  NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     235268
  Seq. ID
                     LIB3272-052-P1-K1-A12
  Method
                     BLASTX
  NCBI GI
                     g167367
  BLAST score
                     567
  E value
                     1.0e-58
  Match length
                     132
  % identity
                     84
  NCBI Description (L08199) peroxidase [Gossypium hirsutum]
  Seq. No.
                     235269
Seq. ID
                     LIB3272-052-P1-K1-A3
  Method
                     BLASTX
  NCBI GI
                     g2738949
  BLAST score
                     508
  E value
                     1.0e-51
  Match length
                     107
  % identity
                     91
  NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                     ananassa]
  Seq. No.
                     235270
  Seq. ID
                    LIB3272-052-P1-K1-A4
                    BLASTX
  Method
  NCBI GI
                     q4103324
  BLAST score
                     329
  E value
                     1.0e-30
                    73
  Match length
                     93
  % identity
  NCBI Description (AF022716) GDP-mannose pyrophosphorylase [Solanum
                     tuberosum]
  Seq. No.
                     235271
  Seq. ID
                     LIB3272-052-P1-K1-A5
  Method
                     BLASTX
  NCBI GI
                     q1491776
  BLAST score
                     353
  E value
                     1.0e-33
  Match length
                     81
                     83
  % identity
  NCBI Description (M37636) cationic peroxidase [Arachis hypogaea]
  Seq. No.
                     235272
```

34049

LIB3272-052-P1-K1-A7

BLASTX



NCBI GI q2493144 BLAST score 412 2.0e-40 E value 97 Match length 57 % identity VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE NCBI Description 16 KD PROTEOLIPID SUBUNIT) >gi 2118221 pir S60132

H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi 926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis

thaliana]

235273 Seq. No.

Seq. ID LIB3272-052-P1-K1-A8

Method BLASTX NCBI GI q4455364 BLAST score 336 E value 2.0e-31 Match length 107 59 % identity

NCBI Description (AL035524) senescence-associated protein-like [Arabidopsis

thalianal

235274 Seq. No.

Seq. ID LIB3272-052-P1-K1-A9

BLASTX Method NCBI GI g4056469 BLAST score 576 E value 1.0e-59 Match length 112 % identity 100

NCBI Description (AC005990) Strong similarity to gb\_M95166 ADP-ribosylation

factor from Arabidopsis thaliana. ESTs gb\_Z25826,

gb\_R90191, gb\_N65697, gb\_AA713150, gb\_T46332, gb\_AA040967,

gb AA712956, gb T46403, gb T46050, gb AI100391 and

gb Z25043 come from t

235275 Seq. No.

Seq. ID LIB3272-052-P1-K1-B11

Method BLASTX NCBI GI g464981 BLAST score 438 E value 2.0e-43Match length 84 % identity 95

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >qi 388207 (L23762)

ubiquitin carrier protein [Lycopersicon esculentum]

235276 Seq. No.

LIB3272-052-P1-K1-B12 Seq. ID

Method BLASTX NCBI GI q1709498 BLAST score 515 E value 2.0e-52 Match length 112 % identity 83



NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR

>gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis thaliana >gi\_887390\_emb\_CAA61411\_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No. 235277
Seq. ID LIB3272-052-P1-K1-B2
Method BLASTX

Method BLASTX
NCBI GI g3319921
BLAST score 267
E value 2.0e-23
Match length 95
% identity 60

NCBI Description (AJ223388) Hev b 3 [Hevea brasiliensis]

>gi\_3319923\_emb\_CAA11304 (AJ223389) Hev b 3 [Hevea
brasiliensis] >gi\_3319925\_emb\_CAA11305 (AJ223390) Hev b 3
[Hevea brasiliensis] >gi\_3818475 (AF051317) small rubber

particle protein [Hevea brasiliensis]

Seq. No. 235278

Seq. ID LIB3272-052-P1-K1-B3

Method BLASTX
NCBI GI g1076274
BLAST score 295
E value 1.0e-26
Match length 102
% identity 59

NCBI Description cucumisin (EC 3.4.21.25) precursor - muskmelon (fragment)

Seq. No. 235279

Seq. ID LIB3272-052-P1-K1-B4

Method BLASTX
NCBI GI g2495155
BLAST score 152
E value 6.0e-10
Match length 112
% identity 39

NCBI Description GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR)

>gi\_1694926\_dbj\_BAA08910\_ (D50407) glutamyl-tRNA reductase

[Cucumis sativus]

Seq. No. 235280

Seq. ID LIB3272-052-P1-K1-C10

Method BLASTX
NCBI GI g3377797
BLAST score 282
E value 3.0e-25
Match length 125
% identity 50

NCBI Description (AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA

R90691 [Ara

Seq. No. 235281

Seq. ID \_\_LIB3272-052-P1-K1-C12



Method BLASTX NCBI GI g4006827 BLAST score 523 E value 2.0e-53 Match length 132 75 % identity NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana] Seq. No. 235282 Seq. ID LIB3272-052-P1-K1-C2 Method BLASTX NCBI GI g3915031 BLAST score 231 E value 3.0e-19 Match length 118

% identity 46

NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi 1217628 emb CAA65232

(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase

[Gossypium hirsutum]

Seq. No. 235283

Seq. ID LIB3272-052-P1-K1-C4

Method BLASTX NCBI GI g3785971 BLAST score 341 E value 4.0e-32 Match length 120 % identity 61

NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]

>gi\_4262248\_gb\_AAD14541\_ (AC006200) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 235284

Seq. ID LIB3272-052-P1-K1-C6

Method BLASTX NCBI GI g170753 BLAST score 523 E value 2.0e-53 Match length 110 % identity 81

NCBI Description (M95819) initiation factor (iso) 4F p28 subunit [Triticum

aestivum]

Seq. No. 235285

Seq. ID LIB3272-052-P1-K1-C8

Method BLASTX NCBI GI q1657948 BLAST score 430 E value 1.0e-42 Match length 122 % identity 72

NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]

Seq. No. 235286

Seq. ID LIB3272-052-P1-K1-D10

Method BLASTX

```
NCBI GI
                   q3193297
BLAST score
                   480
E value
                   2.0e-48
Match length
                  125
% identity
                  66
                  (AF069298) similar to epoxide hydrolases [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  235287
Seq. ID
                  LIB3272-052-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3288821
BLAST score
                  504
E value
                  3.0e-51
Match length
                  123
                  77
% identity
NCBI Description (AF063901) alanine:glyoxylate aminotransferase;
                  transaminase [Arabidopsis thaliana]
Seq. No.
                  235288
Seq. ID
                  LIB3272-052-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g3273828
BLAST score
                  305
E value
                  7.0e-28
Match length
                  126
% identity
                  54
NCBI Description (AF068686) nodule-enhanced malate dehydrogenase [Glycine
                  max]
                  235289
Seq. No.
Seq. ID
                  LIB3272-052-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q3334147
BLAST score
                  463
E value
                  2.0e-46
Match length
                  129
% identity
                  71
NCBI Description ENDOCHITINASE 1 PRECURSOR >qi 1469788 (U60197) class I
                  chitinase [Gossypium hirsutum]
Seq. No.
                  235290
Seq. ID
                  LIB3272-052-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q3335341
BLAST score
                  320
E value
                  1.0e-29
Match length
                  132
% identity
                  54
NCBI Description (AC004512) T8F5.10 [Arabidopsis thaliana]
```

Seq. No. 235291

Seq. ID LIB3272-052-P1-K1-D5

Method BLASTX
NCBI GI g3123271
BLAST score 492
E value 8.0e-50

```
Match length
                   112
% identity
                   84
NCBI Description 40S RIBOSOMAL PROTEIN S6 >qi 2224751 emb CAA74381 (Y14052)
                   ribosomal protein S6 [Arabidopsis thaliana]
Seq. No.
                   235292
Seq. ID
                  LIB3272-052-P1-K1-D6
Method
                  BLASTX
NCBI GI
                   g2274915
BLAST score
                   423
E value
                   1.0e-41
Match length
                   115
                   70
% identity
NCBI Description (AJ000081) beta-1,3-glucanase [Citrus sinensis]
Seq. No.
                  235293
Seq. ID
                  LIB3272-052-P1-K1-D8
Method
                  BLASTX
NCBI GI
                   q730526
BLAST score
                   505
E value
                   3.0e-51
Match length
                   117
% identity
                   79
NCBI Description
                  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
                  >gi_480787_pir__S37271 ribosomal protein L13 - Arabidopsis
                   thaliana >gi_404166_emb_CAA53005_ (X75162) BBC1 protein
                   [Arabidopsis thaliana]
Seq. No.
                   235294
Seq. ID
                  LIB3272-052-P1-K1-E11
Method
                  BLASTX
NCBI GI
                   g4539292
BLAST score
                   438
                  2.0e-43
E value
Match length
                  95
% identity
                   84
NCBI Description (AL049480) putative ribosomal protein S10 [Arabidopsis
                  thaliana]
Seq. No.
                  235295
Seq. ID
                  LIB3272-052-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1657948
BLAST score
                  320
E value
                  1.0e-29
Match length
                  110
% identity
                   63
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
                  235296
Seq. No.
```

 Seq. No.
 235296

 Seq. ID
 LIB3272-052-P1-K1-E2

 Method
 BLASTX

 NCBI GI
 g3915031

 BLAST score
 708

E value 4.0e-75
Match length 133
% identity 100



NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi 1217628 emb CAA65232

(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase

[Gossypium hirsutum]

Seq. No. 235297

Seq. ID LIB3272-052-P1-K1-E3

Method BLASTX
NCBI GI g234327
BLAST score 311
E value 1.0e-28
Match length 117
% identity 32

NCBI Description (S57889) putative regulatory protein=YGL023 [Saccharomyces

cerevisiae, Peptide, 888 aa] [Saccharomyces cerevisiae] >gi 4261598 gb AAD13898\_S58126\_1111111 (S58126) Unknown

[Saccharomyces cerevisiae]

Seq. No. 235298

Seq. ID LIB3272-052-P1-K1-E4

Method BLASTX
NCBI GI g1402912
BLAST score 487
E value 3.0e-49
Match length 129
% identity 71

NCBI Description (X98317) peroxidase [Arabidopsis thaliana]

Seq. No. 235299

Seq. ID LIB3272-052-P1-K1-E7

Method BLASTX
NCBI GI g508304
BLAST score 241
E value 2.0e-20
Match length 82
% identity 57

NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 235300

Seq. ID LIB3272-052-P1-K1-E8

Method BLASTX
NCBI GI g1706547
BLAST score 407
E value 8.0e-40
Match length 115
% identity 68

NCBI Description GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM

PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi\_2129912\_pir\_\_S65077 beta-1,3-glucanase class I precursor - Para rubber tree >gi\_1184668 (U22147)

beta-1,3-glucanase [Hevea brasiliensis]

Seq. No. 235301

Seq. ID LIB3272-052-P1-K1-F1

Method BLASTX NCBI GI g124224



```
BLAST score
E value
                  2.0e-64
Match length
                  122
                  94
% identity
NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
                  >gi_100345_pir__S21060 translation initiation factor eIF-5A
                   - common tobacco >gi 19887 emb CAA45105 (X63543)
                  eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
Seq. No.
                  235302
                  LIB3272-052-P1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3168840
                  298
BLAST score
                  4.0e-27
E value
                  74
Match length
                  74
% identity
NCBI Description (U88711) copper homeostasis factor [Arabidopsis thaliana]
Seq. No.
                  235303
Seq. ID
                  LIB3272-052-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g1657948
BLAST score
                  574
E value
                  2.0e-59
Match length
                  127
                  87
% identity
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
                  235304
Seq. No.
Seq. ID
                  LIB3272-052-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3786017
BLAST score
                  264
                   4.0e-23
E value
Match length
                  112
                   49
% identity
NCBI Description (AC005499) putative non-green plastid inner envelope
                  membrane protein [Arabidopsis thaliana]
Seq. No.
                  235305
Seq. ID
                  LIB3272-052-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g3269293
                  281
BLAST score
E value
                   4.0e-25
Match length
                  90
% identity
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
```

Seq. No. 235306

Seq. ID LIB3272-052-P1-K1-F4 Method BLASTX

NCBI GI g1657948
BLAST score 457
E value 1.0e-45
Match length 116

```
% identity
NCBI Description
                 (U73466) MipC [Mesembryanthemum crystallinum]
Seq. No.
                  235307
                  LIB3272-052-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1168196
BLAST score
                  314
E value
                  6.0e-29
Match length
                  69
% identity
                  88
NCBI Description 14-3-3-LIKE PROTEIN >gi 555974 (U15036) 14-3-3-like protein
                  [Pisum sativum]
Seq. No.
                  235308
                  LIB3272-052-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2811026
BLAST score
                  372
E value
                  1.0e-35
Match length
                  80
% identity
                  89
NCBI Description TCP1-CHAPERONIN COFACTOR A HOMOLOG >gi_1946375 (U93215)
                  TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]
                  >gi 2347204 (AC002338) TCP1-chaperonin cofactor A isolog
                  [Arabidopsis thaliana]
                  235309
Seq. No.
                  LIB3272-052-P1-K1-G1
Seq. ĮD
Method
                  BLASTX
NCBI GI
                  g3894186
BLAST score
                  294
E value
                  1.0e-26
Match length
                  116
% identity
                  53
NCBI Description (AC005662) putative embryo-abundant protein [Arabidopsis
                  thaliana] (
                  235310
Seq. No.
Seq. ID
                  LIB3272-052-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g4210948
BLAST score
                  571
E value
                  5.0e-59
Match length
                  109
```

97 % identity

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

235311 Seq. No.

Seq. ID LIB3272-052-P1-K1-G11

Method BLASTX NCBI GI g4263712 BLAST score 388 E value 1.0e-37 Match length 93

% identity

NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis



## thaliana]

```
235312
Seq. No.
                  LIB3272-052-P1-K1-G12
Seq. ID
Method
                  BLASTX
                  g1843527
NCBI GI
                  659
BLAST score
                  2.0e-69
E value
                  132
Match length
                  51
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
                  235313
Seq. No.
                  LIB3272-052-P1-K1-G2
Seq. ID
Method
                  BLASTX
                  q3805854
NCBI GI
                  196
BLAST score
                  4.0e-15
E value
                  68
Match length
                  56
% identity
NCBI Description (AL031986) putative protein [Arabidopsis thaliana]
                  235314
Seq. No.
                  LIB3272-052-P1-K1-G5
Seq. ID
                  BLASTX
Method
                  g4263712
NCBI GI
BLAST score
                  396
                  1.0e-38
E value
                  94
Match length
                  78
% identity
NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis
                  thaliana]
                  235315
Seq. No.
                  LIB3272-052-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2497538
                  223
BLAST score
                  3.0e-18
E value
                  70
Match length
                  64
% identity
NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632)
                  pyruvate kinase [Glycine max]
                  235316
Seq. No.
                  LIB3272-052-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2914706
BLAST score
                  468
E value
                  5.0e-47
Match length
                  98
% identity
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]
```

Seq. No. 235317

Seq. ID LIB3272-052-P1-K1-H1

Method BLASTX

34058



```
g2661840
NCBI GI
BLAST score
                   371
                   1.0e - 35
E value
                   96
Match length
% identity
                   70
                   (Y15430) adenosine kinase [Physcomitrella patens]
NCBI Description
                   235318
Seq. No.
                   LIB3272-052-P1-K1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4417280
BLAST score
                   265
                   3.0e-23
E value
                   70
Match length
                   77
% identity
                  (AC007019) putative ATP synthase [Arabidopsis thaliana]
NCBI Description
                   235319
Seq. No.
                   LIB3272-052-P1-K1-H11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g417148
                    403
BLAST score
                    2.0e-39
E value
                   130
Match length
                    61
% identity
NCBI Description PROBABLE GLUTATHIONE S-TRANSFERASE (HEAT SHOCK PROTEIN 26A)
                    (G2-4) >gi_99912_pir__A33654 heat shock protein 26A -
                    soybean >g\overline{1}_{169981} (\overline{M2}_{0363}) Gmhsp26-A [Glycine max]
                    235320
Seq. No.
                   LIB3272-052-P1-K1-H3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g113621
                    439
BLAST score
                    1.0e-43
E value
Match length
                    102
% identity
                    86
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                    >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
                    4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
                    bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
                    cytoplasmic aldolase [Zea mays]
Seq. No.
                    235321
Seq. ID
                    LIB3272-052-P1-K1-H4
Method
                    BLASTX
                    g266936
NCBI GI
                    397
BLAST score
                    1.0e-38
E value
                    113
Match length
                    74
% identity
NCBI Description 50S RIBOSOMAL PROTEIN L27, CHLOROPLAST PRECURSOR (CL27)
                    >gi 282960 pir A42840 ribosomal protein L27 - common
                    tobacco >gi 170306 (M98473) ribosomal protein L27
```

34059

L27 [Nicotiana tabacum]

[Nicotiana tabacum] >gi 170326 (M75731) ribosomal protein

```
235322
Seq. No.
Seq. ID
                  LIB3272-052-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g1107526
BLAST score
                  429
E value
                  2.0e-42
Match length
                  111
% identity
                  73
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
Seq. No.
                  235323
                  LIB3272-052-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                  421
E value
                  2.0e-41
Match length
                  106
% identity
                  73
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                  235324
                  LIB3272-052-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204303
BLAST score
                  462
E value
                  3.0e-46
Match length
                  95
                  87
% identity
NCBI Description (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  235325
                  LIB3272-053-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499945
BLAST score
                  411
E value '
                  3.0e-40
Match length
                  121
% identity
                  64
NCBI Description URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
                  PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                  DECARBOXYLASE >gi 1076363 pir__S46440 orotate
                  phosphoribosyltransferase (EC 2.4.2.10) /
                  orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                  Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842)
                  pyrE-F [Arabidopsis thaliana]
```

Seq. No. 235326 Seq. ID Method BLASTX

LIB3272-053-P1-K1-A12

NCBI GI g4376088 378 BLAST score E value 2.0e-36 Match length 136 % identity 52

NCBI Description (Z99707) cytochrome P450-like protein [Arabidopsis

Seq. No.

235332



## thaliana]

```
Seq. No.
                  235327
Seq. ID
                  LIB3272-053-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2583128
BLAST score
                  562
                  6.0e-58
E value
Match length
                  141
                  74
% identity
NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]
                  235328
Seq. No.
                  LIB3272-053-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500354
BLAST score
                  683
                  4.0e-72
E value
Match length
                  132
% identity
                  95
NCBI Description 60S RIBOSOMAL PROTEIN L10 (EQM) >gi_1902894_dbj_BAA19462_
                  (AB001891) QM family protein [Solanum melongena]
Seq. No.
                  235329
                  LIB3272-053-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914002
BLAST score
                  134
E value
                  7.0e-15
Match length
                  81
% identity
                  57
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_2935279
                  (AF033862) Lon protease [Arabidopsis thaliana]
Seq. No.
                  235330
                  LIB3272-053-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4217999
BLAST score
                  475
                  9.0e-48
E value
Match length
                  116
% identity
                  81
NCBI Description (AC006135) putative ubiquitin--protein ligase
                   (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
Seq. No.
                   235331
                  LIB3272-053-P1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3885515
BLAST score
                  388
E value
                   9.0e-38
                  77
Match length
                   95
% identity
NCBI Description (AF084202) similar to ribosomal protein S26 [Medicago
                  sativa]
```



LIB3272-053-P1-K1-B12 Seq. ID BLASTX Method g541816 NCBI GI 177 BLAST score 4.0e-13 E value Match length 60 62 % identity protein kinase - common ice plant >gi\_457689 emb\_CAA82990 NCBI Description (Z30329) protein kinase [Mesembryanthemum crystallinum] Seq. No. 235333 LIB3272-053-P1-K1-B2 Seq. ID BLASTX Method g2499945 NCBI GI 367 BLAST score 3.0e - 35E value Match length 112 63 % identity URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE NCBI Description PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi\_1076363\_pir\_\_S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -Arabidopsis thaliana >gi\_443818\_emb\_CAA50686\_ (X71842) pyrE-F [Arabidopsis thaliana] Seq. No. 235334 LIB3272-053-P1-K1-B4 Seq. ID BLASTX Method g1928981 NCBI GI 297 BLAST score E value 4.0e-32 113 Match length % identity (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica NCBI Description oleracea var. botrytis] 235335 Seq. No. LIB3272-053-P1-K1-B5 Seq. ID BLASTX Method NCBI GI g1170747 BLAST score 380 1.0e-36 E value 86 Match length 85 % identity NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi\_167345 (M88324) late embryogenesis-abundant protein [Gossypium hirsutum] >gi 167347 (M37697) Lea5-A late embryogenesis-abundant protein [Gossypium hirsutum] 235336 Seq. No.

Seq. ID LIB3272-053-P1-K1-B6

Method BLASTX
NCBI GI g2462763
BLAST score 148
E value 2.0e-09
Match length 54



```
% identity
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                  (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  235337
                  LIB3272-053-P1-K1-B7
Seq. ID
                  BLASTX
Method
                  g2780225
NCBI GI
                  223
BLAST score
                  2.0e-18
E value
                  74
Match length
                  53
% identity
NCBI Description (AJ223281) alpha-hydroxynitrile lyase [Manihot esculenta]
                  235338
Seq. No.
                  LIB3272-053-P1-K1-B8
Seq. ID
Method
                  BLASTX
                  g114420
NCBI GI
                  181
BLAST score
                  2.0e-13
E value
                  70
Match length
                  54
% identity
NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi_100882_pir__S11491 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - maize
                  >gi_22173_emb_CAA38140_ (X54233) ATPase F1 subunit protein
                  [Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea
                  mays]
                  235339
Seq. No.
                  LIB3272-053-P1-K1-C11
Seq. ID
Method
                  BLASTX
                  q4098647
NCBI GI
                  745
BLAST score
E value
                  2.0e-79
Match length
                  142
% identity
                  (U80668) homogentisate 1,2-dioxygenase [Arabidopsis
NCBI Description
                  thaliana]
                   235340
Seq. No.
                  LIB3272-053-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g464986
BLAST score
                   541
E value
                   2.0e-55
Match length
                  104
% identity
                   96
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >qi 421857 pir S32674 ubiquitin--protein ligase (EC
                   6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi 297884 emb CAA78714 (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi 600391 emb CAA51201 (X72626) ubiquitin conjugating
```

enzyme E2 [Arabidopsis thaliana]



>gi\_4455355\_emb\_CAB36765.1\_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

 Seq. No.
 235341

 Seq. ID
 LIB3272-053-P1-K1-C4

 Method
 BLASTX

 NCBI GI
 g3738283

 BLAST score
 402

 E value
 3.0e-39

E value 3.0 Match length 82 % identity 85

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 235342

Seq. ID LIB3272-053-P1-K1-C6

Method BLASTX
NCBI GI g4454479
BLAST score 176
E value 1.0e-12
Match length 40
% identity 82

NCBI Description (AC006234) putative riboflavin synthase alpha chain

[Arabidopsis thaliana]

Seq. No. 235343

Seq. ID LIB3272-053-P1-K1-C7

Method BLASTX
NCBI GI g4538945
BLAST score 533
E value 1.0e-54
Match length 134
% identity 74

NCBI Description (AL049483) putative thioredoxin [Arabidopsis thaliana]

Seq. No. 235344

Seq. ID LIB3272-053-P1-K1-D1

Method BLASTX
NCBI GI g3986750
BLAST score 190
E value 9.0e-25
Match length 92
% identity 66

NCBI Description (AF107464) serine/threonine protein phosphatase type 2A

[Hevea brasiliensis]

Seq. No. 235345

Seq. ID LIB3272-053-P1-K1-D6

Method BLASTX
NCBI GI g2662310
BLAST score 331
E value 6.0e-31
Match length 116
% identity 62

NCBI Description (AB009307) bpwl [Hordeum vulgare]

Seq. No. 235346

Seq. ID LIB3272-053-P1-K1-D7

34064



```
BLASTX
Method
                   q1928981
NCBI GI
                   404
BLAST score
                   3.0e-54
E value
                  124
Match length
                   62
% identity
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                   235347
Seq. No.
                  LIB3272-053-P1-K1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3868758
                   483
BLAST score
                   1.0e-48
E value
                   117
Match length
                   74
% identity
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                   235348
Seq. No.
                   LIB3272-053-P1-K1-E11
Seq. ID
                   BLASTX
Method
                   g4406780
NCBI GI
                   369
BLAST score
                   2.0e-35
E value
                   84
Match length
                   82
% identity
                  (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                   235349
Seq. No.
                   LIB3272-053-P1-K1-E2
Seq. ID
                   BLASTX
Method
                   g1724102
NCBI GI
                   283
BLAST score
                   2.0e-25
E value
Match length
                   70
                   81
% identity
                   (U79766) S-adenosyl-L-homocystein hydrolase; SAH
NCBI Description
                   [Mesembryanthemum crystallinum]
                   235350
Seq. No.
                   LIB3272-053-P1-K1-E4
Seq. ID
                   BLASTX
Method
                   g1928981
NCBI GI
                   600
BLAST score
E value
                   2.0e-62
Match length
                   126
 % identity
                   63
                   (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
NCBI Description
                   oleracea var. botrytis]
                    235351
 Seq. No.
                   LIB3272-053-P1-K1-E5
 Seq. ID
```

34065

BLASTX

357

g4530585

Method

NCBI GI

BLAST score



```
6.0e - 34
E value
                   85
Match length
                   74
% identity
                   (AF130978) B12D protein [Ipomoea batatas]
NCBI Description
                   235352
Seq. No.
                   LIB3272-053-P1-K1-E6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3024127
                   545
BLAST score
E value
                   5.0e-56
                   109
Match length
                   95
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)
                   >gi_1655578_emb_CAA95857_ (Z71272) S-adenosyl-L-methionine synthetase 2 [Catharanthus roseus]
                   235353
Seq. No.
                   LIB3272-053-P1-K1-E7
Seq. ID
                   BLASTX
Method
                   q303730
NCBI GI
BLAST score
                   536
                   6.0e-55
E value
                   117
Match length
                   89
% identity
                   (D12540) GTP-binding protein [Pisum sativum]
NCBI Description
                   >gi_738933_prf__2001457A GTP-binding protein [Pisum
                   sativum]
                   235354
Seq. No.
                   LIB3272-053-P1-K1-F1
Seq. ID
                   BLASTX
Method
                    q167367
NCBI GI
                    556
BLAST score
                    3.0e-57
E value
Match length
                    137
                    80
% identity
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                    235355
                    LIB3272-053-P1-K1-F10
Seq. ID
                    BLASTX
Method
                    g629483
NCBI GI
                    357
BLAST score
                    6.0e-34
E value
Match length
                    134
 % identity
                    54
                    gene 1-Sc3 protein - European white birch
NCBI Description
                    >gi 534898 emb CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                    >qi 1584322 prf 2122374C allergen Bet v 1-Sc3 [Betula
                    pendula]
```

Seq. No. 235356

Seq. ID LIB3272-053-P1-K1-F11

Method BLASTX NCBI GI g543905



```
673
BLAST score
                  6.0e-71
E value
                  124
Match length
                  95
% identity
                  BRASSINOSTEROID-REGULATED PROTEIN BRU1 >gi_347459 (L22162)
NCBI Description
                  brassinosteroid-regulated protein [Glycine max]
                  235357
Seq. No.
                  LIB3272-053-P1-K1-F3
Seq. ID
                  BLASTX
Method
                  g3114658
NCBI GI
                  206
BLAST score
                  3.0e-16
E value
                  98
Match length
                  41
% identity
                  (AF060871) hypothetical alcohol dehydrogenase [Rhodococcus
NCBI Description
                  rhodochrous]
                  235358
Seq. No.
                  LIB3272-053-P1-K1-F4
Seq. ID
                   BLASTX
Method
                   g2499946
NCBI GI
                   318
BLAST score
                   2.0e-29
E value
                   75
Match length
                   80
% identity
                  URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
NCBI Description
                   PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                   DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana
                   tabacum]
                   235359
Seq. No.
                   LIB3272-053-P1-K1-F6
Seq. ID
                   BLASTX
Method
                   q2245066
NCBI GI
                   165
BLAST score
                   2.0e-11
E value
Match length
                   87
% identity
                   41
NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]
                   235360
Seq. No.
                   LIB3272-053-P1-K1-F8
Seq. ID
                   BLASTX
Method
                   q135406
NCBI GI
                   523
BLAST score
E value
                   2.0e-53
Match length
                   102
 % identity
                   96
                   TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768 pir_ A32712 tubulin
NCBI Description
                   alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                   alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                   alpha-5 tubulin [Arabidopsis thaliana]
                   235361
 Seq. No.
```

Method BLASTX

Seq. ID

LIB3272-053-P1-K1-F9

34067



```
g1107526
NCBI GI
BLAST score
                   450
                   7.0e-45
E value
Match length
                   114
                   75
% identity
NCBI Description (X87931) SIEP1L protein [Beta vulgaris]
Seq. No.
                   235362
                   LIB3272-053-P1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q629483
BLAST score
                   335
E value
                   2.0e-31
Match length
                   126
                   55
% identity
                  gene 1-Sc3 protein - European white birch
NCBI Description
                   >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula] >gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
                   pendula]
                   235363
Seq. No.
Seq. ID
                   LIB3272-053-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   q133872
BLAST score
                   445
E value
                   3.0e-44
Match length
                   131
                   71
% identity
                   30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1)
NCBI Description
                   >gi 282838_pir__S26494 ribosomal protein S1, chloroplast -
                   spinach >gi_322404_pir__A44121 small subunit ribosomal
                   protein CS1, CS-S2 - spinach >gi_18060_emb_CAA46927_
                   (X66135) ribosomal protein S1 [Spinacia oleracea]
                   >gi 170143 (M82923) chloroplast ribosomal protein S1
                   [Spinacia oleracea]
                   235364
Seq. No.
Seq. ID
                   LIB3272-053-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g1170748
BLAST score
                   284
E value
                   2.0e-25
Match length
                   70
% identity
                   81
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEAS-D >qi 167349
                   (M88323) late embryogenesis-abundant protein [Gossypium
                   hirsutum] >gi 167351 (L01102) late embryogenesis-abundant
                   protein [Gossypium hirsutum]
Seq. No.
                   235365
                   LIB3272-053-P1-K1-G3
Seq. ID
Method
                   BLASTX
```

NCBI GI g1778374

BLAST score 373 E value 8.0e-36 Match length 112 % identity 68

Match length

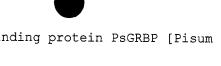
NCBI Description

% identity

140

thalianal





```
NCBI Description
                  (U81287) glycine-rich RNA-binding protein PsGRBP [Pisum
                   sativum]
                   235366
Seq. No.
Seq. ID
                   LIB3272-053-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g3935167
BLAST score
                   334
E value
                   2.0e-31
Match length
                   82
% identity
                   83
NCBI Description (AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.
                   235367
Seq. ID
                   LIB3272-053-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g303730
BLAST score
                   187
E value
                   4.0e-14
                   79
Match length
% identity
                   59
NCBI Description
                  (D12540) GTP-binding protein [Pisum sativum]
                   >gi 738933 prf__2001457A GTP-binding protein [Pisum
                   sativum
Seq. No.
                   235368
Seq. ID
                   LIB3272-053-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g2924509
BLAST score
                   199
E value
                   2.0e-15
Match length
                   91
% identity
                   46
NCBI Description (AL022023) subtilisin proteinase - like [Arabidopsis
                   thaliana]
Seq. No.
                   235369
Seq. ID
                  LIB3272-053-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3367522
BLAST score
                  315
E value
                   5.0e-29
Match length
                  93
% identity
                   62
NCBI Description (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  235370
Seq. ID
                  LIB3272-053-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2529665
BLAST score
                  572
E value
                  4.0e-59
```

34069

(AC002535) putative ribosomal protein L7A [Arabidopsis

Seq. ID

Method

```
Seq. No.
                   235371
Seq. ID
                   LIB3272-054-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g126770
BLAST score
                   141
E value
                   3.0e-09
Match length
                   59
% identity
                   49
NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi 68218 pir SYCNMU malate
                   synthase (EC 4.1.3.2) - upland cotton >gi_18507_emb_CAA36546_ (X52305) malate synthase (AA 1-567)
                   [Gossypium hirsutum]
Seq. No.
                   235372
Seq. ID
                   LIB3272-054-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g508304
BLAST score
                   215
E value
                   3.0e-17
                   73
Match length
% identity
                   60
NCBI Description (L22305) corC [Medicago sativa]
Seq. No.
                   235373
Seq. ID
                   LIB3272-054-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g2792297
BLAST score
                   197
E value
                   2.0e-15
Match length
                   55
% identity
                   60
NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]
                   235374
Seq. No.
Seq. ID
                   LIB3272-054-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g167367
BLAST score
                   436
E value
                   3.0e-43
Match length
                   123
% identity
                   68
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   235375
Seq. ID
                   LIB3272-054-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q3759184
BLAST score
                   331
E value
                   6.0e-31
Match length
                   135
% identity
                   52
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   235376
```

34070

LIB3272-054-P1-K1-B10

BLASTX



```
NCBI GI
                  g625509
BLAST score
                  602
E value
                  1.0e-62
Match length
                  121
                  25
% identity
NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)
Seq. No.
                  235377
                  LIB3272-054-P1-K1-B2
Seq. ID
Method
                  BLASTX
                  g464707
                  648
```

NCBI GI BLAST score E value 4.0e-68 Match length 135 % identity 93

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273 (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A
[Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A. thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and gb\_R30430 come from this gene. [Arabidopsis thaliana] >gi\_4538910 emb CAB39647.1 (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 235378

Seq. ID LIB3272-054-P1-K1-B4

Method BLASTX NCBI GI g2764574 BLAST score 503 E value 4.0e-51 Match length 138 % identity 70

NCBI Description (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]

Seq. No. 235379

Seq. ID LIB3272-054-P1-K1-B5

Method BLASTX NCBI GI q4090257 BLAST score 293 E value 1.0e-40 Match length 91 % identity

NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

Seq. No. 235380

Seq. ID LIB3272-054-P1-K1-B7

Method BLASTX NCBI GI g2244797 BLAST score 166 E value 1.0e-11



```
Match length
                  61
% identity
NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  235381
                  LIB3272-054-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4090257
BLAST score
                  286
E value
                  8.0e-40
Match length
                  91
% identity
                  95
NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
Seq. No.
                  235382
                  LIB3272-054-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1545805
BLAST score
                  207
E value
                  2.0e-16
Match length
                  71
% identity
                  63
NCBI Description (D64052) cytochrome P450 like TBP [Nicotiana tabacum]
Seq. No.
                  235383
                  LIB3272-054-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1419090
BLAST score
                  389
E value
                  1.0e-37
Match length
                  121
% identity
                  64
NCBI Description (X94968) 37kDa chloroplast inner envelope membrane
                  polypeptide precursor [Nicotiana tabacum]
Seq. No.
                  235384
Seq. ID
                  LIB3272-054-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q3337356
BLAST score
                  228
E value
                  7.0e-19
                  90
Match length
% identity
                  64
NCBI Description (AC004481) putative protein transport protein SEC61 alpha
                  subunit [Arabidopsis thaliana]
                  235385
Seq. No.
                  LIB3272-054-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1724100
BLAST score
                  255
E value
                  2.0e-22
                  70
Match length
                  70
% identity
NCBI Description (U79765) porin [Mesembryanthemum crystallinum]
```

Seq. No. 235386



```
LIB3272-054-P1-K1-C7
Seq. ID
                  BLASTX
Method
                  q3421102
NCBI GI
                  493
BLAST score
                  6.0e-50
E value
                  109
Match length
                  83
% identity
                  (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis
NCBI Description
                  thaliana]
                  235387
Seq. No.
                  LIB3272-054-P1-K1-C8
Seq. ID
                  BLASTX
Method
                  q4510363
NCBI GI
                  569
BLAST score
                  8.0e-59
E value
                  117
Match length
                  87
% identity
                  (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  235388
Seq. No.
                  LIB3272-054-P1-K1-D1
Seq. ID
                  BLASTX
Method
                  q1172555
NCBI GI
                  414
BLAST score
                  8.0e-41
E value
                  96
Match length
                  83
% identity
NCBI Description 34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
                   (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                   (POM 34) >gi_629720_pir__S46936 34K porin - potato
                   >gi 1076682_pir__A55364_porin (clone pPOM-34) - potato
                   mitochondrion >gi_516166_emb_CAA56599_ (X80386) 34 kDA
                   porin [Solanum tuberosum]
Seq. No.
                   235389
                   LIB3272-054-P1-K1-D12
Seq. ID
                   BLASTX
Method
                   g1351014
NCBI GI
                   232
BLAST score
                   1.0e-19
E value
                   76
Match length
                   64
 % identity
NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010)
                   ribosomal protein S8 [Oryza sativa]
 Seq. No.
                   235390
                   LIB3272-054-P1-K1-D2
 Seq. ID
                   BLASTX
Method
                   q464981
 NCBI GI
                   737
 BLAST score
 E value
                   2.0e-78
 Match length
                   137
                   98
 % identity
 NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
```

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762)



## ubiquitin carrier protein [Lycopersicon esculentum]

```
235391
Seq. No.
                  LIB3272-054-P1-K1-D3
Seq. ID
                  BLASTX
Method
                  q3738285
NCBI GI
                  303
BLAST score
                  1.0e-27
E value
                  78
Match length
                  74
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
                  235392
Seq. No.
                  LIB3272-054-P1-K1-D5
Seq. ID
Method
                  BLASTX
                  g1313968
NCBI GI
                  395
BLAST score
                  2.0e-38
E value
Match length
                  113
                   67
% identity
NCBI Description (Z72426) major allergen Mal d 1 [Malus domestica]
                   235393
Seq. No.
                  LIB3272-054-P1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                   q4432835
                   148
BLAST score
                   2.0e-09
E value
                   76
Match length
% identity
                   39
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
                   235394
Seq. No.
                   LIB3272-054-P1-K1-D8
Seq. ID
                   BLASTX
Method
                   q1351365
NCBI GI
                   185
BLAST score
                   8.0e-14
E value
                   56
Match length
                   62
% identity
NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 6.7 KD PROTEIN
                   (CR6) >gi_2130002 pir__S68969 ubiquinol--cytochrome-c
                   reductase (EC 1.10.2.2) - potato >gi_633683_emb_CAA57768
                   (X82325) cytochrome c reductase subunit [Solanum tuberosum]
 Seq. No.
                   235395
                   LIB3272-054-P1-K1-E1
 Seq. ID
                   BLASTX
Method
                   g3980412
NCBI GI
                   638
 BLAST score
                   7.0e-67
 E value
                   138
 Match length
 % identity
 NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
 Seq. No.
                   235396
                   LIB3272-054-P1-K1-E2
 Seq. ID
```

34074



```
BLASTX
Method
                   g4539292
NCBI GI
                    452
BLAST score
                    4.0e-45
E value
                   96
Match length
                    86
% identity
                    (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                    thaliana]
                    235397
Seq. No.
                   LIB3272-054-P1-K1-E3
Seq. ID
                   BLASTX
Method
                    g2815246
NCBI GI
                    225
BLAST score
                    2.0e-18
E value
                    55
Match length
                    73
% identity
                   (X95709) class I type 2 metallothionein [Cicer arietinum]
NCBI Description
                    235398
Seq. No.
                    LIB3272-054-P1-K1-E7
Seq. ID
                    BLASTX
Method
                    g2129495
NCBI GI
                    274
BLAST score
                    3.0e-24
E value
                    54
Match length
                    89
% identity
                    fiber protein E6 (clone SIE6-2A) - sea-island cotton
NCBI Description
                    >gi 1000088 (U30507) E6 [Gossypium barbadense] >gi_1000090
                    (U3\overline{0}508) E6 [Gossypium barbadense]
                    235399
Seq. No.
                    LIB3272-054-P1-K1-E9
Seq. ID
                    BLASTX
Method
                    q549063
NCBI GI
                    367
BLAST score
                    4.0e - 35
E value
                    112
Match length
                    65
% identity
                    TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                    >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                    21kd polypeptide [Oryza sativa]
                    235400
Seq. No.
                    LIB3272-054-P1-K1-F11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3450889
                    253
BLAST score
                    9.0e-22
E value
Match length
                    60
                    80
 % identity
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
```

34075

235401

BLASTX

LIB3272-054-P1-K1-F4

Seq. No.

Seq. ID

Method

BLAST score

E value Match length 274 3.0e-24

111



```
q3805854
NCBI GI
                  233
BLAST score
                  2.0e-19
E value
                  109
Match length
% identity
                  48
NCBI Description (AL031986) putative protein [Arabidopsis thaliana]
Seq. No.
                  235402
                  LIB3272-054-P1-K1-F5
Seq. ID
Method
                  BLASTX
                  g3493172
NCBI GI
BLAST score
                  514
                  2.0e-52
E value
Match length
                  117
% identity
                  85
NCBI Description (U89609) fiber annexin [Gossypium hirsutum]
                  235403
Seq. No.
                  LIB3272-054-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3450889
BLAST score
                  212
                  2.0e-17
E value
Match length
                  51
% identity
                  80
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
Seq. No.
                  235404
                  LIB3272-054-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024020
BLAST score
                  639
E value
                  5.0e-67
                  126
Match length
                  94
% identity
                  INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D)
NCBI Description
                  >qi 2225881 dbj BAA20877 (AB004824) eukaryotic initiation
                  factor 5A3 [Solanum tuberosum]
                  235405
Seq. No.
Seq. ID
                  LIB3272-054-P1-K1-F9
                  BLASTX
Method
NCBI GI
                  g3319882
BLAST score
                  615
E value
                   3.0e-64
                  121
Match length
                   98
% identity
NCBI Description (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
                  arietinum]
                   235406
Seq. No.
                  LIB3272-054-P1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2370459
```

34076



```
% identity
                 (Y11987) FPF1 protein [Sinapis alba]
NCBI Description
                  235407
Seq. No.
                  LIB3272-054-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3860277
BLAST score
                  400
E value
                  5.0e-39
Match length
                  95
                  82
% identity
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
                  235408
Seq. No.
                  LIB3272-054-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4519673
BLAST score
                  696
                  1.0e-73
E value
Match length
                  140
% identity
                  83
NCBI Description (AB017694) WREBP-2 [Nicotiana tabacum]
                , 235409
Seq. No.
                  LIB3272-054-P1-K1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4204793
BLAST score
                  636
                  1.0e-66
E value
                  135
Match length
                  47
% identity
NCBI Description (U52079) P-glycoprotein [Solanum tuberosum]
                  235410
Seq. No.
Seq. ID
                  LIB3272-054-P1-K1-G9
                  BLASTX
Method
NCBI GI
                  g3158372
BLAST score
                  436
                  2.0e-43
E value
                  90
Match length
                  53
% identity
NCBI Description (AF035383) polyubiquitin [Arabidopsis thaliana]
                  235411
Seq. No.
                  LIB3272-054-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120669
                  497
BLAST score
                  2.0e-50
E value
                  99
Match length
                   93
% identity
```

34077

>gi\_66014\_pir\_\_DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
>gi 19566 emb CAA42905 (X60347) glyceraldehyde

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

NCBI Description

pendula]





## 3-phosphate dehydrogenase [Magnolia liliiflora]

```
Seq. No.
                  235412
                  LIB3272-054-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3982596
BLAST score
                  261
E value
                  5.0e-23
Match length
                  83
% identity
                  63
NCBI Description (AF039027) cationic peroxidase 2 [Glycine max]
                  235413
Seq. No.
                  LIB3272-054-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3860247
BLAST score
                  396
                  2.0e-39
E value
Match length
                  100
% identity
                  84
NCBI Description (AC005824) unknown protein [Arabidopsis thaliana]
Seq. No.
                  235414
                  LIB3272-054-P1-K1-H7
Seq. ID
Method
                  BLASTX
                  g2827713
NCBI GI
BLAST score
                  309
                  2.0e-28
E value
Match length
                  111
% identity
                  60
NCBI Description (AL021684) pyridoxal-phosphate-dependent aminotransferase -
                  like protein [Arabidopsis thaliana]
Seq. No.
                  235415
Seq. ID
                  LIB3272-054-P1-K1-H9
                  BLASTX
Method
                  q120777
NCBI GI
BLAST score
                  159
E value
                  9.0e-11
                  75
Match length
                   44
% identity
NCBI Description SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)
                  >gi 147901 (M88334) succinic semialdehyde dehydrogenase
                   [Escherichia coli] >gi 1789015 (AE000351)
                   succinate-semialdehyde dehydrogenase, NADP-dependent
                   activity [Escherichia coli]
                  235416
Seq. No.
Seq. ID
                  LIB3272-055-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g4006957
BLAST score
                  267
E value
                   2.0e-23
Match length
                   97
% identity
```

34078

(AJ006910) pollen allergen Betv1, isoform at45 [Betula



```
Seq. No.
                   235417
                   LIB3272-055-P1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g629483
                   228
BLAST score
E value
                   9.0e-19
Match length
                   115
% identity
                   44
                   gene 1-Sc3 protein - European white birch
NCBI Description
                   >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
>gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
                   pendula]
Seq. No.
                   235418
                   LIB3272-055-P1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2982452
BLAST score
                   250
E value
                   1.0e-21
Match length
                   113
                   7
% identity
                   (AL022223) receptor protein kinase-like protein
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   235419
                   LIB3272-055-P1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g862931
BLAST score
                   341
                   3.0e-32
E value
Match length
                   103
% identity
                    68
NCBI Description (U27179) acidic glucanase [Medicago sativa subsp. sativa]
Seq. No.
                   235420
                   LIB3272-055-P1-K1-A6
Seq. ID
                   BLASTX
Method
                   q2462762
NCBI GI
BLAST score
                   341
                    4.0e-32
E value
Match length
                   126
                   57
% identity
NCBI Description (AC002292) Highly similar to auxin-induced protein
                    (aldo/keto reductase family) [Arabidopsis thaliana]
                   235421
Seq. No.
Seq. ID
                   LIB3272-055-P1-K1-A7
                   BLASTX
Method
NCBI GI
                   g3915826
BLAST score
                   456
E value
                   1.0e-45
                   119
Match length
                   74
% identity
```

Seq. No. 235422

NCBI Description 60S.RIBOSOMAL PROTEIN L5



Seq. ID

LIB3272-055-P1-K1-A8

```
BLASTX
Method
NCBI GI
                   g1769887
BLAST score
                   305
                   4.0e-28
E value
                  82
Match length
                   73
% identity
                  (X95736) amino acid permease 6 [Arabidopsis thaliana]
NCBI Description
                   235423
Seq. No.
                   LIB3272-055-P1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3415115
BLAST score
                   334
                   2.0e-31
E value
Match length
                   120
                   34
% identity
                  (AF081202) villin 2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   235424
                   LIB3272-055-P1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1531758
BLAST score
                   714
                   8.0e-76
E value
Match length
                   139
                   92
% identity
                   (X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028)
NCBI Description
                   unknown protein [Arabidopsis thaliana]
                   235425
Seq. No.
                   LIB3272-055-P1-K1-B12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2811025
BLAST score
                   289
E value
                   5.0e-26
                   90
Match length
                   63
% identity
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi 1944181 dbj BAA19607
                   (AB002695) aspartic endopeptidase [Cucurbita pepo]
                   235426
Seq. No.
                   LIB3272-055-P1-K1-B3
Seq. ID
                   BLASTX
Method
                   q710308
NCBI GI
BLAST score
                   643
                   2.0e-67
E value
                   141
Match length
                   86
% identity
NCBI Description (U11693) victorin binding protein [Avena sativa]
                   235427
Seq. No.
                   LIB3272-055-P1-K1-B5
Seq. ID
                   BLASTX
Method
                   g3241945
NCBI GI
BLAST score
                   265
E value
                   4.0e-23
```



```
Match length
                  128
% identity
                   44
                 (AC004625) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  235428
Seq. ID
                  LIB3272-055-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q3413706
BLAST score
                  148
E value
                  7.0e-17
                  87
Match length
% identity
                  61
NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  235429
Seq. ID
                  LIB3272-055-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g3694872
BLAST score
                  445
E value
                  3.0e-44
Match length
                  112
% identity
                  75
NCBI Description (AF092547) profilin [Ricinus communis]
Seq. No.
                  235430
Seq. ID
                  LIB3272-055-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g2565305
BLAST score
                  209
E value
                  9.0e-17
Match length
                  104
                  45
% identity
NCBI Description (AF024589) glycine decarboxylase P subunit [Hordeum sp. x
                  Triticum sp.]
                  235431
Seq. No.
Seq. ID
                  LIB3272-055-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3646373
BLAST score
                  636
E value
                  1.0e-66
Match length
                  124
% identity
                  94
NCBI Description (AJ011078) RGP1 protein [Oryza sativa]
Seq. No.
                  235432
Seq. ID
                  LIB3272-055-P1-K1-C10
Method
                  BLASTX
```

NCBI GI g2738949 BLAST score 463 2.0e-46 E value Match length 96 % identity

NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x

ananassa]

Seq. No. 235433

```
Seq. ID
                   LIB3272-055-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g2735017
BLAST score
                   457
E value
                   1.0e-45
Match length
                   124
% identity
                   70
NCBI Description (U82481) KI domain interacting kinase 1 [Zea mays]
Seq. No.
                   235434
Seq. ID
                   LIB3272-055-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g1332579
BLAST score
                   626
E value
                   2.0e-65
Match length
                   126
% identity
                   10
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                   235435
Seq. ID
                  LIB3272-055-P1-K1-C6
Method
                  BLASTX
NCBI GI
                   g3721926
BLAST score
                   530
E value
                   3.0e-54
Match length
                  105
% identity
                   99
NCBI Description
                 (AB017480) chloroplast FtsH protease [Nicotiana tabacum]
Seq. No.
                   235436
Seq. ID
                  LIB3272-055-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3158474
BLAST score
                  308
E value
                  2.0e-28
Match length
                  77
% identity
                  82
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
Seq. No.
                  235437
Seq. ID
                  LIB3272-055-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1408471
BLAST score
                  517
                  9.0e-53
E value
Match length
                  115
% identity
                  82
NCBI Description
```

(U48938) actin depolymerizing factor 1 [Arabidopsis

thaliana] >gi\_3851707 (AF102173) actin depolymerizing

factor 1 [Arabidopsis thaliana]

Seq. No. 235438

Seq. ID LIB3272-055-P1-K1-D10

Method BLASTX NCBI GI g1170747 BLAST score 345 E value 1.0e-32



Match length 76 % identity 91

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi\_167345 (M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi\_167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 235439

Seq. ID LIB3272-055-P1-K1-D2

Method BLASTX
NCBI GI g3281853
BLAST score 181
E value 3.0e-13
Match length 37
% identity 95

NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 235440

Seq. ID LIB3272-055-P1-K1-D5

Method BLASTX
NCBI GI g3482980
BLAST score 326
E value 3.0e-30
Match length 140
% identity 51

NCBI Description (AL031369) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235441

Seq. ID LIB3272-055-P1-K1-D7

Method BLASTX
NCBI GI g3241945
BLAST score 192
E value 1.0e-14
Match length 109
% identity 39

NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]

Seq. No. 235442

Seq. ID LIB3272-055-P1-K1-E1

Method BLASTX
NCBI GI g167367
BLAST score 406
E value 1.0e-39
Match length 109
% identity 72

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

Seq. No. 235443

Seq. ID LIB3272-055-P1-K1-E10

Method BLASTX
NCBI GI g1621268
BLAST score 379
E value 1.0e-36
Match length 114
% identity 69

NCBI Description (Z81012) unknown [Ricinus communis]



```
Seq. No.
                   235444
Seq. ID
                  LIB3272-055-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q1076668
BLAST score
                   480
E value
                   2.0e-48
Match length
                   124
% identity
                   73
NCBI Description
                  NADH dehydrogenase (EC 1.6.99.3) - potato
                  >gi_639834 emb CAA58823 (X83999) NADH dehydrogenase
                   [Solanum tuberosum]
Seq. No.
                  235445
Seq. ID
                  LIB3272-055-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g132944
BLAST score
                  657
E value
                  4.0e-69
Match length
                  131
% identity
                  92
NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_81658_pir__JQ0772 ribosomal
                  protein L3 (ARP2) - Arabidopsis thaliana >gi_806279
                  (M32655) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                  235446
Seq. ID
                  LIB3272-055-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  548
E value
                  2.0e-56
Match length
                  112
% identity
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                  235447
Seq. ID
                  LIB3272-055-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g1657948
BLAST score
                  349
E value
                  4.0e-33
Match length
                  96
% identity
                  73
NCBI Description (U73466) MipC [Mesembryanthemum crystallinum]
Seq. No.
                  235448
Seq. ID
                  LIB3272-055-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3123271
BLAST score
                  407
E value
                  6.0e-40
Match length
                  101
```

74 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S6 >gi 2224751 emb CAA74381 (Y14052)

ribosomal protein S6 [Arabidopsis thaliana]

Seq. No. 235449

Seq. ID LIB3272-055-P1-K1-F4



Method BLASTX
NCBI GI g549063
BLAST score 493
E value 7.0e-50
Match length 113
% identity 82

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 235450

Seq. ID LIB3272-055-P1-K1-F6

Method BLASTX
NCBI GI g3868758
BLAST score 484
E value 8.0e-49
Match length 136
% identity 65

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 235451

Seq. ID LIB3272-055-P1-K1-F7

Method BLASTX
NCBI GI 94210948
BLAST score 514
E value 2.0e-52
Match length 100
% identity 96

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No. 235452

Seq. ID LIB3272-055-P1-K1-F8

Method BLASTX
NCBI GI g3142698
BLAST score 362
E value 1.0e-34
Match length 88
% identity 78

NCBI Description (AF064542) protein farnesyltransferase subunit A

[Arabidopsis thaliana]

Seq. No. 235453

Seq. ID LIB3272-055-P1-K1-F9

Method BLASTX
NCBI GI g2088651
BLAST score 313
E value 6.0e-29
Match length 101
% identity 61

NCBI Description (AF002109) hypersensitivity-related gene 201 isolog

[Arabidopsis thaliana]

Seq. No. 235454

Seq. ID LIB3272-055-P1-K1-G1

Method BLASTX NCBI GI g4567267



BLAST score 313 E value 5.0e-43Match length 95 % identity 60

NCBI Description (AC006841) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No.

235455

Seq. ID

LIB3272-055-P1-K1-G10

Method BLASTX NCBI GI g417103 BLAST score 645 E value 1.0e-67 Match length 129 % identity 100

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957 (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958 (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 ( $\overline{\text{U}}$ 09460)

histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2 [Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911 emb\_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi\_1435157 emb\_CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.

235456 Seq. ID

LIB3272-055-P1-K1-G12

Method BLASTX NCBI GI q2995384 BLAST score 167 E value 9.0e-12 Match length 59 % identity 57

(AJ004810) cytochrome P450 monooxygenase [Zea mays] NCBI Description

Seq. No. 235457

Seq. ID LIB3272-055-P1-K1-G3

Method BLASTX NCBI GI g464444 BLAST score 466 E value 7.0e-47Match length 100 % identity 89

NCBI Description PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX 30 KD SUBUNIT) >gi 541889 pir S39900 proteasome -

Arabidopsis thaliana >gi 166830 (M98495) proteasome

[Arabidopsis thaliana]

Method

NCBI GI

BLASTX

g3851636

```
Seq. No.
                   235458
Seq. ID
                  LIB3272-055-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2739168
BLAST score
                  311
E value
                  2.0e-36
Match length
                  115
% identity
                   67
NCBI Description (AF032386) aldose-1-epimerase-like protein [Nicotiana
                  tabacum]
Seq. No.
                  235459
Seq. ID
                  LIB3272-055-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g4455207
BLAST score
                  440
E value
                  1.0e-43
Match length
                  95
% identity
                  91
NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
Seq. No.
                  235460
Seq. ID
                  LIB3272-055-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g1076737
BLAST score
                  414
E value
                  8.0e-41
Match length
                  81
% identity
                  98
NCBI Description beta-tubulin R1623 - rice
Seq. No.
                  235461
Seq. ID
                  LIB3272-055-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q4455207
BLAST score
                  339
E value
                  8.0e-32
Match length
                  96
% identity
                  75
NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]
Seq. No.
                  235462
Seq. ID
                  LIB3272-055-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g544437
BLAST score
                  374
E value
                  6.0e-36
Match length
                  85
% identity
                  86
NCBI Description GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN)
                  >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]
Seq. No.
                  235463
Seq. ID
                  LIB3272-055-P1-K1-H9
```



BLAST score 383 E value 4.0e-37 Match length 91 % identity 79

NCBI Description (AF098519) unknown [Avicennia marina] >gi\_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No. 235464

Seq. ID LIB3272-058-P1-K1-A10

Method BLASTX
NCBI GI g549063
BLAST score 377
E value 3.0e-36
Match length 114
% identity 66

NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)

>gi\_1072464\_pir\_\_A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi\_303835\_dbj\_BAA02151\_ (D12626)

21kd polypeptide [Oryza sativa]

Seq. No. 235465

Seq. ID LIB3272-058-P1-K1-A11

Method BLASTX
NCBI GI g464707
BLAST score 663
E value 8.0e-70
Match length 132
% identity 96

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi\_480908 pir S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi\_434343\_emb\_CAA82273\_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A. thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and gb\_R30430 come from this gene. [Arabidopsis thaliana] >gi\_4538910\_emb\_CAB39647.1\_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 235466

Seq. ID LIB3272-058-P1-K1-A12

Method BLASTX
NCBI GI g3021265
BLAST score 200
E value 2.0e-15
Match length 140
% identity 36

NCBI Description (AL022347) protein kinase - like protein [Arabidopsis

thaliana] >gi\_3292839\_emb\_CAA19829\_ (AL031018) protein

kinase - like protein [Arabidopsis thaliana]



Seq. ID LIB3272-058-P1-K1-A2 Method BLASTX

NCBI GI g1705812
BLAST score 475
E value 9.0e-48

Match length 141 % identity 64

NCBI Description ACIDIC CHITINASE PRECURSOR >gi\_1150686\_emb\_CAA92207\_

(Z68123) acidic chitinase [Vitis vinifera]

Seq. No. 235468

Seq. ID LIB3272-058-P1-K1-A3

Method BLASTX
NCBI GI g1170747
BLAST score 385
E value 3.0e-37
Match length 87
% identity 85

NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA5-A >gi\_167345

(M88324) late embryogenesis-abundant protein [Gossypium

hirsutum] >gi\_167347 (M37697) Lea5-A late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No. 235469

Seq. ID LIB3272-058-P1-K1-A4

Method BLASTX
NCBI GI g2500347
BLAST score 254
E value 2.0e-26
Match length 117
% identity 60

NCBI Description NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG

>gi\_3878691\_emb\_CAA90127\_ (Z49911) similar to ribosomal
protein (L7AE family); cDNA EST EMBL:D73957 comes from this
gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST
EMBL:D74077 comes from this gene; cDNA EST EMBL:D71393

comes from this gene; cD

Seq. No. 235470

Seq. ID LIB3272-058-P1-K1-A5

Method BLASTX
NCBI GI g136636
BLAST score 543
E value 9.0e-56
Match length 105
% identity 95

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN

LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)

>gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 -

Arabidopsis thaliana >gi\_442594\_pdb\_1AAK\_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi\_2981894\_pdb\_2AAK\_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi\_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi\_431260 (L19351) ubiquitin conjugating enzyme

[Arabidopsis thaliana]



Seq. ID LIB3272-058-P1-K1-A6 Method BLASTX NCBI GI q1709498 BLAST score 566 E value 2.0e-58 Match length 127 80 % identity NCBI Description OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi\_1362001\_pir\_\_S57524 osmotin precursor - Arabidopsis thaliana >gi\_887390\_emb\_CAA61411\_ (X89008) osmotin [Arabidopsis thaliana] Seq. No. 235472 Seq. ID LIB3272-058-P1-K1-A8 Method BLASTX NCBI GI q1220196 BLAST score 612 E value 7.0e-64 Match length 133 % identity NCBI Description (U49061) alcohol dehydrogenase 2a [Gossypium hirsutum] Seq. No. 235473 Seq. ID LIB3272-058-P1-K1-B10 Method BLASTX NCBI GI q2497702 BLAST score 197 E value 3.0e-15 Match length 133 % identity 36 NCBI Description OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi\_2121019\_pir\_\_I40710 outer membrane lipoprotein -Citrobacter freundii >gi\_717136 (U21727) lipocalin precursor [Citrobacter freundii] Seq. No. 235474 LIB3272-058-P1-K1-B12 Seq. ID Method BLASTX NCBI GI q1657948 BLAST score 468 E value 6.0e-47 Match length 103 % identity 87 NCBI Description (U73466) MipC [Mesembryanthemum crystallinum] Seq. No. 235475 Seq. ID LIB3272-058-P1-K1-B2 Method BLASTX NCBI GI g2459417

Method BLASTX
NCBI GI g2459417
BLAST score 542
E value 1.0e-55
Match length 118
% identity 86

NCBI Description (AC002332) putative pre-mRNA splicing factor PRP19

[Arabidopsis thaliana]



Seq. ID LIB3272-058-P1-K1-B4 Method BLASTX NCBI GI g3193285 BLAST score 143 E value 7.0e-09 Match length 85 % identity 33 NCBI Description (AF069298) T14P8.18 gene product [Arabidopsis thaliana] 235477 Seq. No. Seq. ID LIB3272-058-P1-K1-B7 Method BLASTX NCBI GI g1431629 BLAST score 380 E value 1.0e-36 99 Match length % identity 70 NCBI Description (X99348) pectinacetylesterase precursor [Vigna radiata] Seq. No. 235478 Seq. ID LIB3272-058-P1-K1-B8 Method BLASTX NCBI GI q4455129 BLAST score 277 E value 1.0e-24 84 Match length % identity 62 NCBI Description (AF127761) ribonucleoprotein ZRNP1 [Homo sapiens] Seq. No. 235479 Seq. ID LIB3272-058-P1-K1-B9 Method BLASTX NCBI GI g1769903 BLAST score 414 E value 1.0e-40 Match length 127 % identity 61 NCBI Description (X95738) proline transporter 2 [Arabidopsis thaliana] Seq. No. 235480 Seq. ID LIB3272-058-P1-K1-C1 Method BLASTX NCBI GI g2792297 BLAST score 261 1.0e-22 E value Match length 77 % identity NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa] Seq. No. 235481 Seq. ID LIB3272-058-P1-K1-C11 Method BLASTX

NCBI GI g3023180
BLAST score 460
E value 5.0e-46
Match length 114
% identity 82





NCBI Description 14-3-3-LIKE PROTEIN 10 >gi 1771166 emb CAA67374.1 (X98866) 14-3-3 protein [Lycopersicon esculentum] Seq. No. 235482 Seq. ID LIB3272-058-P1-K1-C3 Method BLASTX NCBI GI g3738257 BLAST score 580 E value 4.0e-60 Match length 124 % identity 91 NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra] 235483 Seq. No. Seq. ID LIB3272-058-P1-K1-C5 Method BLASTX NCBI GI g1166450 BLAST score 302 E value 2.0e-27 Match length 66 % identity 82 NCBI Description (X95262) Tfm5 [Lycopersicon esculentum] Seq. No. 235484 Seq. ID LIB3272-058-P1-K1-C7 Method BLASTX NCBI GI g529353 BLAST score 221 E value 4.0e-18 80 Match length % identity 57 NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus] Seq. No. 235485 Seq. ID LIB3272-058-P1-K1-D1 Method BLASTX NCBI GI g3805964 BLAST score 593 E value 1.0e-61 Match length 140 % identity 76 NCBI Description (Y13773) laccase [Populus balsamifera subsp. trichocarpa] Seq. No. 235486 Seq. ID LIB3272-058-P1-K1-D11 Method BLASTX NCBI GI q3023847 BLAST score 575 E value 2.0e-59 Match length 119 % identity 36

PROTEIN >gi\_2385376\_emb\_CAA69934\_ (Y08678) G protein beta

235487

Seq. No.

34092

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

subunit-like [Medicago sativa]

NCBI Description

sapiens]



```
Seq. ID
                  LIB3272-058-P1-K1-D12
                  BLASTX
Method
NCBI GI
                  g1130682
BLAST score
                  723
E value
                  7.0e-77
Match length
                  139
% identity
                  99
                 (Z46959) acetohydroxyacid synthase [Gossypium hirsutum]
NCBI Description
                  235488
Seq. No.
Seq. ID
                  LIB3272-058-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g124224
BLAST score
                  682
E value
                  5.0e-72
Match length
                  135
                  95
% identity
                  INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi 100345 pir S21060 translation initiation factor eIF-5A
                  - common tobacco >gi 19887 emb CAA45105 (X63543)
                  eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
Seq. No.
                  235489
Seq. ID
                  LIB3272-058-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q586797
BLAST score
                  236
E value
                  9.0e-20
                  100
Match length
% identity
                  44
NCBI Description HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III
Seq. No.
                  235490
Seq. ID
                  LIB3272-058-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g3023316
BLAST score
                  248
E value
                  4.0e-21
Match length
                  123
% identity
                  45
NCBI Description
                 ALTERNATIVE OXIDASE 1 PRECURSOR >gi 558054 bbs 150257
                  (S71335) alternative oxidase, AOX [Nicotiana
                  tabacum=tobacco, cv Bright Yellow, suspension cells,
                  Peptide Mitochondrial, 353 aa] [Nicotiana tabacum]
                  >gi 1090812 prf 2019465A Aox1 gene [Nicotiana tabacum]
Seq. No.
                  235491
Seq. ID
                  LIB3272-058-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g1620898
BLAST score
                  581
E value
                  3.0e-60
Match length
                  141
% identity
```

(D87957) protein involved in sexual development [Homo



```
Seq. No.
                    235492
Seq. ID
                    LIB3272-058-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    g3694872
BLAST score
                    485
E value
                    6.0e-49
Match length
                   118
% identity
                    77
NCBI Description (AF092547) profilin [Ricinus communis]
Seq. No.
                    235493
Seq. ID
                   LIB3272-058-P1-K1-E1
Method
                   BLASTX
NCBI GI
                    q445613
BLAST score
                    410
E value
                    4.0e-40
Match length
                   122
% identity
                    69
NCBI Description ribosomal protein L7 [Solanum tuberosum]
Seq. No.
                    235494
Seq. ID
                   LIB3272-058-P1-K1-E11
Method
                   BLAŞTX
NCBI GI
                    g135406
BLAST score
                    552
E value
                    8.0e-57
Match length
                    107
% identity
                    96
NCBI Description
                   TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin
                    alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                    alpha-5 tubulin [Arabidopsis thaliana]
                    235495
Seq. No.
Seq. ID
                   LIB3272-058-P1-K1-E12
Method
                   BLASTX
NCBI GI
                    g1706918
BLAST score
                   258
E value
                   2.0e-22
Match length
                   105
% identity
                    46
NCBI Description FLAVONOL SULFOTRANSFERASE-LIKE >gi 498647 (U10277)
                   sulfotransferase-like flavonol [Flaveria bidentis]
Seq. No.
                   235496
Seq. ID
                   LIB3272-058-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g2244806
BLAST score
                   151
E value
                   9.0e-10
                   80
Match length
% identity
                    35
```

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No. Seq. ID LIB3272-058-P1-K1-E3

235497

Method BLASTX



```
NCBI GI
                   g1703028
BLAST score
                   167
E value
                   1.0e-11
                   87
Match length
% identity
                   43
NCBI Description
                   CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 (CLATHRIN
                   COAT ASSOCIATED PROTEIN AP47 HOMOLOG 2) (GOLGI ADAPTOR AP-1
                   47 KD PROTEIN HOMOLOG 2) (HA1 47 KD SUBUNIT HOMOLOG 2)
                   (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPL...
                   >gi_2134919_pir__A57170 clathrin-associated protein AP47
homolog CLA20 - human >gi_807815_dbj_BAA07415_ (D38293)
                   clathrin-like protein [Homo sapiens]
Seq. No.
                   235498
Seq. ID
                   LIB3272-058-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g1843527
BLAST score
                   509
E value
                   9.0e-52
Match length
                   132
% identity
                   45
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                   235499
Seq. ID
                   LIB3272-058-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g3355468
BLAST score
                   540
E value
                   2.0e-55
Match length
                   123
                   90
% identity
NCBI Description
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
                   thaliana]
Seq. No.
                   235500
                   LIB3272-058-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1173218
BLAST score
                   567
                   1.0e-58
E value
Match length
                   113
% identity
                   97
NCBI Description
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
                   protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                   cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                   235501
Seq. ID
                   LIB3272-058-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q629483
```

Method BLASTX
NCBI GI g629483
BLAST score 323
E value 6.0e-30
Match length 121
% identity 54

NCBI Description gene 1-Sc3 protein - European white birch

>gi\_534898\_emb\_CAA54696\_ (X77601) 1 Sc-3 [Betula pendula]
>gi\_1584322 prf\_\_2122374C allergen Bet v 1-Sc3 [Betula

NCBI Description



## pendula]

```
Seq. No.
                   235502
Seq. ID
                   LIB3272-058-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2950478
BLAST score
                   223
E value
                   3.0e-18
Match length
                   103
% identity
                   47
NCBI Description (AL022070) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                   235503
Seq. ID
                   LIB3272-058-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g2995384
BLAST score
                   300
E value
                   2.0e-27
Match length
                   90
% identity
                   67
NCBI Description (AJ004810) cytochrome P450 monooxygenase [Zea mays]
Seq. No.
                   235504
Seq. ID
                   LIB3272-058-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g418596
BLAST score
                   242
E value
                   2.0e-20
Match length
                   99
% identity
                   43
NCBI Description PUTATIVE 40S RIBOSOMAL PROTEIN YHR148W
                   >gi 485540 pir S33911 hypothetical protein YHR148w - yeast
                   (Saccharomyces cerevisiae) >gi_4014_emb_CAA49237_ (X69480)
                   uORF1 [Saccharomyces cerevisiae] >gi 500654 (U10397)
                   Yhr148wp [Saccharomyces cerevisiae]
Seq. No.
                   235505
Seq. ID
                   LIB3272-058-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g1666228
BLAST score
                   672
                   7.0e-71
E value
Match length
                  126
% identity
                  (U76190) actin [Pisum sativum] >gi 1666230 (U76191) actin
NCBI Description
                   [Pisum sativum] >gi_1724137 (U8104\overline{6}) actin [Pisum sativum]
                  >gi_1724139 (U81047) actin [Pisum sativum]
Seq. No.
                  235506
Seq. ID
                  LIB3272-058-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1657948
BLAST score
                  492
E value
                  9.0e-50
Match length
                  125
% identity
                  78
```

(U73466) MipC [Mesembryanthemum crystallinum]



```
Seq. No.
                   235507
Seq. ID
                   LIB3272-058-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g124224
BLAST score
                   620
E value
                   9.0e-65
Match length
                   122
% identity
                   94
NCBI Description INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
                   >gi_100345_pir__S21060 translation initiation factor eIF-5A
                   - common tobacco >gi 19887 emb CAA45105 (X63543)
                   eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
Seq. No.
                   235508
Seq. ID
                   LIB3272-058-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   402
E value
                   3.0e-39
Match length
                   119
                   67
% identity
NCBI Description TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                   235509
Seq. ID
                   LIB3272-058-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   q508304
BLAST score
                   218
E value
                   1.0e-17
                   76
Match length
% identity
NCBI Description (L22305) corC [Medicago sativa]
Seq. No.
                   235510
Seq. ID
                   LIB3272-058-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g3023847
BLAST score
                   561
E value
                   7.0e-58
Match length
                   116
% identity
                   35
NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN >gi_2385376_emb_CAA69934_ (Y08678) G protein beta
                   subunit-like [Medicago sativa]
Seq. No.
                   235511
Seq. ID
                   LIB3272-058-P1-K1-G12
```

Method BLASTX NCBI GI q4239845 BLAST score 240 E value 3.0e-21

Match length 130 % identity 44





```
NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]
                  235512
Seq. No.
Seq. ID
                  LIB3272-058-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g4510398
BLAST score
                  346
E value
                  1.0e-32
                  130
Match length
% identity
                  50
NCBI Description (AC006587) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  235513
Seq. ID
                  LIB3272-058-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g548852
BLAST score
                  361
E value
                  2.0e-34
Match length
                  82
% identity
                  80
NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi 481227_pir_ S38357 ribosomal
                  protein S21 - rice >gi 303839 dbj BAA02158 (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
Seq. No.
                  235514
Seq. ID
                  LIB3272-058-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g2388578
BLAST score
                  481
E value
                  2.0e-48
                  135
Match length
% identity
                  72
NCBI Description
                  (AC000098) Similar to Mycobacterium RlpF (gb Z84395). ESTs
                  gb_T75785,gb_R30580,gb_T04698 come from this gene.
                  [Arabidopsis thaliana]
                  235515
Seq. No.
Seq. ID
                  LIB3272-058-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2244769
BLAST score
                  209
E value
                  7.0e-17
Match length
                  70
% identity
                  59
NCBI Description
                 (Z97335) xyloglucan endotransglycosylase-related protein
                  XTR-7 [Arabidopsis thaliana]
Seq. No.
                  235516
Seq. ID
                  LIB3272-058-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  653
E value
                  1.0e-68
Match length
                  131
% identity
```

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]



```
235517
Seq. No.
Seq. ID
                 LIB3272-058-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2160166
                  332
BLAST score
                  5.0e-31
E value
Match length
                  131
                  57
% identity
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]
Seq. No.
                  235518
Seq. ID
                  LIB3272-058-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q2462929 .
BLAST score
                  330
E value
                  8.0e-31
                  135
Match length
                  56
% identity
NCBI Description (Y12295) glutathione transferase [Arabidopsis thaliana]
Seq. No.
                  235519
Seq. ID
                  LIB3272-058-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q2970051
BLAST score
                  502
E value
                  6.0e-51
                  107
Match length
% identity
                  90
NCBI Description (AB012110) ARG10 [Vigna radiata]
                  235520
Seq. No.
Seq. ID
                  LIB3272-058-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g4426565
BLAST score
                  140
E value
                  3.0e-10
                  123
Match length
% identity
                  31
NCBI Description (AF031483) unknown [Rattus norvegicus]
Seq. No.
                  235521
Seq. ID
                  LIB3272-058-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q1173104
BLAST score
                  447
E value
                  2.0e-44
Match length
                  94
                  78
% identity
NCBI Description RIBONUCLEASE 2 PRECURSOR > gi 289210 (M98336) ribonuclease
                  [Arabidopsis thaliana] >gi 2642160 (AC003000) ribonuclease,
                  RNS2 [Arabidopsis thaliana]
Seq. No.
                  235522
Seq. ID
                  LIB3272-058-P1-K1-H2
```

Method BLASTX NCBI GI q4185140 BLAST score 406



E value 1.0e-39 Match length 88 % identity 91

NCBI Description (AC005724) putative small nuclear ribonucleoprotein E

(snRNP-E) [Arabidopsis thaliana]

Seq. No. 235523

Seq. ID LIB3272-058-P1-K1-H3

Method BLASTX NCBI GI g135406 BLAST score 507 E value 2.0e-51 99 Match length 96 % identity

NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >qi 99768 pir A32712 tubulin

alpha-5 chain - Arabidopsis thaliana >gi\_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi\_166918 (M84698)

alpha-5 tubulin [Arabidopsis thaliana]

Seq. No. 235524

Seq. ID LIB3272-058-P1-K1-H4

Method BLASTX NCBI GI g1730843 BLAST score 187 E value 5.0e-14Match length 140 % identity 14

NCBI Description HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC

REGION >gi\_2131945\_pir\_\_S63228 hypothetical protein YNL255c
- yeast (Saccharomyces cerevisiae)

>gi\_1255963\_emb\_CAA65489\_ (X96722) ORF N0852 [Saccharomyces cerevisiae] >gi 1302303 emb CAA96162 (Z71531) ORF YNL255c

[Saccharomyces cerevisiae]

Seq. No. 235525

Seq. ID LIB3272-058-P1-K1-H5

Method BLASTX NCBI GI q3882081 BLAST score 685 E value 2.0e-72 Match length 139 % identity 39

NCBI Description (AJ012552) polyubiquitin [Vicia faba]

Seq. No. 235526

Seq. ID LIB3272-058-P1-K1-H6 Method

BLASTX NCBI GI q1076660 BLAST score 229 6.0e-19 E value Match length 47 % identity 89

NCBI Description D13F(MYBST1) protein - potato >gi\_786426\_bbs\_159122

(S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes,

leaf, Peptide, 342 aa] [Solanum tuberosum]



```
Seq. No.
                  235527
Seq. ID
                  LIB3272-058-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2541886
BLAST score
                  141
E value
                  1.0e-08
Match length
                  52
% identity
                  58
NCBI Description (D63675) acetolactate synthase [Cyanidioschyzon merolae]
Seq. No.
                  235528
Seq. ID
                  LIB3272-058-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q3860272
BLAST score
                  423
E value
                  1.0e-59
Match length
                  136
% identity
                  78
NCBI Description
                  (AC005824) putative suppressor protein [Arabidopsis
                  thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
Seq. No.
                235529
Seq. ID
                  LIB3272-058-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  *g3335365
BLAST score
                  233
E value
                  2.0e-19
Match length
                  87
% identity
                  60
NCBI Description (AC003028) high affinity calcium antiporter [Arabidopsis
                  thaliana]
Seq. No.
                  235530
Seq. ID
                  uC-gsflmaxxa001a11b1
Method
                  BLASTX
NCBI GI
                  g3121825
BLAST score
                  166
E value
                  1.0e-11
Match length
                  42
                  83
% identity
NCBI Description
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
                  ANTIOXIDANT PROTEIN) >gi_1498247 emb CAA63910 (X94219)
                  bas1 protein [Spinacia oleracea]
Seq. No.
                  235531
Seq. ID
                  uC-gsflmaxxa001c04b1
Method
                  BLASTX
NCBI GI
                  q4309884
BLAST score
                  148
E value
                  1.0e-09
Match length
                  44
% identity
                  64
```

Seq. No. 235532

NCBI Description

factor; similar to PID:3395591 [Homo sapiens]

(AC006389) similar to Schizosaccharomyces pombe splicing

A\$ 15

BLAST score

E value

241

2.0e-20



```
Seq. ID
                   uC-gsflmaxxa001c12b1
Method
                   BLASTX
NCBI GI
                   g3355483
BLAST score
                   298
E value
                   4.0e-27
Match length
                   59
% identity
                   81
NCBI Description
                  (AC004218) gibberellin-regulated protein (GASA5)-like
                   [Arabidopsis thaliana]
                   235533
Seq. No.
Seq. ID
                   uC-gsflmaxxa001d12b1
Method
                   BLASTX
NCBI GI
                   q2894558
BLAST score
                   246
E value
                   5.0e-21
Match length
                   121
% identity
                   60
NCBI Description (AL021890) putative protein [Arabidopsis thaliana]
Seq. No.
                   235534
Seq. ID
                   uC-gsflmaxxa001f01b1
Method
                   BLASTX
NCBI GI
                   g1922246
BLAST score
                   190
E value
                   2.0e-14
Match length
                  105
% identity
                   42
NCBI Description (Y10086) putative dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   235535
Seq. ID
                  uC-gsflmaxxa001f05b1
Method
                  BLASTX
NCBI GI
                  g3402690
BLAST score
                  153
E value
                   3.0e-10
Match length
                  101
% identity
                   40
                  (AC004697) hypothetical protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   235536
Seq. ID
                  uC-gsflmaxxa001f12b1
Method
                  BLASTX
NCBI GI
                  q3522937
BLAST score
                  234
                  9.0e-20
E value
Match length
                  77
% identity
NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]
Seq. No.
                  235537
Seq. ID
                  uC-gsflmaxxa001h05b1
Method
                  BLASTX
                  q3776015
NCBI GI
```



```
Match length
                  110
% identity
                   52
NCBI Description
                  (AJ010471) RNA helicase [Arabidopsis thaliana]
                  >gi 4249378 gb_AAD14475 (AC005966) Identical to
                   gb_AJ010471 mRNA for DEAD box RNA helicase (RH22) from
                  Arabidopsis thaliana. EST gb_Y11191 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  235538
Seq. ID
                  uC-qsflmaxxa001h12b1
Method
                  BLASTX
NCBI GI
                  g4056457
BLAST score
                  268
E value
                  1.0e-23
Match length
                  68
% identity
                  75
NCBI Description (AC005990) ESTs gb 234051 and gb F13722 come from this
                  gene. [Arabidopsis thaliana]
                  235539
Seq. No.
Seq. ID
                  uC-gsflmaxxa002b04b1
Method
                  BLASTX
NCBI GI
                  g2213587
BLAST score
                  301
E value
                  1.0e-27
Match length
                  107
% identity
                  63
NCBI Description (AC000348) T7N9.7 [Arabidopsis thaliana]
                  235540
Seq. No.
Seq. ID
                  uC-gsflmaxxa002b11b1
Method
                  BLASTX
NCBI GI
                  g2781345
BLAST score
                  453
E value
                  2.0e-45
Match length
                  104
% identity
NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]
Seq. No.
                  235541
Seq. ID
                  uC-gsflmaxxa002d05b1
Method
                  BLASTX
NCBI GI
                  g4539420
BLAST score
                  237
E value
                  8.0e-20
Match length
                  79
% identity
NCBI Description
                  (AL049171) putative protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                  235542
```

Seq. ID uC-gsflmaxxa002d06b1

Method BLASTX
NCBI GI g1449179
BLAST score 334
E value 3.0e-31
Match length 116



```
% identity
NCBI Description
                    (D86506) N-ethylmaleimide sensitive fusion protein
                    [Nicotiana tabacum]
                    235543
Seq. No.
Seq. ID
                   uC-gsflmaxxa002e06b1
Method
                   BLASTX
NCBI GI
                   g1703446
BLAST score
                   194
E value
                   5.0e-15
                   70
Match length
% identity
                   57
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
                   >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana
>gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis
                   thaliana]
                   235544
Seq. No.
Seq. ID
                   uC-gsflmaxxa002e07b1
Method
                   BLASTX
NCBI GI
                   g3004565
BLAST score
                   526
E value
                   9.0e-54
Match length
                   145
% identity
                   29
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   235545
Seq. ID
                   uC-gsflmaxxa002e10b1
                   BLASTX
Method
NCBI GI
                   q1143445
BLAST score
                   308
E value
                   3.0e-28
Match length
                   72
% identity
NCBI Description (X88797) cinnamyl alcohol dehydrogenase [Eucalyptus gunnii]
Seq. No.
                   235546
Seq. ID
                   uC-gsflmaxxa002e11b1
Method
                   BLASTX
NCBI GI
                   q3327393
BLAST score
                   150
E value
                   1.0e-09
Match length
                   93
% identity
NCBI Description (AC004483) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   235547
Seq. ID
                   uC-gsflmaxxa002e12b1
Method
                   BLASTX
NCBI GI
                   g2342683
BLAST score
                   285
E value
                   1.0e-25
Match length
                   57
```

% identity 88
NCBI Description (AC000106) Contains similarity to Bos beta-mannosidase (gb U46067). [Arabidopsis thaliana]

BLAST score

364

```
Seq. No.
                     235548
   Seq. ID
                     uC-gsflmaxxa002f06b1
   Method
                     BLASTX
   NCBI GI
                     g1495802
   BLAST score
                     772
   E value
                     2.0e-82
   Match length
                     170
                     78
   % identity
   NCBI Description (X96405) 13-lipoxygenase [Solanum tuberosum]
   Seq. No.
                     235549
   Seq. ID
                     uC-gsflmaxxa002f07b1
   Method
                     BLASTX
   NCBI GI
                     g1703375
   BLAST score
                     664
   E value
                     8.0e-70
   Match length
                     130
   % identity
                     100
   NCBI Description ADP-RIBOSYLATION FACTOR 1 >gi_965483_dbj_BAA08259_ (D45420)
                     DcARF1 [Daucus carota]
   Seq. No.
                     235550
   Seq. ID
                     uC-gsflmaxxa002f08b1
  Method
                     BLASTX
  NCBI GI
                     q541847
   BLAST score
                     242
  E value
                     4.0e-21
                     58
  Match length
   % identity
                     78
   NCBI Description alcohol dehydrogenase (EC 1.1.1.1) - Arabidopsis thaliana
   Seq. No.
                     235551
   Seq. ID
                     uC-gsflmaxxa002g02b1
  Method
                     BLASTX
  NCBI GI
                     g3288883
   BLAST score
                     374
  E value
                     5.0e-36
  Match length
                     102
   % identity
                     75
  NCBI Description (AB015431) SAR DNA binding protein [Oryza sativa]
   Seq. No.
                     235552
   Seq. ID
                     uC-gsflmaxxa002g03b1
  Method
                     BLASTX
  NCBI GI
                     g3540194
  BLAST score
                     253
  E value
                     7.0e-22
  Match length
                     64
  % identity
  NCBI Description (AC004260) AtVPS45p [Arabidopsis thaliana]
  Seq. No.
                     235553
  Seq. ID
                     uC-gsflmaxxa002h10b1
  Method
                     BLASTX
  NCBI GI
                     g2213601
```

```
E value
                  9.0e-35
Match length
                  129
% identity
                  57
NCBI Description (AC000348) T7N9.21 [Arabidopsis thaliana]
Seq. No.
                  235554
Seq. ID
                  uC-gsflmaxxa002h11b1
```

Method BLASTX

NCBI GI q2407800 BLAST score 520 E value 6.0e-53 Match length 130 % identity 82

NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No. 235555

Seq. ID uC-gsflmaxxa003d07b1

Method BLASTX NCBI GI g2342690 BLAST score 442 E value 7.0e-44Match length 135 % identity 67

NCBI Description (AC000106) Similar to Homo copine I (gb\_U83246).

[Arabidopsis thaliana]

Seq. No. 235556

uC-qsflmaxxa003d09b1 Seq. ID

Method BLASTX NCBI GI q2880043 BLAST score 439 E value 1.0e-43 Match length 129 % identity

NCBI Description (AC002340) putative 3-hydroxyisobutyryl-coenzyme A

hydrolase [Arabidopsis thaliana]

Seq. No. 235557

Seq. ID uC-gsflmaxxa003e06b1

Method BLASTX NCBI GI g4512661 BLAST score 273 E value 3.0e-24 Match length 97 % identity 55

NCBI Description (AC006931) hypothetical protein [Arabidopsis thaliana]

>gi\_4544468\_gb\_AAD22375.1\_AC006580\_7 (AC006580) putative

DNA binding protein [Arabidopsis thaliana]

Seq. No. 235558

Seq. ID uC-gsflmaxxa003e10b1

Method BLASTX NCBI GI g2341039 BLAST score 342 E value 3.0e-32 Match length 97 % identity 67



NCBI Description (AC000104) Similar to Nicotiana lesion-inducing ORF (gb\_U66269). [Arabidopsis thaliana]

Seq. No. 235559

Seq. ID uC-gsflmaxxa003e12b1

Method BLASTX
NCBI GI g2582665
BLAST score 499
E value 8.0e-51
Match length 105
% identity 94

NCBI Description (Z82983) thi [Citrus sinensis]

Seq. No. 235560

Seq. ID uC-gsflmaxxa003f01b1

Method BLASTX
NCBI GI g3452263
BLAST score 358
E value 3.0e-34
Match length 99
% identity 70

NCBI Description (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis

thaliana]

Seq. No. 235561

Seq. ID uC-gsflmaxxa003f02b1

Method BLASTX
NCBI GI g3738257
BLAST score 191
E value 1.0e-14
Match length 42
% identity 95

NCBI Description (AB018410) cytosolic phosphoglycerate kinase 1 [Populus

nigra]

Seq. No. 235562

Seq. ID uC-gsflmaxxa003f03b1

Method BLASTX
NCBI GI g3892059
BLAST score 272
E value 5.0e-24
Match length 76
% identity 59

NCBI Description (AC002330) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 235563

Seq. ID uC-gsflmaxxa003f08b1

Method BLASTX
NCBI GI g3618343
BLAST score 369
E value 3.0e-35
Match length 148
% identity 47

NCBI Description (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]

>gi\_4506223\_ref\_NP\_002808.1\_pPSMD13\_ proteasome (prosome,

macropain) 26S subunit, non-ATPase,



```
Seq. No.
                  235564
Seq. ID
                  uC-gsflmaxxa003g03b1
Method
                  BLASTX
NCBI GI
                  g4580388
BLAST score
                  224
E value
                  3.0e-18
Match length
                  130
% identity
                  43
NCBI Description (AC007171) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  235565
Seq. ID
                  uC-gsflmaxxa003g08b1
Method
                  BLASTX
NCBI GI
                  g4033424
BLAST score
                  363
E value
                  8.0e-35
Match length
                  82
% identity
                  87
NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                  PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
Seq. No.
                  235566
Seq. ID
                  uC-gsflmaxxa003q10b1
Method
                  BLASTX
NCBI GI
                  g3582002
BLAST score
                  153
                  5.0e-10
E value
Match length
                  94
% identity
                  40
NCBI Description (AJ010943) tomato invertase inhibitor [Lycopersicon
                  esculentum]
Seq. No.
                  235567
                  uC-gsflmaxxa003h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432839
BLAST score
                  355
                  9.0e-34
E value
Match length
                  78
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seg. No.
                  235568
Seq. ID
                  uC-gsflmaxxa004d06b1
Method
                  BLASTX
                  g4220524
                  180
                  2.0e-13
```

NCBI GI BLAST score E value

Match length 40 % identity 78

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 235569

Seq. ID uC-gsflmaxxa004e02b1

Method BLASTX

NCBI GI

E value

BLAST score

g2498886

2.0e-19

234



```
NCBI GI
                   q231586
BLAST score
                   191
E value
                   2.0e-14
Match length
                   40
% identity
                   93
NCBI Description
                   ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi_82027_pir__S20504 H+-transporting ATP synthase (EC
                   3.6.1.34) beta chain, mitochondrial - Para rubber tree
                   >gi_18831_emb_CAA41401 (X58498) mitochondrial ATP synthase
                   beta-subunit [Hevea brasiliensis]
Seq. No.
                   235570
Seq. ID
                   uC-gsflmaxxa004e04b1
Method
                   BLASTX
NCBI GI
                   q3860321
BLAST score
                   242
E value
                   6.0e-43
Match length
                   109
% identity
                   75
NCBI Description (AJ012687) beta-galactosidase [Cicer arietinum]
Seq. No.
                   235571
Seq. ID
                   uC-gsflmaxxa004e10b1
Method
                   BLASTX
NCBI GI
                   q3877252
BLAST score
                   265
E value
                   4.0e-23
Match length
                   125
% identity
                   46
NCBI Description
                 (Z93382) F45G2.10 [Caenorhabditis elegans]
Seq. No.
                   235572
Seq. ID
                   uC-gsflmaxxa004f04b1
Method
                   BLASTX
NCBI GI
                   q4539335
BLAST score
                   349
E value
                   5.0e - 33
Match length
                   136
% identity
                   52
NCBI Description
                  (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                   235573
Seq. ID
                  uC-gsflmaxxa004f12b1
Method
                  BLASTX
NCBI GI
                  g4220475
BLAST score
                  197
E value
                   4.0e-15
Match length
                  154
% identity
NCBI Description
                  (AC006069) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  235574
Seq. ID
                  uC-gsflmaxxa004g06b1
Method
                  BLASTX
```



Match length 85 % identity 45

NCBI Description PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM B

>gi\_1296666\_emb\_CAA65775\_ (X97065) Sec23 protein [Homo

sapiens]

Seq. No. 235575

Seq. ID uC-gsflmaxxa004g09b1

Method BLASTX
NCBI GI g3236235
BLAST score 317
E value 3.0e-29
Match length 93
% identity 69

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

>gi\_4056501 (AC005896) unknown protein [Arabidopsis

thaliana]

Seq. No. 235576

Seq. ID uC-gsflmaxxa005a01b1

Method BLASTX
NCBI GI g2827718
BLAST score 211
E value 1.0e-16
Match length 86
% identity 56

NCBI Description (AL021684) retrotransposon - like protein [Arabidopsis

thaliana]

Seq. No. 235577

Seq. ID uC-gsflmaxxa005b08b1

Method BLASTX
NCBI GI g3746063
BLAST score 218
E value 1.0e-17
Match length 95
% identity 43

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No. 235578

Seq. ID uC-gsflmaxxa005b12b1

Method BLASTX
NCBI GI g4262229
BLAST score 140
E value 7.0e-09
Match length 68
% identity 44

NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]

Seq. No. 235579

Seq. ID uC-gsflmaxxa005c03b1

Method BLASTX
NCBI GI g3702331
BLAST score 269
E value 1.0e-23
Match length 139
% identity 48

```
NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   235580
Seq. ID
                   uC-gsflmaxxa005c05b1
Method
                   {\tt BLASTX}
NCBI GI
                   g2842490
BLAST score
                   276
E value
                   6.0e-25
Match length
                   71
                   70
% identity
NCBI Description (AL021749) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                   235581
Seq. ID
                   uC-gsflmaxxa005d04b1
Method
                   BLASTX
NCBI GI
                   g3249095
BLAST score
                   230
E value
                   4.0e-19
Match length
                   69
% identity
                   67
NCBI Description
                  (AC003114) Contains similarity to dihydrofolate reductase
                   (dfr1) gb L13703 from Schizosaccharomyces pombe. ESTs
                   gb N37567 and gb T43002 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   235582
Seq. ID
                   uC-gsflmaxxa005d08b1
Method
                  BLASTX
NCBI GI
                   g897638
BLAST score
                   278
E value
                   8.0e-25
Match length
                   56
% identity
                   96
NCBI Description
                  (M10124) unknown protein [Nicotiana tabacum]
                  >gi_224349_prf__1102209C ORF 3 [Nicotiana sp.]
Seq. No.
                  235583
Seq. ID
                  uC-gsflmaxxa006a04b1
Method
                  BLASTX
```

NCBI GI g2880049 BLAST score 391 E value 4.0e-38 Match length 97 % identity

(AC002340) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 235584

Seq. ID uC-gsflmaxxa006a07b1

Method BLASTX NCBI GI g4522012 BLAST score 406 E value 1.0e - 39Match length 111 % identity 70

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

NCBI GI

E value

BLAST score

g1362086

1.0e-15

153



```
Seq. ID
                   uC-gsflmaxxa006a08b1
Method
                   BLASTX
NCBI GI
                   q99807
BLAST score
                   233
E value
                   9.0e-28
Match length
                   111
% identity
                   59
NCBI Description gene Bp10 protein - rape >gi_17782_emb_CAA47176_ (X66607)
                   Bplo [Brassica napus]
Seq. No.
                   235586
Seq. ID
                   uC-gsflmaxxa006a10b1
Method
                   BLASTX
NCBI GI
                   g2880049
BLAST score
                   378
E value
                  2.0e-36
Match length
                  111
% identity
                   67
NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   235587
Seq. ID
                  uC-qsflmaxxa006b06b1
Method
                  BLASTX
NCBI GI
                  g3757522
BLAST score
                  208
E value
                  1.0e-16
Match length
                  110
% identity
                  47
NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]
Seq. No.
                  235588
Seq. ID
                  uC-gsflmaxxa006c12b1
Method
                  BLASTX
NCBI GI
                  q3063396
BLAST score
                  369
E value
                  2.0e-35
Match length
                  85
% identity
                  81
NCBI Description (AB012947) vcCyP [Vicia faba]
Seq. No.
                  235589
Seq. ID
                  uC-gsflmaxxa006d04b1
Method
                  BLASTX
NCBI GI
                  g3297824
BLAST score
                  220
E value
                  7.0e-18
Match length
                  76
% identity
                  66
                  (AL031032) bZIP transcription factor - like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  235590
Seq. ID
                  uC-gsflmaxxa009a06b1
Method
                  BLASTX
```



```
Match length
% identity
                   67
NCBI Description
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi_2129919_pir__$65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                  >gi_886471_emb_CAA58474_ (X83499) methionine synthase
                   [Catharanthus roseus]
Seq. No.
                  235591
Seq. ID
                  uC-gsflmaxxa009a12b1
Method
                  BLASTX
NCBI GI
                  g124712
BLAST score
                  375
E value
                  5.0e-36
Match length
                  91
% identity
                  73
NCBI Description BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 1 PRECURSOR
                   (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) (CELL WALL
                  BETA-FRUCTOSIDASE 1) >gi_100159_pir__J00991
                  beta-fructofuranosidase (EC 3.2.1.26) precursor - carrot
                  >gi_167551 (M58362) beta-fructosidase [Daucus carota]
Seq. No.
                  235592
Seq. ID
                  uC-gsflmaxxa009b09b1
Method
                  BLASTX
NCBI GI
                  g4263787
BLAST score
                  212
E value
                  5.0e-17
Match length
                  92
                  46
% identity
NCBI Description (AC006068) unknown protein [Arabidopsis thaliana]
Seq. No.
                  235593
Seq. ID
                  uC-gsflmaxxa009b12b1
Method
                  BLASTX
NCBI GI
                  g4455301
BLAST score
                  243
E value
                  9.0e-21
Match length
                  71
% identity
                  75
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
Seq. No.
                  235594
Seq. ID
                  uC-qsflmaxxa009c04b1
Method
                  BLASTX
NCBI GI
                  g441457
BLAST score
                  335
                  2.0e-31
```

E value

Match length % identity

74

NCBI Description

(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon

esculentum]

Seq. No.

235595

Seq. ID

uC-qsflmaxxa009c07b1



Method BLASTX NCBI GI g132944 BLAST score 352 E value 1.0e-33 Match length 85 79 % identity NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi\_81658 pir JQ0772 ribosomal protein L3 (ARP2) - Arabidopsis thaliana >gi 806279

(M32655) ribosomal protein [Arabidopsis thaliana] Seq. No. 235596

Seq. ID uC-gsflmaxxa009c10b1 Method BLASTX NCBI GI g464981 BLAST score 241 E value 6.0e-21 Match length 46 % identity 98

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762)

ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 235597

Seq. ID uC-gsflmaxxa009d04b1

Method BLASTX NCBI GI g2961346 BLAST score 429 E value 2.0e-42 Match length 111 % identity 67

NCBI Description (AL022140) pectinesterase like protein [Arabidopsis

thaliana]

Seq. No. 235598

Seq. ID uC-gsflmaxxa009d07b1

Method BLASTX NCBI GI q2335096 BLAST score 191 E value 1.0e-14 Match length 90 % identity 51

NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235599

Seq. ID uC-gsflmaxxa009d08b1

Method BLASTX NCBI GI g1710188 BLAST score 264 E value 3.0e-23 Match length 94 % identity 51

NCBI Description (U79241) unknown [Homo sapiens]

Seq. No. 235600

Seq. ID uC-gsflmaxxa009e01b1

Method BLASTX NCBI GI g2500521



BLAST score 252
E value 1.0e-21
Match length 56
% identity 86
NCBI Description EUKARYOTIC INITIATION FACTOR 4A-15 (EIF-4A-15)
>gi\_485945\_emb\_CAA55739\_ (X79138) NeIF-4A15 [Nicotiana tabacum]

Seq. No.

235601

Seq. ID uC-gsflmaxxa009e08b1
Method BLASTX
NCBI GI g3822223
BLAST score 309
E value 6.0e-29
Match length 70
% identity 79

NCBI Description (AF077955) branched-chain alpha keto-acid dehydrogenase E1

alpha subunit [Arabidopsis thaliana]

 Seq. No.
 235602

 Seq. ID
 uC-gsflmaxxa009f01b1

 Method
 BLASTX

 NCBI GI
 g2618686

 BLAST score
 193

 E value
 4.0e-15

 Match length
 70

Match length 70 % identity 47

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235603

Seq. ID uC-gsflmaxxa009f03b1

Method BLASTX
NCBI GI g267075
BLAST score 412
E value 2.0e-40
Match length 82
% identity 89

NCBI Description TUBULIN BETA-2 CHAIN >gi\_388254\_emb\_CAA38614\_ (X54845)

beta-tubulin 2 [Pisum sativum]

Seq. No. 235604

Seq. ID uC-gsflmaxxa009f06b1

Method BLASTX
NCBI GI g1419758
BLAST score 357
E value 2.0e-34
Match length 75
% identity 84

NCBI Description (X98795) geranylgeranyl pyrophosphate synthase [Sinapis

alba]

Seq. No. 235605

Seq. ID uC-gsflmaxxa009f09b1

Method BLASTX
NCBI GI g2344887
BLAST score 292
E value 2.0e-26



Match length 83 % identity 69

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 235606

Seq. ID uC-gsflmaxxa009g05b1

Method BLASTX
NCBI GI g129231
BLAST score 466
E value 9.0e-47
Match length 128
% identity 59

NCBI Description ORYZAIN ALPHA CHAIN PRECURSOR >gi\_67644\_pir\_KHRZOA oryzain

(EC 3.4.22.-) alpha precursor - rice

>gi\_218181\_dbj\_BAA14402 (D90406) oryzain alpha precursor

[Oryza sativa]

Seq. No. 235607

Seq. ID uC-gsflmaxxa009g08b1

Method BLASTX
NCBI GI g2764941
BLAST score 286
E value 9.0e-26
Match length 79
% identity 65

NCBI Description (X98255) transcriptionally stimulated by gibberellins;

expressed in meristematic region, and style [Arabidopsis

thaliana]

Seq. No. 235608

Seq. ID uC-gsflmaxxa009g11b1

Method BLASTX
NCBI GI g4210332
BLAST score 203
E value 6.0e-16
Match length 50
% identity 80

NCBI Description (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit

[Arabidopsis thaliana]

Seq. No. 235609

Seq. ID uC-qsflmaxxa010b04b1

Method BLASTX
NCBI GI 94325345
BLAST score 336
E value 2.0e-31
Match length 144
% identity 35

NCBI Description (AF128393) similar to thioredoxin-like proteins (Pfam:

PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,

N=1) [Arabidopsis thaliana]

Seq. No. 235610

Seq. ID uC-gsflmaxxa010d02b1

Method BLASTX NCBI GI g3157949



BLAST score 401 E value 5.0e-39 Match length 112 % identity 72

NCBI Description (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185

and gb\_AA605362 come from this gene. [Arabidopsis thaliana]

Seq. No. 235611

Seq. ID uC-gsflmaxxa010d09b1

Method BLASTX
NCBI GI g1351838
BLAST score 179
E value 6.0e-14
Match length 51
% identity 86

NCBI Description ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT

BETA >gi\_984309 (U26948) beta-carboxyltransferase subunit

[Glycine max]

Seq. No. 235612

Seq. ID uC-gsflmaxxa011a02b1

Method BLASTX
NCBI GI g2739004
BLAST score 381
E value 1.0e-36
Match length 143
% identity 49

NCBI Description (AF022461) CYP82C1p [Glycine max]

Seq. No. 235613

Seq. ID uC-gsflmaxxa011a03b1

Method BLASTX
NCBI GI g626010
BLAST score 216
E value 1.0e-35
Match length 122
% identity 60

NCBI Description disease resistance protein kinase Pto - tomato >gi\_430992

(U02271) protein kinase [Solanum pimpinellifolium]

>gi\_1809261 (U59315) serine/threonine protein kinase Pto
[Lycopersicon pimpinellifolium] >gi 1096879 prf 2112354A

Pto gene [Lycopersicon esculentum]

Seq. No. 235614

Seq. ID uC-gsflmaxxa011b08b1

Method BLASTX
NCBI GI 94206765
BLAST score 195
E value 6.0e-15
Match length 101
% identity 47

NCBI Description (AF104329) putative type 1 membrane protein [Arabidopsis ]

thaliana]

Seq. No. 235615

Seq. ID uC-gsflmaxxa011b11b1

```
Method
                   BLASTX
NCBI GI
                   q3540193
BLAST score
                   446
E value
                   2.0e-44
Match length
                   106
                   79
% identity
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  235616
Seq. ID
                  uC-gsflmaxxa012a04b1
Method
                  BLASTX
NCBI GI
                  q1730566
BLAST score
                  497
                  2.0e-50
E value
Match length
                  141
% identity
                  69
NCBI Description
                  PHYTOCHROME E >gi 1145714 (U39787) phytochrome E [Ipomoea
                  nil]
Seq. No.
                  235617
Seq. ID
                  uC-gsflmaxxa012b04b1
Method
                  BLASTX
NCBI GI
                  g2315153
BLAST score
                  317
                  2.0e-29
E value
Match length
                  84
                  73
% identity
NCBI Description (Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
                  235618
Seq. No.
                  uC-gsflmaxxa012b08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3522939
BLAST score
                  210
E value
                  9.0e-17
Match length
                  68
% identity
                  60
NCBI Description
                   (AC004411) putative squamosa-promoter binding protein
                   [Arabidopsis thaliana]
Seq. No.
                  235619
Seq. ID
                  uC-gsflmaxxa012c04b1
Method
                  BLASTX
NCBI GI
                  g1621268
BLAST score
                  230
```

E value 3.0e-19 Match length 62 % identity

NCBI Description (Z81012) unknown [Ricinus communis]

Seq. No. 235620

Seq. ID uC-gsflmaxxa012d04b1

Method BLASTX NCBI GI g3643607 BLAST score 354 E value 5.0e-34 Match length 81



% identity 41 NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.

235621

Seq. ID

uC-gsflmaxxa014a11b1

Method NCBI GI BLAST score BLASTX g2252840

BLAST score 136 E value 1.0e-08

Match length 52 % identity 52

NCBI Description (AF013293) contains regions of similarity to Haemophilus

influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.

235622

Seq. ID

uC-gsflmaxxa014b01b1

Method BLASTX
NCBI GI g1332579
BLAST score 358
E value 2.0e-52
Match length 118
% identity 10

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No.

235623

Seq. ID uC-gsflmaxxa014d10b1

Method BLASTX
NCBI GI g2160322
BLAST score 163
E value 9.0e-12
Match length 31
% identity 100

NCBI Description (D16139) cytokinin binding protein CBP57 [Nicotiana

sylvestris]

Seq. No.

235624

Seq. ID uC-gsflmaxxa014e05b1

Method BLASTX
NCBI GI g4210948
BLAST score 225
E value 7.0e-22
Match length 58
% identity 95

NCBI Description (AF085275) DnaJ protein [Hevea brasiliensis]

Seq. No.

235625

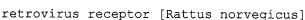
Seq. ID uC-gsflmaxxa015a11b1

Method BLASTX
NCBI GI g1706187
BLAST score 253
E value 5.0e-22
Match length 97
% identity 52

NCBI Description HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1)

(CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR) >gi\_1015327\_dbj\_BAA11090\_ (D67087) ecotropic





Seq. No. 235626 Seq. ID uC-gsflmaxxa015b07b1 Method BLASTX NCBI GI g4335773 BLAST score 151 E value 8.0e-10 Match length 91 % identity 42 NCBI Description (AC006284) unknown protein [Arabidopsis thaliana] Seq. No. 235627 Seq. ID uC-gsflmaxxa015b09b1 Method BLASTX NCBI GI g2623298 BLAST score 310 E value 2.0e-28 Match length 134 % identity 62 NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana] Seq. No. 235628 Seq. ID uC-gsflmaxxa015c03b1 Method BLASTX NCBI GI g3080415 BLAST score 182 E value 6.0e-14Match length 60 % identity 62 NCBI Description (AL022604) cysteine proteinase - like protein [Arabidopsis thaliana] Seq. No. 235629 Seq. ID uC-gsflmaxxa015f04b1 Method BLASTX NCBI GI g130172 BLAST score 190 E value 6.0e-15 Match length 37 % identity 95 NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (STARCH PHOSPHORYLASE L) >gi\_168276 (M64362) starch phosphorylase [Ipomoea batatas] Seq. No. 235630 Seq. ID uC-gsflmaxxa015f11b1 Method BLASTX NCBI GI g322641 BLAST score 322 E value 3.0e-30 Match length 86 % identity 63 beta-1,3-glucanase homolog (clone A6) - rape (fragment) NCBI Description

34120

homologue [Brassica napus]

>gi 17738 emb\_CAA49513\_ (X69887) beta-1,3-glucanase

NCBI GI

```
Seq. No.
                   235631
Seq. ID
                   uC-qsflmaxxa026a11b1
Method
                   BLASTX
NCBI GI
                   q4056507
BLAST score
                   147
E value
                   9.0e-10
Match length
                   65
% identity
NCBI Description (AC005896) putative RNA binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   235632
Seq. ID
                   uC-gsflmaxxa026b01b1
Method
                   BLASTX
NCBI GI
                   q3080391
BLAST score
                   238
E value
                   4.0e-20
Match length
                   75
% identity
                   61
NCBI Description (AL022603) putative protein [Arabidopsis thaliana]
Seq. No.
                   235633
Seq. ID
                   uC-gsflmaxxa026c01b1
Method
                   BLASTX
NCBI GI
                   g1652164
BLAST score
                   333
E value
                   3.0e - 31
Match length
                   111
% identity
NCBI Description (D90903) hypothetical protein [Synechocystis sp.]
Seq. No.
                   235634
Seq. ID
                   uC-qsflmaxxa026e03b1
Method
                  BLASTX
NCBI GI
                   g3150405
BLAST score
                  208
E value
                  8.0e-17
Match length
                  82
% identity
                  51
NCBI Description (AC004165) putative indole-3-acetate
                  beta-glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                  235635
Seq. ID
                  uC-gsflmaxxa026f01b1
Method
                  BLASTX
NCBI GI
                  g2661412
BLAST score
                  223
E value
                  1.0e-18
Match length
                  60
% identity
                  75
NCBI Description (AJ000728) MAP kinase kinase [Lycopersicon esculentum]
Seq. No.
                  235636
Seq. ID
                  uC-gsflmaxxa026g02b1
Method
                  BLASTX
```

34121

q3914826



BLAST score 586 E value 8.0e-61 Match length 128 % identity 81

NCBI Description DNA-DIRECTED RNA POLYMERASE CHLOROPLAST PRECURSOR >gi\_2330560\_emb\_CAA69972\_ (Y08722) chloroplast

single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi\_2330564\_emb\_CAA69717\_ (Y08463) chloroplast single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi\_4115372 (AC005967) chloroplast single subunit

DNA-dependent RNA polymerase [Arabidopsis thaliana]

Seq. No. 235637

Seq. ID uC-gsflmaxxa026g12b1

Method BLASTX
NCBI GI g2760837
BLAST score 237
E value 6.0e-20
Match length 110
% identity 38

NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 235638

Seq. ID uC-gsflmaxxa026h03b1

Method BLASTX
NCBI GI g4539351
BLAST score 183
E value 5.0e-14
Match length 68
% identity 44

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 235639

Seq. ID uC-gsflmaxxa026h06b1

Method BLASTX
NCBI GI g3080396
BLAST score 501
E value 8.0e-51
Match length 136
% identity 69

NCBI Description (AL022603) putative protein [Arabidopsis thaliana]

Seq. No. 235640

Seq. ID uC-gsflmaxxa026h11b1

Method BLASTX
NCBI GI g3859570
BLAST score 327
E value 2.0e-30
Match length 143
% identity 50

NCBI Description (AF098753) unknown [Oryza sativa]

Seq. No. 235641

Seq. ID uC-gsflmaxxa027a08b1

Method BLASTX
NCBI GI g1297187
BLAST score 240



```
E value
                   2.0e-20
Match length
                   74
% identity
                   62
NCBI Description
                  (U53501) similar to protein encoded by GenBank Accession
                  Number U41815, nucleoporin 98 [Arabidopsis thaliana]
Seq. No.
                   235642
Seq. ID
                  uC-gsflmaxxa027b10b1
Method
                  BLASTX
NCBI GI
                  g4455350
BLAST score
                  198
E value
                  2.0e-15
Match length
                  71
% identity
                  58
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                  235643
Seq. ID
                  uC-gsflmaxxa027c08b1
Method
                  BLASTX
NCBI GI
                  g4337025
BLAST score
                  421
E value
                  2.0e-41
Match length
                  107
                  79
% identity
NCBI Description (AF123253) AIM1 protein [Arabidopsis thaliana]
Seq. No.
                  235644
Seq. ID
                  uC-gsflmaxxa027c12b1
Method
                  BLASTX
NCBI GI
                  g3024386
BLAST score
                  420
E value
                  1.0e-41
Match length
                  91
% identity
                  93
NCBI Description POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
                  >gi_2129500_pir S52006 polygalacturonase - upland cotton
                  >gi_606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                  235645
Seq. ID
                  uC-gsflmaxxa027d03b1
Method
                  BLASTX
NCBI GI
                  g3668089
BLAST score
                  228
E value
                  8.0e-19
Match length
                  76
% identity
                  51
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                  235646
```

Seq. ID uC-gsflmaxxa027q11b1

Method BLASTX NCBI GI g2245022 BLAST score 219 E value 6.0e-18 Match length 96 % identity 47

NCBI Description (Z97341) hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
                   235647
Seq. ID
                   uC-qsflmaxxa027h03b1
Method
                   BLASTX
NCBI GI
                   g3513744
BLAST score
                   262
E value
                   6.0e-23
Match length
                   75
% identity
                   60
NCBI Description
                   (AF080118) contains similarity to Medicago truncatula MtN3
                   (GB:Y08726) [Arabidopsis thaliana]
Seq. No.
                   235648
Seq. ID
                   uC-gsflmaxxa027h04b1
Method
                   BLASTX
NCBI GI
                   g2738248
BLAST score
                   411
E value
                   3.0e-40
Match length
                   102
% identity
                   82
NCBI Description
                  (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
Seq. No.
                   235649
Seq. ID
                   uC-gsflmaxxa027h12b1
Method
                  BLASTX
NCBI GI
                   q3036819
BLAST score
                   350
E value
                   3.0e-33
Match length
                  115
% identity
                   63
NCBI Description (AJ000058) MCM3 homolog [Arabidopsis thaliana]
Seq. No.
                  235650
Seq. ID
                  uC-gsflmaxxa028a07b1
Method
                  BLASTX
NCBI GI
                  q3522933
BLAST score
                   229
E value
                   6.0e-25
Match length
                  66
% identity
                  87
NCBI Description
                  (AC004411) putative anion exchange protein 3 [Arabidopsis
                  thaliana]
Seq. No.
                  235651
Seq. ID
                  uC-gsflmaxxa028a08b1
Method
                  BLASTX
NCBI GI
                  g4510426
BLAST score
                  312
E value
                  1.0e-28
Match length
                  128
% identity
                  54
NCBI Description
                 (AC006929) hypothetical protein [Arabidopsis thaliana]
```

Seq. ID uC-gsflmaxxa028b05b1

Method BLASTX



```
q2244949
NCBI GI
BLAST score
                   201
E value
                   8.0e-16
Match length
                   100
% identity
                   42
NCBI Description
                  (Z97339) similarity to ORF - Lilium longiflorum
                   [Arabidopsis thaliana]
Seq. No.
                   235653
Seg. ID
                   uC-gsflmaxxa028b06b1
Method
                   BLASTX
NCBI GI
                   q3881836
BLAST score
                   548
E value
                   2.0e-56
Match length
                  143
% identity
                   73
NCBI Description
                  (Z78019) Similarity to Yeast LPG22P protein (TR:G1151240);
                   cDNA EST EMBL:T00686 comes from this gene; cDNA EST
                   EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728
                   comes from this gene; cDNA EST EMBL:C10626 comes from this
                   ge
Seq. No.
                  235654
Seq. ID
                  uC-gsflmaxxa028b07b1
Method
                  BLASTX
NCBI GI
                  g3241943
BLAST score
                  733
E value
                  6.0e-78
Match length
                  159
% identity
                  81
NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  235655
Seq. ID
                  uC-gsflmaxxa028c01b1
Method
                  BLASTX
NCBI GI
                  g3367585
BLAST score
                  187
E value
                  4.0e-14
Match length
                  91
% identity
NCBI Description
                  (AL031135) putative polygalacturonase [Arabidopsis
                  thalianal
Seq. No.
                  235656
Seq. ID
                  uC-gsflmaxxa028e05b1
Method
                  BLASTX
NCBI GI
                  q2129581
BLAST score
                  456
E value
                  2.0e-45
Match length
                  142
% identity
                  62
```

NCBI Description envelope Ca2+-ATPase precursor - Arabidopsis thaliana >gi 471089 dbj BAA03091 (D13984) chloroplast envelope

Ca2+-ATPase precursor [Arabidopsis thaliana]

>gi\_4165448\_emb\_CAA49558\_ (X69940) envelope Ca2+-ATPase

[Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                    uC-gsflmaxxa028f12b1
Method
                    BLASTX
NCBI GI
                    q1502430
BLAST score
                    233
E value
                    9.0e-26
Match length
                    68
% identity
NCBI Description
                    (U62331) phosphate transporter [Arabidopsis thaliana]
                    >qi 2564661 (AF022872) phosphate transporter [Arabidopsis
                    thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate
Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
                    phosphate transporter, AtPT2 [Arabidopsis thaliana]
Seq. No.
                    235658
Seq. ID
                    uC-gsflmaxxa028g03b1
Method
                    BLASTX
NCBI GI
                    g2244792
BLAST score
                    261
                    1.0e-22
E value
Match length
                    78
% identity
                    64
NCBI Description (Z97336) ankyrin homolog [Arabidopsis thaliana]
Seq. No.
                    235659
Seq. ID
                    uC-gsflmaxxa028q09b1
Method
                    BLASTX
NCBI GI
                    q4558664
BLAST score
                    191
                    2.0e-14
E value
Match length
                    72
% identity
                    28
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    235660
Seq. ID
                   uC-gsflmaxxa028h08b1
Method
                   BLASTX
NCBI GI
                    g2154715
BLAST score
                   321
E value
                   1.0e-42
Match length
                   96
% identity
                   92
NCBI Description (Y09418) CDPK-related protein kinase [Arabidopsis thaliana]
Seq. No.
                   235661
Seq. ID
                   uC-qsflmaxxa029b01b1
Method
                   BLASTX
NCBI GI
                   g1130684
BLAST score
                   429
E value
                   1.0e-42
Match length
                   88
```

% identity 95

NCBI Description (Z46960) acetohydroxyacid synthase [Gossypium hirsutum]

Seq. No. 235662

Seq. ID uC-gsflmaxxa029b10b1

Method BLASTX



```
NCBI GI
                   q3297824
BLAST score
                   161
E value
                   3.0e-11
Match length
                   82
% identity
                   (AL031032) bZIP transcription factor - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   235663
Seq. ID
                   uC-gsflmaxxa029d09b1
Method
                   BLASTX
NCBI GI
                   q3128228
BLAST score
                   337
E value
                   7.0e-32
Match length
                   72
% identity
                   89
NCBI Description
```

(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi\_3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 235664 Seq. ID uC-gsflmaxxa029d10b1 Method BLASTX NCBI GI g2495256 BLAST score 564 E value 3.0e-58 Match length 121 % identity 89

NCBI Description STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 HOMOLOG (HMG PROTEIN) >gi\_481756\_pir\_\_S39242 HMG protein - Madagascar periwinkle >gi\_433872\_emb\_CAA82251\_ (Z28410) HMG protein

[Catharanthus roseus]

Seq. No. 235665

Seq. ID uC-gsflmaxxa029e03b1

Method BLASTX NCBI GI g2760836 BLAST score 291 E value 1.0e-26 Match length 90 % identity

NCBI Description (AC003105) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 235666

Seq. ID uC-gsflmaxxa029e06b1

Method BLASTX NCBI GI g1171642 BLAST score 187 E value 1.0e-14 Match length 45 % identity 80

NCBI Description PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK

>gi 481206\_pir\_\_S38326 protein kinase - Arabidopsis thaliana >gi\_166809 (L07248) protein kinase [Arabidopsis

thaliana]

```
Seq. No.
                   235667
Seq. ID
                   uC-gsflmaxxa029e07b1
Method
                   BLASTX
NCBI GI
                   g1843527
BLAST score
                   182
E value
                   5.0e-14
Match length
                   42
% identity
NCBI Description (U73747) annexin [Gossypium hirsutum]
Seq. No.
                   235668
Seq. ID
                   uC-gsflmaxxa029f04b1
Method
                   BLASTX
NCBI GI
                  g3738338
BLAST score
                  282
E value
                  3.0e-25
Match length
                  113
% identity
                   50
NCBI Description (AC005170) putative polygalacturonase [Arabidopsis
                  thaliana]
Seq. No.
                  235669
Seq. ID
                  uC-gsflmaxxa029f10b1
Method
                  BLASTX
NCBI GI
                  g2911075
BLAST score
                  397
E value
                  8.0e-39
Match length
                  110
% identity
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
Seq. No.
                  235670
Seq. ID
                  uC-gsflmaxxa029f12b1
Method
                  BLASTX
NCBI GI
                  g544426
BLAST score
                  231
E value
                  4.0e-19
Match length
                  85
% identity
NCBI Description
                  GLYCINE-RICH RNA-BINDING PROTEIN >gi_100155 pir S14857
                  glycine-rich protein - carrot >gi_18347_emb_CAA41152
                  (X58146) glycine-rich protein [Daucus carota]
                  >gi_445138_prf__1908438A Gly-rich protein [Daucus carota]
Seq. No.
                  235671
Seq. ID
                  uC-qsflmaxxa029h01b1
Method
                  BLASTX
NCBI GI
                  g3860323
BLAST score
                  158
```

E value 1.0e-10 Match length 38 % identity 82

NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]

Seq. No. 235672

Seq. ID uC-gsflmaxxa029h05b1

Method BLASTX



NCBI GI g124202 BLAST score 263 E value 4.0e-23 Match length 85 % identity 60

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA) >gi\_92416\_pir\_\_A26711 translation initiation

factor eIF-2 alpha chain - rat >gi\_108753\_pir\_\_S18461 translation initiation factor eIF-2 alpha chain - bovine >gi\_325\_emb\_CAA37728\_(X53689) initiation factor 2 alpha [Bos taurus] >gi\_204002 (J02646) translational initiation

factor eIF-2, alpha subunit [Rattus norvegicus]

Seq. No. 235673

Seq. ID uC-gsflmaxxa029h07b1

Method BLASTX
NCBI GI g3702338
BLAST score 307
E value 5.0e-28
Match length 74
% identity 73

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 235674

Seq. ID uC-gsflmaxxa038a03b1

Method BLASTX
NCBI GI g3641312
BLAST score 283
E value 3.0e-25
Match length 65
% identity 78

NCBI Description (AF087412) AJH2 [Arabidopsis thaliana]

Seq. No. 235675

Seq. ID uC-gsflmaxxa038a07b1

Method BLASTX
NCBI GI g2664214
BLAST score 392
E value 4.0e-38
Match length 129
% identity 59

NCBI Description (AJ222646) G2484-1 [Arabidopsis thaliana]

Seq. No. 235676

Seq. ID uC-gsflmaxxa038a12b1

Method BLASTX
NCBI GI g3335375
BLAST score 277
E value 2.0e-24
Match length 60
% identity 90

NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]

Seq. No. 235677

Seq. ID uC-gsflmaxxa038b01b1

Method BLASTX NCBI GI q3928098



BLAST score 212 E value 4.0e-17 Match length 79 % identity 67

NCBI Description (AC005770) similar to guanylate binding protein, 5' partial

[Arabidopsis thaliana]

Seq. No. 235678

Seq. ID uC-gsflmaxxa038b03b1

Method BLASTX
NCBI GI g4263777
BLAST score 517
E value 1.0e-52
Match length 125
% identity 71

NCBI Description (AC006068) putative serine carboxypeptidase II [Arabidopsis

thaliana] >gi\_4510391\_gb\_AAD21479.1\_ (AC007017) putative

serine carboxypeptidase II [Arabidopsis thaliana]

Seq. No. 235679

Seq. ID uC-gsflmaxxa038b05b1

Method BLASTX
NCBI GI g4539470
BLAST score 249
E value 3.0e-21
Match length 82
% identity 59

NCBI Description (AL049500) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235680

Seq. ID uC-gsflmaxxa038b10b1

Method BLASTX
NCBI GI g2760837
BLAST score 300
E value 4.0e-27
Match length 160
% identity 39

NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 235681

Seq. ID uC-gsflmaxxa038e01b1

Method BLASTX
NCBI GI g4432854
BLAST score 150
E value 1.0e-09
Match length 67
% identity 39

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235682

Seq. ID uC-gsflmaxxa038e12b1

Method BLASTX
NCBI GI g2059326
BLAST score 147
E value 3.0e-09
Match length 105
% identity 30



```
NCBI Description (D67067) thymic epithelial cell surface antigen [Mus musculus]

Seq. No. 235683
Seq. ID uC-gsflmaxxa038f02b1
```

Method BLASTX
NCBI GI g2253582
BLAST score 230
E value 5.0e-19
Match length 60
% identity 70

NCBI Description (U78721) Serine proteinase (stubble) isolog [Arabidopsis

thaliana]

 Seq. No.
 235684

 Seq. ID
 uC-gsflmaxxa038f11b1

Method BLASTX
NCBI GI 94580471
BLAST score 194
E value 8.0e-15
Match length 124
% identity 35

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 235685

Seq. ID uC-gsflmaxxa038g01b1

Method BLASTX
NCBI GI g4539301
BLAST score 234
E value 5.0e-20
Match length 70
% identity 70

NCBI Description (ALO49480) putative mitochondrial protein [Arabidopsis

thaliana]

Seq. No. 235686

Seq. ID uC-gsflmaxxa038g09b1

Method BLASTX
NCBI GI g256810
BLAST score 157
E value 7.0e-11
Match length 55
% identity 62

NCBI Description Myb oncoprotein homolog {clone 308} [Antirrhinum

majus=snapdragons, Jl:522, flowers, Peptide Partial, 117

aa, segment 2 of 2]

Seq. No. 235687

Seq. ID uC-gsflmaxxa038h02b1

Method BLASTX
NCBI GI g3157949
BLAST score 188
E value 4.0e-14
Match length 83
% identity 46

NCBI Description (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb\_Z28697 from Nicotiana tabacum. ESTs gb\_Z18185

Seq. ID

Method

235693

BLASTX

uC-qsflmaxxa039a08b1



and gb\_AA605362 come from this gene. [Arabidopsis thaliana]

```
Seq. No.
                   235688
Seq. ID
                   uC-gsflmaxxa038h05b1
Method
                   BLASTX
NCBI GI
                   g2244771
BLAST score
                   201
E value
                   1.0e-15
Match length
                   69
% identity
                   59
NCBI Description (Z97335) kinesin homolog [Arabidopsis thaliana]
Seq. No.
                   235689
Seq. ID
                   uC-gsflmaxxa038h11b1
Method
                   BLASTX
NCBI GI
                   g3046815
BLAST score
                   427
E value
                   3.0e-42
Match length
                   83
% identity
                   92
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   235690
Seq. ID
                   uC-gsflmaxxa038h12b1
Method
                   BLASTX
NCBI GI
                   g167367
BLAST score
                   299
E value
                   2.0e-51
Match length
                   124
% identity
                   84
NCBI Description (L08199) peroxidase [Gossypium hirsutum]
Seq. No.
                   235691
Seq. ID
                   uC-gsflmaxxa039a02b1
Method
                   BLASTX
NCBI GI
                   g2832664
BLAST score
                   182
E value
                   1.0e-13
Match length
                   67
% identity
                   54
NCBI Description
                 (AL021710) pollen-specific protein - like [Arabidopsis
                  thaliana]
Seq. No.
                   235692
Seq. ID
                  uC-gsflmaxxa039a04b1
Method
                  BLASTX
NCBI GI
                  g4545262
BLAST score
                  185
E value
                  2.0e-15
Match length
                  56
% identity
                  70
NCBI Description
                  (AF118230) metallothionein-like protein [Gossypium
                  hirsutum]
```

Method

NCBI GI

BLAST score

BLASTX

418

g2688619



```
NCBI GI
                    g4218122
BLAST score
                   283
E value
                   3.0e-25
Match length
                   135
% identity
                   46
NCBI Description (AL035353) putative protein [Arabidopsis thaliana]
Seq. No.
                   235694
Seq. ID
                   uC-gsflmaxxa039b03b1
Method
                   BLASTX
NCBI GI
                   q584825
BLAST score
                   289
E value
                   5.0e-26
Match length
                   60
% identity
                   90
NCBI Description
                   B2 PROTEIN >gi 322726 pir S32124 B2 protein - carrot
                   >gi 297889 emb CAA51078 (X72385) B2 protein [Daucus
Seq. No.
                   235695
Seq. ID
                   uC-gsflmaxxa039c11b1
Method
                   BLASTX
NCBI GI
                   g2565277
BLAST score
                   205
E value
                   2.0e-16
Match length
                   43
% identity
                   81
NCBI Description (AF023612) Dim1p homolog [Homo sapiens]
Seq. No.
                   235696
Seq. ID
                   uC-gsflmaxxa039f07b1
Method
                   BLASTX
NCBI GI
                   g2492506
BLAST score
                   282
E value
                   9.0e-26
Match length
                   66
% identity
                   40
NCBI Description PEROXISOME ASSEMBLY FACTOR-2 (PAF-2) (PEROXISOMAL-TYPE
                   ATPASE 1) (PEROXIN-6) >gi_2135899_pir_S71090 peroxisome biogenesis disorder group 4 protein PXAAA1 - human
                   >gi 1354753 (U56602) Pxaaalp [Homo sapiens]
Seq. No.
                   235697
Seq. ID
                   uC-gsflmaxxa039g09b1
Method
                   BLASTX
NCBI GI
                   g4433616
BLAST score
                   246
                   2.0e-21
E value
Match length
                   78
% identity
                   54
NCBI Description (AF107018) alpha-mannosidase IIx [Mus musculus]
Seq. No.
                   235698
Seq. ID
                   uC-gsflmaxxa040a07b1
```

Match length

% identity

104

89



```
E value
                    4.0e-41
 Match length
                    123
 % identity
                    57
 NCBI Description
                   (AE001169) conserved hypothetical protein [Borrelia
                    burgdorferi]
 Seq. No.
                    235699
 Seq. ID
                    uC-gsflmaxxa040b02b1
 Method
                    BLASTX
 NCBI GI
                    g3810596
 BLAST score
                    263
 E value
                    4.0e-23
 Match length
                    101
 % identity
                    50
 NCBI Description (AC005398) reverse-transcriptase-like protein [Arabidopsis
                    thaliana]
 Seq. No.
                    235700
 Seq. ID
                    uC-gsflmaxxa040b03b1
 Method
                    BLASTX
 NCBI GI
                    g3702314
 BLAST score
                    255
 E value
                    4.0e-22
 Match length
                   81
% identity
                    59
 NCBI Description (AC002535) similar to SWI/SNF complex subunit BAF170
                    [Arabidopsis thaliana]
 Seq. No.
                    235701
 Seq. ID
                   uC-gsflmaxxa040c04b1
 Method
                   BLASTX
 NCBI GI
                   g3776013
 BLAST score
                   260
 E value
                    4.0e-23
 Match length
                   52
 % identity
                    94
 NCBI Description (AJ010470) RNA helicase [Arabidopsis thaliana]
 Seq. No.
                   235702
 Seq. ID
                   uC-gsflmaxxa040c06b1
 Method
                   BLASTX
 NCBI GI
                   g3786011
 BLAST score
                   216
 E value
                   5.0e-18
 Match length
                   45
 % identity
                   91
 NCBI Description (AC005499) putative elongation factor [Arabidopsis
                   thaliana]
 Seq. No.
                   235703
 Seq. ID
                   uC-gsflmaxxa040e02b1
 Method
                   BLASTX
 NCBI GI
                   g2244810
 BLAST score
                   467
 E value
                   7.0e-47
```



NCBI Description (Z97336) CCAAT-binding transcription factor subunit A(CBF-A) [Arabidopsis thaliana]

Seq. No. 235704

Seq. ID uC-gsflmaxxa040e07b1

Method BLASTX
NCBI GI g3183445
BLAST score 299
E value 4.0e-27
Match length 140
% identity 46

NCBI Description HYPOTHETICAL 30.8 KD PROTEIN IN PPHB-RPOS INTERGENIC REGION

>gi\_882629 (U29579) ORF\_o302 [Escherichia coli] >gi 1789092

(AE000357) putative dehydrogenase [Escherichia coli]

Seq. No. 235705

Seq. ID uC-gsflmaxxa040e09b1

Method BLASTX
NCBI GI g3056595
BLAST score 247
E value 3.0e-21
Match length 103
% identity 50

NCBI Description (AC004255) T1F9.16 [Arabidopsis thaliana]

Seq. No. 235706

Seq. ID uC-gsflmaxxa040f01b1

Method BLASTX
NCBI GI g3892059
BLAST score 529
E value 5.0e-54
Match length 146
% identity 71

NCBI Description (AC002330) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 235707

Seq. ID uC-gsflmaxxa040f05b1

Method BLASTX
NCBI GI g2191175
BLAST score 450
E value 8.0e-45
Match length 141
% identity 61

NCBI Description (AF007270) A\_IG002P16.24 gene product [Arabidopsis

thaliana]

Seq. No. 235708

Seq. ID uC-gsflmaxxa040g09b1

Method BLASTX
NCBI GI g3881189
BLAST score 419
E value 3.0e-41
Match length 96

% identity 77

NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337



comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No. 235709 Seq. ID uC-gsflmaxxa040h08b1 Method BLASTX NCBI GI g1483228 BLAST score 139 E value 1.0e-08 Match length 31 % identity 81 NCBI Description (X99653) MADS3 protein [Betula pendula] Seq. No. 235710 Seq. ID uC-gsflmaxxa040h10b1 Method BLASTX

Method BLASTX
NCBI GI 94240385
BLAST score 302
E value 1.0e-27
Match length 122
% identity 52

NCBI Description (AF061027) omega-3 fatty acid desaturase precursor

[Vernicia fordii]

Seq. No. 235711

Seq. ID uC-gsflmaxxa041a05b1

Method BLASTX
NCBI GI g1763279
BLAST score 543
E value 1.0e-55
Match length 141
% identity 70

NCBI Description (U73657) tryptophan decarboxylase [Camptotheca acuminata]

Seq. No. 235712

Seq. ID uC-gsflmaxxa041a08b1

Method BLASTX
NCBI GI g1351856
BLAST score 617
E value 2.0e-64
Match length 128
% identity 95

NCBI Description ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)

(ACONITASE) >gi\_868003\_dbj\_BAA06108\_ (D29629) aconitase

[Cucurbita sp.]

Seq. No. 235713

Seq. ID uC-gsflmaxxa041a09b1

Method BLASTX
NCBI GI g1707032
BLAST score 305
E value 7.0e-28
Match length 126
% identity 32

NCBI Description (U80445) coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA



by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8

Seq. No. 235714

Seq. ID uC-gsflmaxxa041a12b1

Method BLASTX
NCBI GI g4490752
BLAST score 286
E value 8.0e-26
Match length 65

Match length 65 % identity 82

NCBI Description (AL035708) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 235715

Seq. ID uC-gsflmaxxa041b01b1

Method BLASTX
NCBI GI g2281330
BLAST score 259
E value 2.0e-22
Match length 95
% identity 53

NCBI Description (U85646) putative pectate lyase Nt59 [Nicotiana tabacum]

Seq. No. 235716

Seq. ID uC-gsflmaxxa041b04b1

Method BLASTX
NCBI GI g2317910
BLAST score 475
E value 9.0e-48
Match length 141
% identity 62

NCBI Description (U89959) CER1 protein [Arabidopsis thaliana]

Seq. No. 235717

Seq. ID uC-gsflmaxxa041b09b1

Method BLASTX
NCBI GI g3004551
BLAST score 165
E value 2.0e-11
Match length 71

% identity 51

NCBI Description (AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235718

Seq. ID uC-gsflmaxxa041b12b1

Method BLASTX
NCBI GI g4544372
BLAST score 129
E value 7.0e-17
Match length 104
% identity 42

NCBI Description (AC006920) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No. 235719

Seq. ID uC-gsflmaxxa041c08b1

34137

114100



```
Method
                   BLASTX
NCBI GI
                   g2244847
BLAST score
                   158
E value
                   1.0e-10
Match length
                   125
% identity
                   30
NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog
                   [Arabidopsis thaliana]
Seq. No.
                   235720
Seq. ID
                   uC-gsflmaxxa041d06b1
Method
                   BLASTX
NCBI GI
                   g4160280
BLAST score
                   365
E value
                   8.0e-35
Match length
                   124
% identity
                   54
NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]
Seq. No.
                   235721
Seq. ID
                  uC-gsflmaxxa041d08b1
Method
                  BLASTX
NCBI GI
                   g3334230
BLAST score
                  206
                   3.0e-16
E value
Match length
                  75
% identity
                   51
NCBI Description D-HYDANTOINASE (DIHYDROPYRIMIDINASE) (DHPASE) >gi 2828803
                  (U84197) D-hydantoinase [Pseudomonas putida]
Seq. No.
                   235722
Seq. ID
                  uC-gsflmaxxa041e04b1
Method
                  BLASTX
NCBI GI
                  q4160280
BLAST score
                  296
E value
                  8.0e-27
Match length
                  95
% identity
                  56
NCBI Description (AJ006224) purple acid phosphatase [Ipomoea batatas]
Seq. No.
                  235723
Seq. ID
                  uC-gsflmaxxa041f08b1
Method
                  BLASTX
NCBI GI
                  g4335751
BLAST score
                  510
E value
                  7.0e-52
Match length
                  139
% identity
                  68
NCBI Description
                  (AC006284) putative methyltransferase [Arabidopsis
                  thaliana]
```

Seq. ID uC-gsflmaxxa041g05b1

Method BLASTX q1076715 NCBI GI BLAST score 222 E value 3.0e-18



```
Match length
                   69
% identity
                   58
NCBI Description abscisic acid-induced protein HVA22 - barley >gi 404589
                   (L19119) A22 [Hordeum vulgare]
                   235725
Seq. No.
Seq. ID
                   uC-gsflmaxxa041h03b1
Method
                   BLASTX
NCBI GI
                   g2262116
BLAST score
                   270
E value
                   5.0e-24
Match length
                   89
% identity
                   56
NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
                   235726
Seq. No.
Seq. ID
                   uC-gsflmaxxa041h05b1
Method
                   BLASTX
NCBI GI
                   g401189
BLAST score
                   388
E value
                   8.0e-38
Match length
                   83
% identity
                   90
NCBI Description
                  WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP)
                   (TURGOR-RESPONSIVE PROTEIN 7A) >gi_485511_pir___$33617
                   trg-31 protein - garden pea >gi_20426_emb_CAA79159_
(Z18288) trg-31 [Pisum sativum]
Seq. No.
                   235727
Seq. ID
                   uC-gsflmaxxa041h10b1
Method
                   BLASTX
NCBI GI
                   g3426062
BLAST score
                   236
E value
                   8.0e-20
                   104
Match length
% identity
                   52
NCBI Description (AJ007587) monooxygenase [Arabidopsis thaliana]
Seq. No.
                   235728
Seq. ID
                   uC-gsflmaxxa041h12b1
Method
                   BLASTX
NCBI GI
                   g2104685
BLAST score
                   285
E value
                   1.0e-25
Match length
                  129
% identity
                   52
NCBI Description (X97909) transcripteion factor [Vicia faba]
```

Seq. ID uC-gsflmaxxa042a02b1

Method BLASTX NCBI GI g3914191 BLAST score 313 E value 9.0e-29. Match length 147

% identity

NCBI Description UDP-N-ACETYLGLUCOSAMINE--PEPTIDE



N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT) >gi 1931579 (U76557) O-GlcNAc transferase, p110 subunit [Rattus norvegicus]

Seq. No. 235730 Seq. ID uC-gsflmaxxa042a08b1 Method BLASTX NCBI GI g3928543 BLAST score 279 E value 6.0e-25 Match length 83 % identity 60

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 235731

Seq. ID uC-gsflmaxxa042e08b1

Method BLASTX NCBI GI g2792297 BLAST score 275 E value 2.0e-24 Match length 56 % identity 77

NCBI Description (AF039183) GAST-like gene product [Fragaria x ananassa]

Seq. No. 235732

Seq. ID uC-gsflmaxxa042e10b1

Method BLASTX NCBI GI g3292830 .BLAST score 223 E value 3.0e-18Match length 116 % identity 47

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 235733

Seq. ID uC-gsflmaxxa042f06b1

Method BLASTX q3033375 NCBI GI BLAST score 520 E value 4.0e-53 Match length 122 % identity 73

(AC004238) putative berberine bridge enzyme [Arabidopsis NCBI Description

thaliana]

Seq. No. 235734

Seq. ID uC-gsflmaxxa042q01b1

Method BLASTX NCBI GI g2507619 BLAST score 184 E value 1.0e-13 Match length 94 % identity 35

NCBI Description (U90342) PrLTP1 [Pinus radiata]

Seq. No. 235735

```
Seq. ID
                   uC-gsflmaxxa042g02b1
Method
                   BLASTX
NCBI GI
                   g4417293
BLAST score
                   328
E value
                   1.0e-30
Match length
                   94
% identity
                   67
NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]
Seq. No.
                   235736
Seq. ID
                   uC-gsflmaxxa042g03b1
Method
                   BLASTX
NCBI GI
                   q4510376
BLAST score
                   314
E value
                   6.0e-29
Match length
                   97
                   59
% identity
NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                   235737
Seq. ID
                   uC-gsflmaxxa042q06b1
Method
                   BLASTX
NCBI GI
                   g2809241
BLAST score
                   434
E value
                   6.0e-43
Match length
                   125
                   70
% identity
NCBI Description (AC002560) F21B7.10 [Arabidopsis thaliana]
Seq. No.
                   235738
Seq. ID
                  uC-gsflmaxxa042g10b1
Method
                  BLASTX
NCBI GI
                  g1922242
BLAST score
                  195
E value
                   5.0e-15
                  71
Match length
% identity
                   65
NCBI Description (Y10084) hypothetical protein [Arabidopsis thaliana]
                  235739
Seq. No.
Seq. ID
                  uC-gsflmaxxa042h02b1
Method
                  BLASTX
NCBI GI
                  g3695403
```

Method BLASTX
NCBI GI g3695403
BLAST score 623
E value 5.0e-65
Match length 149
% identity 79

NCBI Description (AF096373) contains similarity to the pfkB family of

carbohydrate kinases (Pfam: PF00294, E=1.6e-75)
[Arabidopsis thaliana] >gi\_4538955\_emb\_CAB39779.1

(AL049488) fructokinase-like protein [Arabidopsis thaliana]

Seq. No. 235740

Seq. ID uC-gsflmaxxa042h04b1

Method BLASTX NCBI GI g3738298 BLAST score 299

```
E value
                   4.0e-27
Match length
                   108
% identity
                   56
NCBI Description
                   (AC005309) unknown protein [Arabidopsis thaliana]
                   >gi 4249394 (AC006072) unknown protein [Arabidopsis
                   thaliana]
Seq. No.
                   235741
Seq. ID
                   uC-gsflmaxxa043b07b1
Method
                   BLASTX
NCBI GI
                   g4455293
BLAST score
                   248
E value
                   2.0e-21
Match length
                  68
                   74
% identity
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
Seq. No.
                   235742
Seq. ID
                  uC-gsflmaxxa043b09b1
Method
                  BLASTX
NCBI GI
                  q557474
BLAST score
                  154
E value
                   4.0e-10
                  99
Match length
% identity
                   35
NCBI Description (U15179) ORF1 [Bacteroides ovatus]
Seq. No.
                  235743
Seq. ID
                  uC-gsflmaxxa043e10b1
Method
                  BLASTX
NCBI GI
                  g4432835
BLAST score
                  200
E value
                  1.0e-15
Match length
                  83
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
                              ۵,
Seq. No.
                  235744
Seq. ID
                  uC-gsflmaxxa043f02b1
Method
                  BLASTX
NCBI GI
                  g2623298
BLAST score
                  323
E value
                  7.0e-30
Match length
                  75
% identity
NCBI Description (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis
                  thaliana]
```

Seq. ID uC-gsflmaxxa043f07b1

Method BLASTX NCBI GI g2760830 BLAST score 228 E value 8.0e-19 Match length 99 % identity

NCBI Description (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis

Seq. ID

235751

uC-gsflmaxxa045e12b1



## thaliana]

```
Seq. No.
                   235746
Seq. ID
                   uC-gsflmaxxa043h03b1
Method
                   BLASTX
NCBI GI
                   q541816
BLAST score
                   208
E value
                   5.0e-17
Match length
                   45
% identity
                   84
NCBI Description protein kinase - common ice plant >gi_457689 emb CAA82990
                   (Z30329) protein kinase [Mesembryanthemum crystallinum]
Seq. No.
                   235747
Seq. ID
                   uC-gsflmaxxa043h07b1
Method
                   BLASTX
NCBI GI
                   g4406777
BLAST score
                   184
                   3.0e-14
E value
Match length
                   37
% identity
                   92
NCBI Description
                  (AC006532) putative zinc-finger protein [Arabidopsis
                   thaliana]
                   235748
Seq. No.
Seq. ID
                   uC-gsflmaxxa045b03b1
Method
                   BLASTX
NCBI GI
                   g2832679
BLAST score
                   398
E value
                   6.0e-39
Match length
                   112
% identity
                   65
                  (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   235749
Seq. ID
                  uC-gsflmaxxa045d05b1
Method
                  BLASTX
NCBI GI
                  g2505870
BLAST score
                   604
E value
                  7.0e-63
Match length
                  138
% identity
NCBI Description
                 (Y12227) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  235750
Seq. ID
                  uC-qsflmaxxa045d11b1
Method
                  BLASTX
NCBI GI
                  g4544387
BLAST score
                  184
E value
                  1.0e-20
Match length
                  90
% identity
                  62
                  (AC007047) putative purple acid phosphatase precursor
NCBI Description
                  [Arabidopsis thaliana]
```

34143

```
Method
                  BLASTX
NCBI GI
                  g4510354
BLAST score
                  163
E value
                   3.0e-11
Match length
                  138
% identity
                  37
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                  235752
Seq. ID
                  uC-gsflmaxxa045h04b1
Method
                  BLASTX
NCBI GI
                  q4455169
BLAST score
                  269
E value
                  1.0e-23
Match length
                  83
% identity
                  64
NCBI Description (AL035521) putative aldehyde dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  235753
Seq. ID
                  uC-gsflmaxxa045h11b1
Method
                  BLASTX
NCBI GI
                  g2191144
BLAST score
                  397
E value
                  1.0e-38
                  124
Match length
% identity
                  64
NCBI Description (AF007269) A_IG002N01.24 gene product [Arabidopsis
                  thaliana]
Seq. No.
                  235754
Seq. ID
                  uC-gsflmaxxa046b05b1
Method
                  BLASTX
NCBI GI
                  g3928862
BLAST score
                  213
E value
                  4.0e-17
Match length
                  112
                  38
% identity
NCBI Description (AF089710) disease resistance protein RPP8 [Arabidopsis
                  thaliana]
Seq. No.
                  235755
Seq. ID
                  uC-gsflmaxxa046b06b1
Method
                  BLASTX
NCBI GI
                  g134891
BLAST score
                  144
                  5.0e-09
E value
Match length
                  99
% identity
                  35
NCBI Description SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
                  (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
                  >gi 89066 pir _A24570 signal recognition particle receptor
                  precursor - dog >gi_997_emb_CAA26945_ (X03184) signal
```

recognition particle receptor [Canis sp.] >gi\_224778\_prf 1112224A signal recognition particle

receptor [Canis familiaris]



```
Seq. No.
                    235756
Seq. ID
                    uC-gsflmaxxa046b09b1
Method
                    BLASTX
NCBI GI
                    g3123209
BLAST score
                    300
E value
                    1.0e-32
                    88
Match length
% identity
                    83
NCBI Description ELONGATION FACTOR G, MITOCHONDRIAL 1 PRECURSOR (MEF-G-1)
                    >gi 2119928 pir S61642 translation elongation factor G,
                    mitochondrial - yeast (Saccharomyces cerevisiae)
                    >gi_1181289_emb_CAA64315_ (X94607) Mef1 protein [Saccharomyces cerevisiae] >gi_1360422_emb_CAA97626_
                    (Z73241) ORF YLR069c [Saccharomyces cerevisiae]
Seq. No.
                    235757
Seq. ID
                   uC-gsflmaxxa046c03b1
Method
                   BLASTX
NCBI GI
                   g125568
BLAST score
                    287
E value
                    1.0e-25
Match length
                    134
% identity
                    44
NCBI Description PROTEIN KINASE PVPK-1 >gi_100013_pir__ A30311 protein kinase C (EC 2.7.1.-) homolog - kidney bean >gi_169361 (J04555)
                    PVPK-1 protein [Phaseolus vulgaris]
Seq. No.
                    235758
Seq. ID
                   uC-gsflmaxxa046c08b1
Method
                   BLASTX
NCBI GI
                   g3738316
BLAST score
                   455
E value
                    2.0e-45
Match length
                   128
% identity
NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
Seq. No.
                   235759
Seq. ID
                   uC-gsflmaxxa046c10b1
Method
                   BLASTX
NCBI GI
                   q3024386
BLAST score
                   402
E value
                   2.0e-39
Match length
                   85
% identity
                    92
NCBI Description POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
                   >gi 2129500_pir__S52006 polygalacturonase - upland cotton
                   >gi 606650 (U09717) polygalacturonase [Gossypium hirsutum]
Seq. No.
                    235760
Seq. ID
                   uC-gsflmaxxa046d02b1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g4416307
BLAST score 182
E value 3.0e-13
Match length 151
% identity 29



```
NCBI Description (AF105716) hypothetical protein [Zea mays]
Seq. No.
                   235761
Seq. ID
                   uC-gsflmaxxa046d10b1
Method
                   BLASTX
NCBI GI
                   g2739004
BLAST score
                   249
E value
                   3.0e-21
Match length
                   81
% identity
                   57
NCBI Description (AF022461) CYP82Clp [Glycine max]
Seq. No.
                   235762
Seq. ID
                   uC-gsflmaxxa046e05b1
Method
                   BLASTX
NCBI GI
                   g4191774
BLAST score
                   335
E value
                   3.0e-31
Match length
                   129
% identity
                   50
NCBI Description
                  (AC005917) putative beta-1,3-endoglucanase [Arabidopsis
                   thaliana]
                   235763
Seq. No.
Seq. ID
                   uC-gsflmaxxa046e08b1
Method
                  BLASTX
NCBI GI
                   g4539323
BLAST score
                   271
E value
                   6.0e-24
Match length
                   90
% identity
                   63
NCBI Description (AL035679) putative protein [Arabidopsis thaliana]
                  235764
Seq. No.
Seq. ID
                  uC-gsflmaxxa046f02b1
Method
                  BLASTX
NCBI GI
                  q3320379
BLAST score
                   410
                   4.0e-40
E value
Match length
                  81
% identity
                   96
NCBI Description
                  (AF014375) putative JUN kinase activation domain binding
                  protein [Medicago sativa]
Seq. No.
                  235765
Seq. ID
                  uC-gsflmaxxa046f03b1
Method
                  BLASTX
NCBI GI
                  g2499612
BLAST score
                  228
E value
                  7.0e-19
Match length
                  72
% identity
                  65
NCBI Description
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 1 (PMEK1)
                  >gi_1076650_pir__S52989 mitogen-activated,
```

34146

kinase 1 [Petunia  $\bar{x}$  hybri $\bar{d}a$ ]

extracelluar-regulated protein kinase 1 (EC 2.7.1.-) - garden petunia >gi 603871\_emb CAA58466 (X83440) MAP/ERK

Seq. ID

Method

235771

BLASTX

uC-gsflmaxxa046h10b1



```
Seq. No.
                   235766
Seq. ID
                   uC-qsflmaxxa046f05b1
Method
                   BLASTX
NCBI GI
                   g3213227
BLAST score
                   162
E value
                   4.0e-11
Match length
                   128
% identity
                   30
NCBI Description
                   (AF035209) putative v-SNARE Vtila [Mus musculus]
                  >gi_3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]
Seq. No.
                   235767
Seq. ID
                   uC-gsflmaxxa046f08b1
Method
                  BLASTX
NCBI GI
                   g4335724
BLAST score
                   131
E value
                   8.0e-12
Match length
                   81
% identity
                   62
NCBI Description
                  (AC006248) putative RING-H2 finger protein [Arabidopsis
                   thaliana]
                   235768
Seq. No.
Seq. ID
                  uC-gsflmaxxa046f11b1
Method
                  BLASTX
NCBI GI
                   q3021271
BLAST score
                   263
E value
                   6.0e-23
Match length
                  72
% identity
                   71
NCBI Description
                  (AL022347) serine/threonine kinase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                  235769
Seq. ID
                  uC-gsflmaxxa046g10b1
Method
                  BLASTX
NCBI GI
                  q4415912
BLAST score
                  250
E value
                  2.0e-21
Match length
                  131
% identity
                  35
NCBI Description (AC006282) putative protease [Arabidopsis thaliana]
Seq. No.
                  235770
Seq. ID
                  uC-gsflmaxxa046g12b1
Method
                  BLASTX
NCBI GI
                  g4204297
BLAST score
                  320
                  1.0e-29
E value
Match length
                  64
% identity
                  97
NCBI Description
                  (AC003027) ADK1 [Arabidopsis thaliana]
```

34147

```
NCBI GI
                   q4263522
BLAST score
                   414
E value
                   1.0e-40
                  142
Match length
% identity
                   51
NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  235772
Seq. ID
                  uC-gsflmaxxa047a01b1
Method
                  BLASTX
NCBI GI
                  g3522929
BLAST score
                  226
E value
                  1.0e-18
Match length
                  43
% identity
                  98
NCBI Description
                  (AC002535) putative dTDP-glucose 4-6-dehydratase
                   [Arabidopsis thaliana] >gi 3738279 (AC005309) putative
                  dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.
                  235773
Seq. ID
                  uC-gsflmaxxa047a11b1
Method
                  BLASTX
NCBI GI
                  g2979554
BLAST score
                  245
E value
                  2.0e-21
Match length
                  77
% identity
                  62
NCBI Description (AC003680) CDC4 like protein [Arabidopsis thaliana]
                  235774
Seq. No.
Seq. ID
                  uC-gsflmaxxa047b09b1
Method
                  BLASTX
                  q3941522
NCBI GI
BLAST score
                  465
E value
                  1.0e-46
Match length
                  106
% identity
                  76
NCBI Description
                  (AF062915) putative transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                  235775
Seq. ID
                  uC-gsflmaxxa047b10b1
Method
                  BLASTX
NCBI GI
                  g1346791
BLAST score
                  173
                  2.0e-12
E value
Match length
                  74 .
% identity
                  49
                 PATHOGENESIS-RELATED HOMEODOMAIN PROTEIN (PRHP) >gi_666128
NCBI Description
                  (L21975) homeodomain protein [Petroselinum crispum]
```

Seq. ID uC-gsflmaxxa047c01b1

Method BLASTX
NCBI GI g2208946
BLAST score 376
E value 4.0e-36



Match length 92 % identity 79

NCBI Description (Y10116) signal recognition particle subunit 14

[Arabidopsis thaliana]

Seq. No. 235777

Seq. ID uC-gsflmaxxa047c10b1

Method BLASTX
NCBI GI g4544445
BLAST score 617
E value 2.0e-64
Match length 148
% identity 82

NCBI Description (AC006592) putative pyrophosphate--fructose 6-phosphate

1-phosphotransferase [Arabidopsis thaliana]

Seq. No. 235778

Seq. ID uC-gsflmaxxa047e03b1

Method BLASTX
NCBI GI 94469023
BLAST score 560
E value 1.0e-57
Match length 128
% identity 83

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 235779

Seq. ID uC-gsflmaxxa047e06b1

Method BLASTX
NCBI GI g3935152
BLAST score 237
E value 5.0e-20
Match length 55
% identity 80

NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No. 235780

Seq. ID uC-gsflmaxxa047f04b1

Method BLASTX
NCBI GI g4335731
BLAST score 160
E value 8.0e-11
Match length 126
% identity 31

NCBI Description (AC006248) putative polyprotein [Arabidopsis thaliana]

Seq. No. 235781

Seq. ID uC-gsflmaxxa047f05b1

Method BLASTX
NCBI GI g3062801
BLAST score 477
E value 4.0e-48
Match length 120
% identity 75

NCBI Description (AB012873) arginine decarboxylase [Nicotiana sylvestris]

Seq. No. 235782



Seq. ID uC-gsflmaxxa047f06b1 Method BLASTX NCBI GI g1762584

BLAST score 392 E value 5.0e-38 Match length 115 % identity 64

NCBI Description (U63373) polygalacturonase isoenzyme 1 beta subunit homolog

[Arabidopsis thaliana]

Seq. No. 235783

Seq. ID uC-gsflmaxxa047f10b1

Method BLASTX
NCBI GI g3776559
BLAST score 618
E value 1.0e-64
Match length 131
% identity 87

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi 3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb\_AC003970. ESTs gb\_Z35332 and gb\_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 235784

Seq. ID uC-gsflmaxxa047g04b1

Method BLASTX
NCBI GI g3894197
BLAST score 319
E value 2.0e-29
Match length 88
% identity 72

NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235785

Seq. ID uC-gsflmaxxa047h03b1

Method BLASTX
NCBI GI g3935152
BLAST score 359
E value 2.0e-34
Match length 94
% identity 71

NCBI Description (AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No. 235786

Seq. ID uC-gsflmaxxa047h05b1

Method BLASTX
NCBI GI g2146740
BLAST score 357
E value 5.0e-34
Match length 103
% identity 71

NCBI Description inner mitochondrial membrane protein - Arabidopsis thaliana

>gi\_603056 (U18126) inner mitochondrial membrane protein

[Arabidopsis thaliana]

Seq. No. 235787

Seq. ID uC-gsflmaxxa048a10b1



```
Method
                   BLASTX
NCBI GI
                   g1841355
BLAST score
                   180
E value
                   3.0e-13
Match length
                   34
                   85
% identity
NCBI Description (D85381) cytochrome c oxidase subunit Vb precursor [Oryza
                   sativa]
Seq. No.
                   235788
Seq. ID
                  uC-gsflmaxxa048a12b1
Method
                  BLASTX
NCBI GI
                   q3850587
BLAST score
                  359
E value
                   3.0e-34
Match length
                  123
% identity
                   64
NCBI Description
                  (AC005278) Strong similarity to gi 2244780 hypothetical
                  protein from Arabidopsis thaliana chromosome 4 contig
                  gb_Z97335. [Arabidopsis thaliana]
Seq. No.
                  235789
Seq. ID
                  uC-gsflmaxxa048c03b1
Method
                  BLASTX
NCBI GI
                  g2281633
BLAST score
                  226
E value
                  2.0e-18
Match length
                  55
                  75
% identity
NCBI Description (AF003097) AP2 domain containing protein RAP2.4
                  [Arabidopsis thaliana]
Seq. No.
                  235790
Seq. ID
                  uC-gsflmaxxa048c09b1
Method
                  BLASTX
NCBI GI
                  g130172
BLAST score
                  638
E value
                  9.0e-67
Match length
                  148
% identity
                  78
NCBI Description ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME PRECURSOR (STARCH
                  PHOSPHORYLASE L) >gi 168276 (M64362) starch phosphorylase
                  [Ipomoea batatas]
                  235791
Seq. ID
                  uC-gsflmaxxa048d10b1
```

Method BLASTX NCBI GI g1657619 BLAST score 653 E value 2.0e-68 Match length 173 % identity 67

NCBI Description (U72504) G5p [Arabidopsis thaliana] >gi\_3068710 (AF049236)

putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No. 235792

Seq. ID uC-gsflmaxxa048e03b1

Match length

128

```
Method
                    BLASTX
 NCBI GI
                    g3885338
 BLAST score
                    179
 E value
                    6.0e-13
 Match length
                    80
 % identity
                    39
 NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]
                    235793
 Seq. No.
 Seq. ID
                    uC-gsflmaxxa048e05b1
 Method
                    BLASTX
 NCBI GI
                    g3098603
 BLAST score
                    175
 E value
                    2.0e-12
 Match length
                    111
 % identity
                    33
 NCBI Description
                   (AF052191) katanin p60 subunit [Strongylocentrotus
                    purpuratus]
 Seq. No.
                    235794
 Seq. ID
                    uC-gsflmaxxa048e07b1
 Method
                    BLASTX
 NCBI GI
                    g1621268
 BLAST score
                    221
- E value
                    4.0e-18
 Match length
                    60
 % identity
                    70
 NCBI Description (Z81012) unknown [Ricinus communis]
 Seq. No.
                    235795
 Seq. ID
                    uC-gsflmaxxa048f06b1
 Method
                    BLASTX
 NCBI GI
                    g4038030
 BLAST score
                    382
 E value
                    8.0e-37
 Match length
                    151
 % identity
                    50
 NCBI Description
                   (AC005936) putative protein kinase, 5' partial [Arabidopsis
                    thaliana]
 Seq. No.
                    235796
 Seq. ID
                   uC-gsflmaxxa048f11b1
 Method
                   BLASTX
 NCBI GI
                   g2065531
 BLAST score
                   320
 E value
                   7.0e-30
 Match length
                   60
 % identity
                   92
NCBI Description (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
 Seq. No.
                   235797
 Seq. ID
                   uC-gsflmaxxa048g05b1
Method
                   BLASTX
NCBI GI
                   g4158232
BLAST score
                   581
E value
                   4.0e-60
```



```
% identity
NCBI Description
                   (Y18626) reversibly glycosylated polypeptide [Triticum
                    aestivum]
Seq. No.
                    235798
Seq. ID
                    uC-gsflmaxxa048q07b1
Method
                    BLASTX
NCBI GI
                    q2760320
BLAST score
                    332
E value
                    6.0e - 31
Match length
                    130
% identity
                    52
NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]
Seq. No.
                   235799
Seq. ID
                   uC-gsflmaxxa048h03b1
Method
                   BLASTX
NCBI GI
                   q2739374
BLAST score
                   457
E value
                   1.0e-45
Match length
                   141
% identity
                   32
NCBI Description (AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   235800
Seq. ID
                   uC-gsflmaxxa048h05b1
Method
                   BLASTX
NCBI GI
                   q2147966
BLAST score
                   239
E value
                   5.0e-20
Match length
                   82
% identity
                   57
NCBI Description probable 1-acyl-sn-glycerol-3-phosphate acyltransferase -
                   Limnanthes douglasii >gi_1067138_emb_CAA88620_ (Z48730)
                   1-acyl-sn-glycerol-3-phosphate acyltransferase (putative)
                   [Limnanthes douglasii]
Seq. No.
                   235801
Seq. ID
                   uC-gsflmaxxa048h08b1
Method
                   BLASTX
NCBI GI
                   g586004
BLAST score
                   251
E value
                   9.0e-22
Match length
                   53
% identity
                   91
                   SUPEROXIDE DISMUTASE [CU-ZN] >gi_421962_pir__S34267 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - sweet potato
NCBI Description
                   >gi_542090_pir__S40404 superoxide dismutase (EC 1.15.1.1)
                   (Cu-Zn) - sweet potato >gi_311971_emb_CAA51654 (X73139)
                   superoxide dismutase [Ipomoea batatas]
```

Seq. ID uC-gsflmaxxa049a02b1 Method BLASTX

NCBI GI g1076668 BLAST score 183 E value 1.0e-13

Match length

NCBI Description

% identity

74

47

```
Match length
 % identity
 NCBI Description
                    NADH dehydrogenase (EC 1.6.99.3) - potato
                    >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                    [Solanum tuberosum]
 Seq. No.
                    235803
                    uC-gsflmaxxa049c04b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1161926
 BLAST score
                    161
 E value
                    4.0e-11
 Match length
                    50
 % identity
                    62
                   (U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine
 NCBI Description
 Seq. No.
                    235804
 Seq. ID
                    uC-gsflmaxxa049c07b1
 Method
                    BLASTX
 NCBI GI
                    g3128209
 BLAST score
                    236 -
 E value
                    6.0e-20
 Match length
                    68
 % identity
                    66
 NCBF Description (AC004077) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    235805
 Seq. ID
                    uC-gsflmaxxa049c11b1
Method
                    BLASTX
 NCBI GI
                    g2662343
 BLAST score
                    441
 E value
                    6.0e-44
 Match length
                    85
 % identity
                    100
 NCBI Description (D63581) EF-1 alpha [Oryza sativa]
 Seq. No.
                    235806
 Seq. ID
                    uC-gsflmaxxa049d07b1
 Method
                    BLASTX
 NCBI GI
                    g4580389
 BLAST score
                    404
 E value
                    1.0e-39
 Match length
                    94
 % identity
 NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    235807
 Seq. ID
                   uC-gsflmaxxa049d09b1
 Method
                   BLASTX
 NCBI GI
                    g1497987
 BLAST score
                   161
 E value
                    4.0e-11
```

(U62798) SCARECROW [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                   uC-gsflmaxxa049e08b1
Method
                   BLASTX
NCBI GI
                   q2117725
BLAST score
                   206
                   2.0e-16
E value
Match length
                   44
% identity
                   84
NCBI Description 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) isoform
                   SBE2.2 precursor - Arabidopsis thaliana (fragment)
                   >gi 726490 (U22428) starch branching enzyme class II
                   [Arabidopsis thaliana]
Seq. No.
                   235809
Seq. ID
                   uC-gsflmaxxa049e09b1
Method
                   BLASTX
NCBI GI
                   g136107
BLAST score
                   204
                   4.0e-16
E value
Match length
                   104
% identity
                   44
NCBI Description TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL
                  AMINOPEPTIDASE) >gi_1082875_pir__S54376
tripeptidyl-peptidase II (EC 3.4.14.10) - human >gi_339880
                   (M73047) trípeptidyl peptidase II [Homo sapiens]
                   >gi_4507657_ref_NP_003282.1_pTPP2_ tripeptidyl peptidase II
Seq. No.
                   235810
Seq. ID
                   uC-gsflmaxxa049e10b1
Method
                   BLASTX
NCBI GI
                   g4455329
BLAST score
                   505
                   2.0e-51
E value
Match length
                  109
% identity
NCBI Description
                 (AL035525) lysine-ketoglutarate reductase/saccharopine
                   [Arabidopsis thaliana]
Seq. No.
                   235811
Seq. ID
                   uC-gsflmaxxa049f01b1
Method
                   BLASTX
NCBI GI
                   g1346705
BLAST score
                  246
E value
                   4.0e-21
Match length
                  86
% identity
NCBI Description
                  POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
                   >gi 1085765_pir S40123 endopolygalacturonase (EC 3.2.1.15)
                   - Prunus persica >gi_436420_emb_CAA54150_ (X76735)
                  endopolygalacturonase [Prunus persica]
```

Seq. No. 235812

Seq. ID uC-gsflmaxxa049f03b1

Method BLASTX
NCBI GI g4335722
BLAST score 283
E value 9.0e-26

```
Match length
                   68
% identity
                   76
NCBI Description (AC006248) hypothetical protein [Arabidopsis thaliana]
                   235813
Seq. No.
Seq. ID
                   uC-gsflmaxxa049f05b1
Method
                   BLASTX
NCBI GI
                   g2911047
BLAST score
                   186
E value
                   4.0e-14
Match length
                   70
% identity
                   51
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                   235814
Seq. ID
                   uC-gsflmaxxa049h01b1
Method
                  BLASTX
NCBI GI
                  g1895084
BLAST score
                  509
E value
                   5.0e-52
Match length
                  98
% identity
                   95
NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays]
Seq. No.
                   235815
Seq. ID
                  uC-qsflmaxxa051h09b1
Method
                  BLASTX
NCBI GI
                  g2827715
BLAST score
                  172
E value
                  2.0e-12
Match length
                  70
                  50
% identity
NCBI Description (AL021684) receptor protein kinase - like protein
                  [Arabidopsis thaliana]
Seq. No.
                  235816
Seq. ID
                  uC-gsflmaxxa052h09b1
Method
                  BLASTX
NCBI GI
                  g2213611
BLAST score
                  370
E value
                  8.0e-36
Match length
                  92
% identity
                  76
NCBI Description (AC000103) F21J9.5 [Arabidopsis thaliana]
Seq. No.
                  235817
Seq. ID
                  uC-gsflmaxxa052h11b1
Method
                  BLASTX
NCBI GI
                  g730290
BLAST score
                  348
E value
                  5.0e-33
Match length
                  101
% identity
                  63
NCBI Description
                  PECTATE LYASE PRECURSOR >gi_322883_pir__$29612 pectate
```

34156

pectate lyase [Lilium longiflorum]

lyase - trumpet lily >gi\_19451 emb\_CAA78976 (Z17328) pectate lyase [Lilium longiflorum] >gi\_308902 (L18911)



```
Seq. No.
                   235818
Seq. ID
                   uC-gsflmaxxa054a08b1
Method
                  BLASTX
NCBI GI
                   g3386614
BLAST score
                   247
                   3.0e-21
E value
Match length
                   58
% identity
NCBI Description
```

NCBI Description (AC004665) putative transcription factor SF3 [Arabidopsis thaliana]

Seq. No. 235819

Seq. ID uC-gsflmaxxa054a12b1

Method BLASTX
NCBI GI g4455202
BLAST score 261
E value 7.0e-23
Match length 65
% identity 77

NCBI Description (AL035440) putative APG protein [Arabidopsis thaliana]

Seq. No. 235820

Seq. ID uC-gsflmaxxa054b12b1

Method BLASTX
NCBI GI g3688189
BLAST score 382
E value 3.0e-37
Match length 92
% identity 80

NCBI Description (AL031804) putative protein kinase [Arabidopsis thaliana]

Seq. No. 235821

Seq. ID uC-gsflmaxxa054c02b1

Method BLASTX
NCBI GI g128592
BLAST score 383
E value 6.0e-37
Match length 99
% identity 71

NCBI Description POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR

>gi\_82190\_pir\_\_S22495 pollen-specific protein precursor common tobacco >gi\_19902\_emb\_CAA43454\_ (X61146) pollen

specific protein [Nicotiana Tabacum]

Seq. No. 235822

Seq. ID ... uC-gsflmaxxa054c10b1

Method BLASTX
NCBI GI g2832625
BLAST score 230
E value 3.0e-19
Match length 97
% identity 52

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 235823

Seq. ID uC-gsflmaxxa054e05b1



Method BLASTX
NCBI GI g1488255
BLAST score 197
E value 2.0e-15
Match length 76
% identity 46
NCBI Description (U38416)

NCBI Description (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana] >gi\_2961381\_emb\_CAA18128\_ (AL022141) ferulate-5-hydroxylase

(FAH1) [Arabidopsis thaliana] >gi\_3925365 (AF068574)

ferulate-5-hydroxylase [Arabidopsis thaliana]

Seq. No. 235824

Seq. ID uC-gsflmaxxa054e11b1

Method BLASTX
NCBI GI g3914555
BLAST score 315
E value 5.0e-29
Match length 87
% identity 80

NCBI Description PUTATIVE RIBOSOME-BINDING FACTOR A, CHLOROPLAST PRECURSOR

>gi\_3096942\_emb\_CAA18852.1 (AL023094) putative protein

[Arabidopsis thaliana]

Seq. No. 235825

Seq. ID uC-gsflmaxxa054f09b1

Method BLASTX

NCBI GI g3297821

BLAST score 265

E value 3.0e-23

Match length 107

% identity 50

NCBI Description (AL031032) extensin-like protein [Arabidopsis thaliana]

Seq. No. 235826

Seq. ID uC-gsflmaxxa054f10b1

Method BLASTX
NCBI GI g1352321
BLAST score 151
E value 9.0e-10
Match length 69
% identity 46

NCBI Description UBIQUITIN-LIKE PROTEIN DSK2 >gi\_786151 (L40587)

ubiquitin-like protein [Saccharomyces cerevisiae]

Seq. No. 235827

Seq. ID uC-gsflmaxxa054g12b1

Method BLASTX
NCBI GI g3668089
BLAST score 249
E value 3.0e-21
Match length 79
% identity 66

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 235828

Seq. ID uC-gsflmaxxa054h09b1

Method BLASTX



```
NCBI GI g2673914
BLAST score 294
E value 1.0e-26
Match length 101
% identity 58
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
Seq. No. 235829
Seq. ID uC-gsflmaxxa055a02b1
```

Method BLASTX
NCBI GI g3738319
BLAST score 164
E value 6.0e-12
Match length 54

Match length 54 % identity 59

NCBI Description (AC005170) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235830

Seq. ID uC-gsflmaxxa055c04b1

Method BLASTX
NCBI GI g3355484
BLAST score 249
E value 4.0e-25
Match length 98
% identity 66

NCBI Description (AC004218) putative geranylgeranyl transferase type I beta

subunit [Arabidopsis thaliana]

Seq. No. 235831

Seq. ID uC-gsflmaxxa055d04b1

Method BLASTX
NCBI GI g3157927
BLAST score 267
E value 9.0e-24
Match length 77
% identity 69

NCBI Description (AC002131) Contains similarity to GDP-dissociation

inhibitor gb\_L07918 from Mus musculus. [Arabidopsis

thaliana]

Seq. No. 235832

Seq. ID uC-gsflmaxxa055e12b1

Method BLASTX
NCBI GI g2459421
BLAST score 352
E value 2.0e-33
Match length 89
% identity 69

NCBI Description (AC002332) putative calcium-binding EF-hand protein

[Arabidopsis thaliana]

Seq. No. 235833

Seq. ID uC-gsflmaxxa055f01b1

Method BLASTX
NCBI GI g4455329
BLAST score 159
E value 2.0e-11



Match length 34 % identity 85

NCBI Description (AL035525) lysine-ketoglutarate reductase/saccharopine

[Arabidopsis thaliana]

Seq. No. 235834

Seq. ID uC-gsflmaxxa055g06b1

Method BLASTX
NCBI GI g3337361
BLAST score 183
E value 1.0e-13
Match length 83
% identity 41

NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]

Seq. No. 235835

Seq. ID uC-gsflmaxxa055g08b1

Method BLASTX
NCBI GI 9452593
BLAST score 156
E value 2.0e-13
Match length 83
% identity 59

NCBI Description (D21814) ORF [Lilium longiflorum]

Seq. No. 235836

Seq. ID uC-gsflmaxxa055g11b1

Method BLASTX
NCBI GI g1762584
BLAST score 380
E value 9.0e-37
Match length 115
% identity 22

NCBI Description (U63373) polygalacturonase isoenzyme 1 beta subunit homolog

[Arabidopsis thaliana]

Seq. No. 235837

Seq. ID uC-gsflmaxxa055g12b1

Method BLASTX
NCBI GI g2979544
BLAST score 190
E value 2.0e-14
Match length 72
% identity 54

NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No. 235838

Seq. ID uC-gsflmaxxa057a09b1

Method BLASTX
NCBI GI g1345132
BLAST score 393
E value 4.0e-38
Match length 122
% identity 67

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]

>gi\_1389566\_dbj\_BAA11869\_ (D83257) receptor protein kinase
[Arabidopsis thaliana] >gi 3075386 (AC004484) receptor



## protein kinase, ERECTA [Arabidopsis thaliana]

```
Seq. No.
                   235839
Seq. ID
                   uC-gsflmaxxa057b01b1
Method
                   BLASTX
NCBI GI
                   q2344894
BLAST score
                   191
E value
                   2.0e-14
Match length
                   45
% identity
                   78
NCBI Description (AC002388) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   235840
Seq. ID
                   uC-gsflmaxxa057b03b1
Method
                   BLASTX
NCBI GI
                   g3250675
BLAST score
                   192
E value
                   1.0e-14
Match length
                   82
% identity
                   52
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
                   235841
Seq. ID
                   uC-gsflmaxxa057b07b1
Method
                  BLASTX
NCBI GI
                   g4263527
BLAST score
                   420
E value
                   3.0e-41
Match length
                  157
% identity
                   59
NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   235842
Seq. ID
                  uC-gsflmaxxa057b10b1
Method
                  BLASTX
NCBI GI
                  g3915618
BLAST score
                  242
E value
                  2.0e-20
Match length
                  121
% identity
                  44
NCBI Description ALTERNATIVE OXIDASE PRECURSOR
Seq. No.
                  235843
Seq. ID
                  uC-gsflmaxxa057c07b1
Method
                  BLASTX
NCBI GI
                  g136057
BLAST score
                  515
E value
                  2.0e-52
Match length
                  130
% identity
                  75
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
```

Coptis japonica >gi\_556171 (J04121) triosephosphate

isomerase [Coptis japonica]

Seq. No. 235844

Seq. ID uC-qsflmaxxa057c10b1



```
Method
                   BLASTX
NCBI GI
                   g3779024
BLAST score
                   439
E value
                   1.0e-43
Match length
                   116
% identity
                   78
NCBI Description (AC005171) unknown protein [Arabidopsis thaliana]
Seq. No.
                   235845
Seq. ID
                   uC-gsflmaxxa057d05b1
Method
                   BLASTX
NCBI GI
                   q3080420
BLAST score
                   218
E value
                   1.0e-17
Match length
                   47
% identity
                   87
NCBI Description (AL022604) putative sugar transporter protein [Arabidopsis
                   thaliana]
Seq. No.
                   235846
Seq. ID
                   uC-gsflmaxxa057d10b1
Method
                  BLASTX
NCBI GI
                  g3334162
BLAST score
                  227
E value
                  1.0e-18
Match length
                  97
% identity
                   41
NCBI Description DOWN SYNDROME CRITICAL REGION PROTEIN A
                  >gi_2588993_dbj_BAA23270_ (AB001990) Dcra [Mus musculus]
Seq. No.
                  235847
Seq. ID
                  uC-gsflmaxxa057e12b1
Method
                  BLASTX
NCBI GI
                  g2088658
BLAST score
                  271
E value
                  7.0e-24
Match length
                  91
% identity
                  59
NCBI Description (AF002109) unknown protein [Arabidopsis thaliana]
Seq. No.
                  235848
Seq. ID
                  uC-gsflmaxxa057f05b1
Method
                  BLASTX
NCBI GI
                  g115610
BLAST score
                  636
E value
                  1.0e-66
Match length
                  135
% identity
NCBI Description
                  PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE)
                  >gi_68030_pir__QYNT phosphoenolpyruvate carboxylase (EC
                  4.1.1.31) - common tobacco >gi_22589_emb_CAA41758_ (X59016)
```

phosphoenolpyruvate carboxylase [Nicotiana tabacum]

Seq. No. 235849

Seq. ID uC-gsflmaxxa057f08b1

Method BLASTX NCBI GI q3080369



BLAST score 145 E value 3.0e-09 Match length 54 % identity 54

NCBI Description (AL022580) putative protein [Arabidopsis thaliana]

Seq. No. Seq. ID 235850

Seq. ID uC-gsflmaxxa057g11b1

Method BLASTX
NCBI GI g2558662
BLAST score 151
E value 8.0e-10
Match length 56
% identity 50

NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.

235851

Seq. ID uC-gsflmaxxa057h05b1

Method BLASTX
NCBI GI g3025329
BLAST score 165
E value 2.0e-11
Match length 115
% identity 35

NCBI Description HYPOTHETICAL 25.4 KD PROTEIN F53F4.3 IN CHROMOSOME V

>gi\_3877534\_emb\_CAB01212\_ (Z77663) Similarity to S.pombe hypothetical proteinSPAC4G9.01 (TR:E223656) [Caenorhabditis

elegans]

Seq. No.

235852

Seq. ID uC-gsflmaxxa057h10b1

Method BLASTX
NCBI GI g2760332
BLAST score 337
E value 1.0e-31
Match length 137
% identity 52

NCBI Description (AC002130) F1N21.17 [Arabidopsis thaliana]

Seq. No. 235853

Seq. ID uC-gsflmaxxa057h11b1

Method BLASTX
NCBI GI g3445204
BLAST score 180
E value 4.0e-13
Match length 50
% identity 64

NCBI Description (AC004786) putative GTP-binding protein [Arabidopsis

thaliana]

Seq. No. 235854

Seq. ID uC-gsflmaxxa058a01b1

Method BLASTX
NCBI GI g2497486
BLAST score 471
E value 2.0e-47
Match length 111



% identity

NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi\_2121275 (AF000147) UMP/CMP kinase [Arabidopsis

thaliana]

Seq. No.

235855

Seq. ID

uC-gsflmaxxa058a09b1

Method

BLASTX g3355486

NCBI GI BLAST score

367

E value

4.0e-35

Match length

97

% identity

68

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.

235856

Seq. ID

uC-gsflmaxxa058b04b1

Method NCBI GI

BLASTX q2497953

BLAST score

361

E value

1.0e-34

Match length

98

% identity

73

NCBI Description

MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM

COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi\_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi\_4469123\_emb\_CAB38312\_ (AJ236870) molybdenum

cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No.

235857

Seq. ID

uC-gsflmaxxa058b10b1

Method NCBI GI BLASTX q4185139

BLAST score

299 2.0e-27

E value Match length

93

% identity

62

NCBI Description (AC005724) putative diacylglycerol kinase [Arabidopsis

thaliana]

Seq. No.

235858

Seq. ID

uC-gsflmaxxa058c02b1

Method

BLASTX

NCBI GI

g3169178

BLAST score

E value

199

Match length

2.0e-15

59 63

% identity

NCBI Description (AC004401) hypothetical protein [Arabidopsis thaliana]

Seq. No.

235859

Seq. ID

uC-gsflmaxxa058c03b1

Method NCBI GI BLASTX g2501449

BLAST score

245 1.0e-20

E value Match length

53

34164

```
% identity
NCBI Description
                  UBIQUITIN-LIKE PROTEIN SMT3 >gi 1668773 emb CAA67922
                   (X99608) ubiquitin-like protein [Oryza sativa]
Seq. No.
                   235860
Seq. ID
                   uC-gsflmaxxa058c08b1
Method
                   BLASTX
NCBI GI
                   q4263048
BLAST score
                   335
E value
                   2.0e-31
Match length
                  100
% identity
                   67
NCBI Description (AC005142) putative hydrolase [Arabidopsis thaliana]
Seq. No.
                   235861
Seq. ID
                   uC-gsflmaxxa058e02b1
Method
                  BLASTX
NCBI GI
                  g4455155
BLAST score
                  274
E value
                  2.0e-24
Match length
                  80
% identity
                  70
NCBI Description (AL022023) EF-1 alpha - like protein (fragment)
                   [Arabidopsis thaliana]
Seq. No.
                  235862
Seq. ID
                  uC-gsflmaxxa058e07b1
Method
                  BLASTX
NCBI GI
                  g2832686
BLAST score
                  250
E value
                  2.0e-21
Match length
                  132
% identity
                  34
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
Seq. No.
                  235863
Seq. ID
                  uC-gsflmaxxa058f03b1
Method
                  BLASTX
NCBI GI
                  g2842496
BLAST score
                  146
E value
                  2.0e-09
Match length
                  32
% identity
                  81
NCBI Description (AL021749) NAM / CUC2 -like protein [Arabidopsis thaliana]
Seq. No.
                  235864
Seq. ID
                  uC-gsflmaxxa058f09b1
Method
                  BLASTX
                  g126896
                  416
                  7.0e-41
```

NCBI GI BLAST score E value Match length 88 % identity 92

NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR

>gi\_319831 pir DEPUMW malate dehydrogenase (EC 1.1.1.37)

precursor, mitochondrial - watermelon

>gi\_18297\_emb\_CAA35239\_ (X17362) precursor protein (AA -27



## to 320) [Citrullus lanatus]

Seq. No. 235865 Seq. ID uC-gsflmaxxa058f12b1 Method BLASTX NCBI GI g3822403 BLAST score 203 E value 8.0e-16 Match length 40 85 % identity NCBI Description (AF087932) hydroperoxide lyase [Arabidopsis thaliana]

Seq. No. 235866

Seq. ID uC-gsflmaxxa058g07b1 Method BLASTX

NCBI GI g1663722 BLAST score 386 E value 2.0e-37 Match length 133 % identity 53

NCBI Description (U50845) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No. 235867

Seq. ID uC-gsflmaxxa058h08b1

Method BLASTX
NCBI GI g1491615
BLAST score 261
E value 6.0e-23
Match length 65
% identity 69

NCBI Description (X99923) male sterility 2-like protein [Arabidopsis

thaliana]

Seq. No. 235868

Seq. ID uC-gsflmaxxa058h10b1

Method BLASTX
NCBI GI g2244752
BLAST score 194
E value 7.0e-15
Match length 108
% identity 39

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235869

Seq. ID uC-gsflmaxxa060a04b1

Method BLASTX
NCBI GI g4103152
BLAST score 165
E value 5.0e-12
Match length 59
% identity 56

NCBI Description (AF020716) histidyl-tRNA synthetase [Triticum aestivum]

Seq. No. 235870

Seq. ID uC-gsflmaxxa060a06b1

Method BLASTX NCBI GI g22166

34166

% identity

```
BLAST score
E value
                   2.0e-52
Match length
                   118
% identity
                   81
NCBI Description (X15711) adenine nucleotide translocator [Zea mays]
Seq. No.
                   235871
Seq. ID
                   uC-gsflmaxxa060b09b1
Method
                   BLASTX
NCBI GI
                   g3036816
BLAST score
                   204
E value
                   5.0e-16
Match length
                   131
                   37
% identity
NCBI Description (AL022373) myosin-like protein [Arabidopsis thaliana]
Seq. No.
                   235872
Seq. ID
                   uC-gsflmaxxa060c12b1
Method
                   BLASTX
NCBI GI
                   g2924503
BLAST score
                   213
E value
                   3.0e-17
Match length
                   76
% identity
                   50
NCBI Description (AL022019) glucosyltransferase [Schizosaccharomyces pombe]
Seq. No.
                   235873
Seq. ID
                   uC-gsflmaxxa060e12b1
Method
                   BLASTX
NCBI GI
                   g4309734
BLAST score
                   195
E value
                   5.0e-15
Match length
                   53
% identity
                   66
NCBI Description (AC006439) putative 26S proteosome regulatory subunit 8
                   [Arabidopsis thaliana]
                   235874
Seq. No.
Seq. ID
                   uC-gsflmaxxa060f02b1
Method
                  BLASTX
NCBI GI
                   g2632252
BLAST score
                   345
E value
                   7.0e-33
Match length
                  88
% identity
                   75
NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]
Seq. No.
                   235875
Seq. ID
                  uC-gsflmaxxa060f09b1
Method
                  BLASTX
NCBI GI
                  g4538913
BLAST score
                  317
E value
                   3.0e-29
Match length
                  97
```

NCBI Description (AL049482) putative protein [Arabidopsis thaliana]



```
Seq. No.
                   235876
Seq. ID
                   uC-gsflmaxxa060f11b1
Method
                   {\tt BLASTX}
NCBI GI
                   g2459415
BLAST score
                   146
E value
                   3.0e-09
Match length
                   83
% identity
                   43
NCBI Description (AC002332) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   235877
Seq. ID
                   uC-gsflmaxxa060g02b1
Method
                   BLASTX
NCBI GI
                   q3033393
BLAST score
                   234
E value
                   1.0e-19
Match length
                   66
% identity
                   70
                  (AC004238) putative phosphatidylinositol-glycan-class C
NCBI Description
                   (PIGC) [Arabidopsis thaliana]
Seq. No.
                   235878
Seq. ID
                   uC-gsflmaxxa061a02b1
Method
                   BLASTX
NCBI GI
                   q2146735
BLAST score
                   556
E value
                   2.0e-57
Match length
                   114
% identity
                   92
NCBI Description
                  glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (clone
                  E5) - Arabidopsis thaliana (fragment)
                   >gi_1166405_emb_CAA59011_ (X84229) glucose-6-phosphate
                   1-dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   235879
Seq. ID
                  uC-gsflmaxxa061a09b1
Method
                  BLASTX
NCBI GI
                  g2501182
BLAST score
                  587
                  7.0e-61
E value
Match length
                  147
% identity
                  72
NCBI Description
                  OSMOTIN-LIKE PROTEIN PRECURSOR >gi_2129934 pir JC5237
                  osmotin-like protein - tomato >gi 1220537 (L76632)
                  osmotin-like protein [Lycopersicon esculentum]
Seq. No.
                  235880
Seq. ID
                  uC-gsflmaxxa061a11b1
Method
                  BLASTX
                  g4510383
                  223
```

NCBI GI BLAST score E value 3.0e-18 Match length 69 % identity

NCBI Description (AC007017) unknown protein [Arabidopsis thaliana]

Seq. No. 235881



```
Seq. ID
                   uC-gsflmaxxa061b01b1
Method
                   BLASTX
NCBI GI
                   g585452
BLAST score
                   601
E value
                   5.0e-65
Match length
                   134
% identity
                   90
                   MALATE OXIDOREDUCTASE (NAD), MITOCHONDRIAL 59 KD ISOFORM
NCBI Description
                   PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME)
                   (NAD-ME) >gi_1076666_pir__A53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 59K chain precursor,
                   mitochondrial - potato >gi_438131_emb_CAA80547_ (Z23002)
                   precursor of the 59kDa subunit of the mitochondrial
                   NAD+-dependent malic enzyme [Solanum tuberosum]
Seq. No.
                   235882
Seq. ID
                   uC-gsflmaxxa061b04b1
Method
                   BLASTX
NCBI GI
                   g4467110
BLAST score
                   224
E value
                   2.0e-18
Match length
                   114
% identity
                   36
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                   235883
Seq. ID
                   uC-qsflmaxxa061b08b1
Method
                   BLASTX
NCBI GI
                   g2547036
BLAST score
                   193
E value
                   1.0e-14
Match length
                   90
% identity
NCBI Description (Y13920) ribosomal protein S2 [Triticum aestivum]
Seq. No.
                   235884
Seq. ID
                   uC-gsflmaxxa061b12b1
Method
                   BLASTX
NCBI GI
                   g1495366
BLAST score
                   394
E value
                   3.0e-38
Match length
                   104
% identity
                   69
NCBI Description (Z69370) nitrite transporter [Cucumis sativus]
Seq. No.
                   235885
Seq. ID
                   uC-gsflmaxxa061c06b1
Method
                   BLASTX
```

NCBI GI g4249410 BLAST score 148 E value 3.0e-09 Match length 99

% identity

NCBI Description (AC006072) unknown protein [Arabidopsis thaliana]

Seq. No. 235886

Seq. ID uC-qsflmaxxa061d03b1



Method BLASTX
NCBI GI g508304
BLAST score 340
E value 7.0e-32
Match length 77
% identity 81

NCBI Description (L22305) corC [Medicago sativa]

Seq. No. 235887

Seq. ID uC-gsflmaxxa061e05b1

Method BLASTX
NCBI GI g3122572
BLAST score 348
E value 6.0e-33
Match length 118
% identity 61

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I

SUBUNIT) >gi\_1084434\_pir\_\_S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi\_758340\_emb\_CAA59818\_ (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No. 235888

Seq. ID uC-gsflmaxxa061g05b1

Method BLASTX
NCBI GI g2266947
BLAST score 757
E value 9.0e-81
Match length 146
% identity 99

NCBI Description (AF008939) phosphoenolpyruvate carboxylase 1 [Gossypium

hirsutum]

Seq. No. 235889

Seq. ID uC-gsflmaxxa061g11b1

Method BLASTX
NCBI GI g1143511
BLAST score 653
E value 1.0e-68
Match length 124
% identity 99

NCBI Description (Z47076) Ser/Thr protein phosphatase homologous to PPX

[Malus domestica] >gi\_1586034\_prf\_\_2202340A Ser/Thr protein

phosphatase [Malus domestica]

Seq. No. 235890

Seq. ID uC-gsflmaxxa061h01b1

Method BLASTX
NCBI GI g3121836
BLAST score 164
E value 3.0e-11
Match length 60
% identity 57

NCBI Description PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE

SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE)

(CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE





## CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) >gi\_2181182\_emb\_CAA63969\_ (X94306) CDP-diacylglycerol synthetase [Arabidopsis thaliana]

Seq. No. 235891
Seq. ID uC-gsflmaxxa061h07b1
Method BLASTX
NCBI GI a3641252

NCBI GI g3641252 BLAST score 290 E value 4.0e-26 Match length 133 % identity 6

NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus

domestica]

Seq. No. 235892

Seq. ID uC-gsflmaxxa064a07b1

Method BLASTX
NCBI GI g3757524
BLAST score 217
E value 2.0e-17
Match length 165
% identity 35

NCBI Description (AC005167) tetracycline transporter-like protein

[Arabidopsis thaliana]

Seq. No. 235893

Seq. ID uC-gsflmaxxa064b01b1

Method BLASTX
NCBI GI g4200165
BLAST score 752
E value 3.0e-80
Match length 156
% identity 84

NCBI Description (Y16262) neutral invertase [Daucus carota]

Seq. No. 235894

Seq. ID uC-gsflmaxxa064b02b1

Method BLASTX
NCBI GI g1169451
BLAST score 153
E value 3.0e-10
Match length 58
% identity 55

NCBI Description PROBABLE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A6 PRECURSOR

((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)

(BETA-1,3-ENDOGLUCANASE) >gi\_322510\_pir\_\_S31906 beta-1,3-glucanase homolog - Arabidopsis thaliana

>gi\_22677\_emb\_CAA49853\_ (X70409) A6 [Arabidopsis thaliana]
>gi\_2244764\_emb\_CAB10187\_ (Z97335) AMP-binding protein

[Arabidopsis thaliana]

Seq. No. 235895

Seq. ID uC-gsflmaxxa064b12b1

Method BLASTX NCBI GI g3024386 BLAST score 764



E value 1.0e-81
Match length 144
% identity 98
NCBI Description POLYGAL

NCBI Description POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)

>gi\_2129500\_pir\_\_S52006 polygalacturonase - upland cotton >gi\_606650 (U09717) polygalacturonase [Gossypium hirsutum]

Seq. No. 235896

Seq. ID uC-gsflmaxxa067b02b1

Method BLASTX
NCBI GI g4415916
BLAST score 315
E value 6.0e-29
Match length 152
% identity 41

NCBI Description (AC006282) putative pectin methylesterase [Arabidopsis

thaliana]

Seq. No. 235897

Seq. ID uC-gsflmaxxa067d05b1

Method BLASTX
NCBI GI g4539010
BLAST score 511
E value 6.0e-52
Match length 148
% identity 48

NCBI Description (AL049481) putative DNA-directed RNA polymerase

[Arabidopsis thaliana]

Seq. No. 235898

Seq. ID uC-gsflmaxxa067f08b1

Method BLASTX
NCBI GI g2342679
BLAST score 155
E value 3.0e-10
Match length 136
% identity 38

NCBI Description (AC000106) Similar to Vicia sativa ENBP1 (gb X95995).

[Arabidopsis thaliana]

Seq. No. 235899

Seq. ID uC-gsflmaxxa067q07b1

Method BLASTX
NCBI GI g1172874
BLAST score 213
E value 2.0e-24
Match length 114
% identity 54

NCBI Description DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

>gi\_479589\_pir\_\_S34823 dehydration-induced protein RD22 Arabidopsis thaliana >gi\_391608\_dbj\_BAA01546\_ (D10703) rd22
[Arabidopsis thaliana] >gi\_447134\_prf\_\_1913421A rd22 gene

[Arabidopsis thaliana]

Seq. No. 235900

Seq. ID uC-gsflmaxxa067g09b1

Method BLASTX



```
NCBI GI
                   q2388710
BLAST score
                  530
E value
                  4.0e-54
Match length
                  144
% identity
NCBI Description (AF017150) betaine aldehyde dehydrogenase [Amaranthus
                  hypochondriacus]
                  235901
Seq. No.
Seq. ID
                  uC-gsflmaxxa067g11b1
Method
                  BLASTX
NCBI GI
                  g4185855
BLAST score
                  468
E value
                  7.0e-47
Match length
                  135
% identity
                  73
NCBI Description (AJ132388) Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.
                  235902
Seq. ID
                  uC-gsflmaxxa067g12b1
Method
                  BLASTX
NCBI GI
                  q3046815
BLAST score
                  267
E value
                  3.0e-23
Match length
                  50
% identity
                  88
NCBI Description (AL021687) cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  235903
Seq. ID
                  uC-gsflmaxxa067h06b1
Method
                  BLASTX
NCBI GI
                  q4454051
BLAST score
                  545
E value
                  7.0e-56
Match length
                  163
% identity
                  63
NCBI Description (AL035394) putative polygalacturonase [Arabidopsis
                  thaliana]
                  235904
Seq. No.
Seq. ID
                  uC-gsflmaxxa069b09b1
Method
                  BLASTX
NCBI GI
                  g3212869
BLAST score
                  170
E value
                  1.0e-12
Match length
                  39
% identity
                  82
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
                  235905
Seq. No.
Seq. ID
                  uC-gsflmaxxa069c02b1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2454182
BLAST score 144
E value 2.0e-09
Match length 39
% identity 69



```
NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit
                  [Arabidopsis thaliana]
                  235906
Seq. No.
Seq. ID
                  uC-gsflmaxxa069e04b1
Method
                  BLASTX
NCBI GI
                  g2129639
BLAST score
                  159
E value
                  1.0e-12
Match length
                  48
                  78
% identity
NCBI Description
                  luminal binding protein (BiP) - Arabidopsis thaliana
                  >gi 1303695 dbj BAA12348 (D84414) luminal binding protein
                  (BiP) [Arabidopsis thaliana]
                  235907
Seq. No.
Seq. ID
                  uC-gsflmaxxa070a04b1
Method
                  BLASTX
                  g2244749
NCBI GI
BLAST score
                  315
E value
                  2.0e-29
                  88
Match length
% identity
                  66
NCBI Description (297335) hydroxymethyltransferase [Arabidopsis thaliana].
Seq. No.
                  235908
Seq. ID
                  uC-gsflmaxxa070a11b1
Method
                  BLASTX
NCBI GI
                  g4204265
BLAST score
                  643
E value
                  2.0e-67
Match length
                  143
% identity
                  80
NCBI Description (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                  235909
Seq. ID
                  uC-gsflmaxxa070b02b1
Method
                  BLASTX
NCBI GI
                  g4454015
BLAST score
                  146
E value
                  2.0e-09
Match length
                  80
% identity
                  18
NCBI Description (AL035396) putative protein [Arabidopsis thaliana]
Seq. No.
                  235910
Seq. ID
                  uC-gsflmaxxa070b04b1
                  BLASTX
Method
NCBI GI
                  q3299896
```

Method BLASTX
NCBI GI g3299896
BLAST score 285
E value 2.0e-25
Match length 67

% identity 73

NCBI Description (AF020390) beta-galactosidase [Lycopersicon esculentum]

Seq. No. 235911

Seq. ID uC-gsflmaxxa070b08b1



```
Method
                   BLASTX
NCBI GI
                   g1169451
BLAST score
                   441
E value
                   7.0e-44
Match length
                   125
% identity
                   66
```

NCBI Description PROBABLE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A6 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)

> (BETA-1,3-ENDOGLUCANASE) >gi\_322510\_pir\_\_\$31906 beta-1,3-glucanase homolog - Arabidopsis thaliana

>qi 22677 emb CAA49853 (X70409) A6 [Arabidopsis thaliana] >gi\_2244764\_emb\_CAB10187\_ (Z97335) AMP-binding protein

[Arabidopsis thaliana]

```
Seq. No.
                   235912
```

uC-gsflmaxxa070c06b1 Seq. ID

Method BLASTX NCBI GI q2129944 BLAST score 331 E value 4.0e-31Match length 88 % identity 68

NCBI Description RNA-binding protein RZ-1 - wood tobacco

>gi\_1395193\_dbj\_BAA12064\_ (D83696) RNA-binding protein RZ-1 [Nicotiana sylvestris] >gi\_1435062\_dbj\_BAA06012\_ (D28861) RNA binding protein, RZ-1 [Nicotiana sylvestris]

Seq. No. 235913

Seq. ID uC-gsflmaxxa070c11b1

Method BLASTX NCBI GI q3292827 BLAST score 234 E value 1.0e-19 Match length 51 % identity 82

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 235914

Seq. ID uC-gsflmaxxa070e03b1

Method BLASTX NCBI GI q3256068 BLAST score 164 E value 3.0e-23Match length 109 % identity 50

NCBI Description (Y14068) Heat Shock Factor 3 [Arabidopsis thaliana]

Seq. No. 235915

Seq. ID uC-gsflmaxxa070g12b1

Method BLASTX NCBI GI q3790587 BLAST score 400 E value 4.0e-39 Match length 99 % identity 73

NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis

thaliana]

```
235916
Seq. No.
Seq. ID
                    uC-gsfImaxxa070h02b1
Method
                    BLASTX
NCBI GI
                    g1076282
BLAST score
                    183
E value
                    6.0e-17
Match length
                    61
                    79
% identity
NCBI Description
                    aconitate hydratase (EC 4.2.1.3) - Arabidopsis thaliana
                    (fragment) >gi 599625 emb CAA58046 (X82839) aconitase
                    [Arabidopsis thaliana]
                    235917
Seq. No.
Seq. ID
                    uC-gsflmaxxa070h11b1
Method
                    BLASTX
NCBI GI
                    g1706318
BLAST score
                    572
E value
                    3.0e-59
Match length
                    126
% identity
                    82
NCBI Description
                    GLUTAMATE DECARBOXYLASE (GAD) (ERT D1)
                    >gi_1362098_pir__S56177 probable glutamate decarboxylase -tomato >gi_995555_emb_CAA56812_(X80840) homology to pyroxidal-5'-phosphate-dependant glutamate decarboxylases;
                    putative start codon [Lycopersicon esculentum]
Seq. No.
                    235918
Seq. ID
                    uC-gsflmaxxa070h12b1
Method
                    BLASTX
NCBI GI
                    g2213594
BLAST score
                    371
                    9.0e-36
E value
Match length
                    106
% identity
                    65
NCBI Description (AC000348) T7N9.14 [Arabidopsis thaliana]
Seq. No.
                    235919
Seq. ID
                    uC-gsflmaxxa074h09b1
Method
                    BLASTX
NCBI GI
                    q3249086
BLAST score
                    319
E value
                    2.0e-29
Match length
                    72
% identity
                    85
NCBI Description
                    (AC004473) Contains similarity to 21 KD subunit of the
                    Arp2/3 protein complex (ARC21) gb AF006086 from Homo
                    sapiens. EST gb Z37222 comes [Arabidopsis thaliana]
Seq. No.
                    235920
Seq. ID
                    uC-gsflmaxxa076b01b1
```

Method BLASTX NCBI GI g2708741 BLAST score 613 E válue 7.0e-67 Match length 139 % identity 94



```
NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]
                   235921
Seq. No.
Seq. ID
                   uC-gsflmaxxa076b06b1
Method
                   BLASTX
NCBI GI
                   g1071918
BLAST score
                   261
E value
                   1.0e-22
Match length
                   56
% identity
                   84
NCBI Description
                  phosphoribosylamine--glycine ligase (EC 6.3.4.13) -
                   Arabidopsis thaliana (fragment)
Seq. No.
                   235922
Seq. ID
                   uC-qsflmaxxa076b07b1
Method
                   BLASTX
NCBI GI
                   g3757527
BLAST score
                   155
E value
                   3.0e-10
                   71
Match length
% identity
NCBI Description
                   (AC005167) putative ribosomal protein L27 [Arabidopsis
                   thaliana]
Seq. No.
                   235923
Seq. ID
                   uC-gsflmaxxa076b08b1
Method
                   BLASTX
NCBI GI
                   g4545262
BLAST score
                   159
E value
                   1.0e-10
Match length
                   44
% identity
                   64
NCBI Description
                  (AF118230) metallothionein-like protein [Gossypium
                   hirsutum]
                   235924
Seq. No.
Seq. ID
                   uC-gsflmaxxa076b11b1
Method
                  BLASTX
NCBI GI
                   g3461820
BLAST score
                  180
E value
                   4.0e-13
Match length
                  84
% identity
                   49
NCBI Description
                 (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   235925
Seq. ID
                  uC-gsflmaxxa076c04b1
                  BLASTX
Method
NCBI GI
                  q114332
BLAST score
                  485
                   4.0e-49
E value
Match length
                  105
% identity
                  88
NCBI Description
                  PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
```

>gi\_482389\_pir\_\_A45506 H+-transporting ATPase (EC 3.6.1.35)
LHA1 - tomato >gi\_170464 (M60166) H+-ATPase [Lycopersicon esculentum] >gi\_228405\_prf\_\_1803518A H ATPase [Lycopersicon



## esculentum]

```
Seq. No.
                   235926
Seq. ID
                   uC-gsflmaxxa076c05b1
Method
                   BLASTX
NCBI GI
                   g2914703
BLAST score
                   265
E value
                   4.0e-23
Match length
                   101
% identity
                   28
NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]
Seq. No.
                   235927
Seq. ID
                   uC-qsflmaxxa076c11b1
Method
                   BLASTX
NCBI GI
                   g2493895
BLAST score
                   484
E value
                   8.0e-49
Match length
                   119
                   77
% identity
NCBI Description CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)
                    (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                   >gi_1071911_pir__S46438 cysteine synthase (EC 4.2.99.8) - watermelon >gi_540497_dbj_BAA05965_ (D28777) cysteine
                   synthase [Citrullus lanatus]
                   235928
Seq. No.
Seq. ID
                   uC-gsflmaxxa076d03b1
Method
                   BLASTX
NCBI GI
                   g134891
BLAST score
                   184
E value
                   1.0e-13
Match length
                   99
% identity
                   42
                   SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT
NCBI Description
                   (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA)
                   >gi 89066 pir A24570 signal recognition particle receptor
                   precursor - dog >gi_997_emb_CAA26945_ (X03184) signal
                   recognition particle receptor [Canis sp.]
                   >gi 224778 prf__1112224A signal recognition particle
                   receptor [Canis familiaris]
Seq. No.
                   235929
Seq. ID
                   uC-gsflmaxxa076d05b1
Method
                   BLASTX
NCBI GI
                   g3582344
BLAST score
                   213
E value
                   5.0e-17
                   117
Match length
% identity
                  (AC005496) putative cell division protein [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 235930

Seq. ID uC-gsflmaxxa076e09b1

Method BLASTX NCBI GI g2642428



BLAST score 222 E value 3.0e-18 Match length 118 % identity 47

NCBI Description (AC002391) unknown protein, 3' partial [Arabidopsis

thaliana]

Seq. No. 235931

Seq. ID uC-gsflmaxxa076g01b1

Method BLASTX
NCBI GI g4567282
BLAST score 408
E value 6.0e-40
Match length 116
% identity 66

NCBI Description (AC006841) putative DNAJ protein [Arabidopsis thaliana]

Seq. No. 235932

Seq. ID uC-gsflmaxxa076g03b1

Method BLASTX
NCBI GI g4263771
BLAST score 254
E value 6.0e-22
Match length 64
% identity 73

NCBI Description (AC006218) putative nonspecific lipid-transfer protein

precursor [Arabidopsis thaliana]

Seq. No. 235933

Seq. ID uC-gsflmaxxa076h01b1

Method BLASTX
NCBI GI g1906830
BLAST score 154
E value 5.0e-21
Match length 99
% identity 56

NCBI Description (Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No. 235934

Seq. ID uC-gsflmaxxa076h08b1

Method BLASTX
NCBI GI g4539324
BLAST score 599
E value 2.0e-62
Match length 131
% identity 92

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 235935

Seq. ID uC-gsflmaxxa088b02b1

Method BLASTX
NCBI GI g3193286
BLAST score 173
E value 2.0e-12
Match length 58
% identity 53

NCBI Description (AF069298) T14P8.22 gene product [Arabidopsis thaliana]

NCBI Description

domestica]



```
235936
Seq. No.
Seq. ID
                  uC-gsflmaxxa088b09b1
                  BLASTX
Method
NCBI GI
                  g2244956
BLAST score
                  220
E value
                   5.0e-18
                  133
Match length
% identity
                   38
                  (Z97340) strong similarity to pectinesterase [Arabidopsis
NCBI Description
                  thaliana]
                   235937
Seq. No.
Seq. ID
                  uC-qsflmaxxa088b10b1
                  BLASTX
Method
NCBI GI
                  g3367515
BLAST score
                  279
E value
                  8.0e-25
                   97
Match length
                   56
% identity
NCBI Description (AC004392) Similar to
                  glucose-6-phosphate/phosphate-translocator (GPT)
                  gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
                   235938
Seq. No.
Seq. ID
                  uC-gsflmaxxa088c07b1
Method
                  BLASTX
NCBI GI
                   g3928084
                   485
BLAST score
E value
                   7.0e-49
Match length
                  148
                   66
% identity
NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis
                   thaliana]
                   235939
Seq. No.
Seq. ID
                   uC-gsflmaxxa088d12b1
Method
                  BLASTX
NCBI GI
                   g2832649
                   392
BLAST score
E value
                   7.0e-38
Match length
                   95
% identity
                   79
NCBI Description
                  (AL021710) adenylosuccinate lyase - like protein
                   [Arabidopsis thaliana]
                   235940
Seq. No.
                   uC-gsflmaxxa088e08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3641252
BLAST score
                   404
                   1.0e-39
E value
Match length
                   111
% identity
```

(AF053127) leucine-rich receptor-like protein kinase [Malus



```
235941
Seq. No.
Seq. ID
                  uC-gsflmaxxa088f09b1
Method
                  BLASTX
NCBI GI
                  g3367576
BLAST score
                  310
                  2.0e-28
E value
Match length
                  95
% identity
                  62
NCBI Description (AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]
                  235942
Seq. No.
Seq. ID
                  uC-gsflmaxxa088g04b1
                  {\tt BLASTX}
Method
NCBI GI
                  g3776557
BLAST score
                  463
E value
                  2.0e-46
                  132
Match length
% identity
                  64
                  (AC005388) Contains similarity to gi 2924495 hypothetical
NCBI Description
                  protein Rv1920 from Mycobacterium tuberculosis genome
                  gb AL022020. [Arabidopsis thaliana]
                  235943
Seq. No.
Seq. ID
                  uC-gsflmaxxa088h11b1
Method
                  BLASTX
NCBI GI
                  g1263177
BLAST score
                  186
E value
                  6.0e-14
Match length
                  133
                  35
% identity
NCBI Description (U23438) MAP kinase phosphatase [Rattus norvegicus]
                  235944
Seq. No.
                  uC-gsflmaxxa089a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3927830
BLAST score
                  257
E value
                  2.0e-22
Match length
                  75
                  56
% identity
NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  235945
                  uC-gsflmaxxa089a11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3114573
BLAST score
                  665
E value
                  5.0e-70
Match length
                  154
% identity
                  80
                  (AF019383) 1-deoxyxylulose-5-phosphate synthase [Mentha x
NCBI Description
                  piperita]
```

Seq. No. 235946

Seq. ID uC-gsflmaxxa089c08b1

Method BLASTX NCBI GI g548770



BLAST score 449 E value 1.0e-44 Match length 100 % identity 85

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi\_481228\_pir\_\_S38359 ribosomal

protein L3 - rice >gi\_303853\_dbj\_BAA02155 (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 235947

Seq. ID uC-gsflmaxxa089d10b1

Method BLASTX
NCBI GI g3551954
BLAST score 160
E value 1.0e-10
Match length 103
% identity 31

NCBI Description (AF082030) senescence-associated protein 5 [Hemerocallis

hybrid cultivar]

Seq. No. 235948

Seq. ID uC-gsflmaxxa089e10b1

Method BLASTX
NCBI GI g3420052
BLAST score 465
E value 2.0e-46
Match length 153
% identity 63

NCBI Description (AC004680) putative ubiqinone reductase [Arabidopsis

thaliana]

Seq. No. 235949

Seq. ID uC-gsflmaxxa089f02b1

Method BLASTX
NCBI GI g4432817
BLAST score 318
E value 2.0e-29
Match length 111
% identity 65

NCBI Description (AC006593) unknown protein [Arabidopsis thaliana]

Seq. No. 235950

Seq. ID uC-qsflmaxxa089h06b1

Method BLASTX
NCBI GI g1477480
BLAST score 654
E value 1.0e-68
Match length 167
% identity 48

NCBI Description (U40341) carbamoyl phosphate synthetase large chain

[Arabidopsis thaliana]

Seq. No. 235951

Seq. ID uC-gsflmaxxa089h10b1

Method BLASTX
NCBI GI g544242
BLAST score 158
E value 1.0e-10



Match length 38 % identity 79 NCBI Description EN >g pr

ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi\_485498\_pir\_\_S33533 heat shock protein 90 homolog
precursor - barley >gi 22652 emb CAA48143 (X67960) GRP94

homologue [Hordeum vulgare]

Seq. No. 235952

Seq. ID uC-gsflmaxxa089h11b1

Method BLASTX
NCBI GI g2344901
BLAST score 724
E value 7.0e-77
Match length 164
% identity 82

NCBI Description (AC002388) serine/threonine protein kinase isolog

[Arabidopsis thaliana]

Seq. No. 235953

Seq. ID 'uC-gsflmaxxa090a06b1

Method BLASTX
NCBI GI g2982311
BLAST score 200
E value 5.0e-16
Match length 49
% identity 78

NCBI Description (AF051240) probable ubiquitin-conjugating enzyme E2 [Picea

mariana]

Seq. No. 235954

Seq. ID uC-gsflmaxxa090c04b1

Method BLASTX
NCBI GI g3522942
BLAST score 575
E value 2.0e-59
Match length 155
% identity 66

NCBI Description (AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No. 235955

Seq. ID uC-gsflmaxxa090c06b1

Method BLASTX
NCBI GI g421955
BLAST score 515
E value 6.0e-59
Match length 160
% identity 65

NCBI Description hypothetical protein 4 - potato transposon Tst1

>gi\_21434\_emb\_CAA36616\_ (X52387) ORF4 [Solanum tuberosum]

Seq. No. 235956

Seq. ID uC-gsflmaxxa090c11b1

Method BLASTX
NCBI GI g2529677
BLAST score 492
E value 6.0e-50
Match length 115

34183



% identity (AC002535) kinesin-like protein, heavy chain [Arabidopsis NCBI Description thaliana] Seq. No. 235957 Seq. ID uC-gsflmaxxa090d06b1 Method BLASTX NCBI GI g2952433 BLAST score 363 E value 1.0e-34 Match length 119 % identity 59 NCBI Description (AF051135) putative ubiquitin activating enzyme E1 [Arabidopsis thaliana] Seq. No. 235958 Seq. ID uC-gsflmaxxa090f09b1 Method BLASTX NCBI GI g4263821 BLAST score 258 E value 2.0e-22 Match length 98 % identity 58 NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana] Seq. No. 235959 Seq. ID uC-gsflmaxxa090h10b1 Method BLASTX NCBI GI q2982243 BLAST score 222 E value 4.0e-18 Match length 109 % identity 42 NCBI Description (AF051204) hypothetical protein [Picea mariana] Seq. No. 235960 Seq. ID uC-gsflmaxxa091a03b1 Method BLASTX NCBI GI q1895084 BLAST score 207 E value 2.0e-16 Match length 39 % identity NCBI Description (U89897) golgi associated protein se-wap41 [Zea mays] Seq. No. 235961

Seq. ID uC-gsflmaxxa091a07b1

Method BLASTX NCBI GI g4580395 BLAST score 562 E value 7.0e-58 Match length 167 % identity

NCBI Description (AC007171) putative kinesin-related protein [Arabidopsis

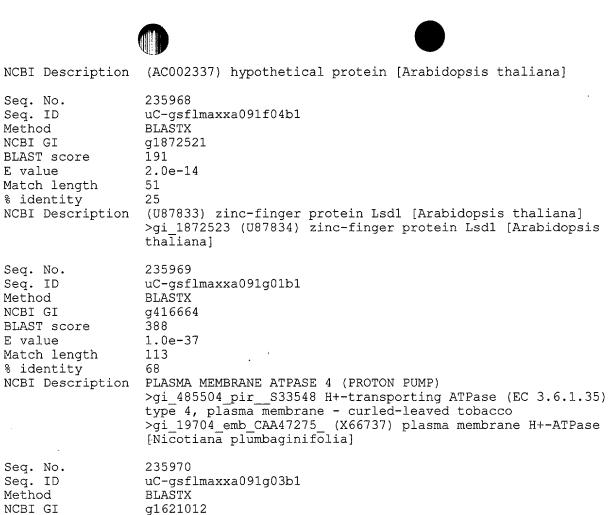
thaliana]

Seq. No. 235962

34184

```
Seq. ID
                   uC-gsflmaxxa091b08b1
Method
                   BLASTX
NCBI GI
                   g3335367
BLAST score
                   188
E value
                   4.0e-14
Match length
                   43
% identity
                   70
NCBI Description
                  (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                   235963
Seq. ID
                   uC-gsflmaxxa091b12b1
Method
                   BLASTX
NCBI GI
                   g1747294
BLAST score
                   494
E value
                   3.0e-50
Match length
                   102
% identity
                   95
NCBI Description (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
Seq. No.
                   235964
Seq. ID
                   uC-gsflmaxxa091d04b1
Method
                  BLASTX
NCBI GI
                   g2673914
BLAST score
                   207
E value
                   6.0e-17
Match length
                   68
% identity
                   60
NCBI Description
                  (AC002561) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   235965
Seq. ID
                  uC-gsflmaxxa091e05b1
Method
                  BLASTX
NCBI GI
                  g2244910
BLAST score
                  148
E value
                   9.0e-10
Match length
                  88
% identity
                   49
NCBI Description
                  (Z97339) unnamed protein product [Arabidopsis thaliana]
Seq. No.
                  235966
Seq. ID
                  uC-gsflmaxxa091e11b1
Method
                  BLASTX
NCBI GI
                  g2739374
BLAST score
                  171
E value
                  3.0e-12
Match length
                  71
% identity
                  54
NCBI Description
                  (AC002505) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  235967
Seq. ID
                  uC-gsflmaxxa091f01b1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2275213
BLAST score 166
E value 1.0e-11
Match length 99
% identity 43



BLAST score 642 E value 2.0e-67 Match length 134 % identity 90

NCBI Description (Y08786) 1,4-alpha-glucan branching enzyme [Solanum

tuberosum]

235971 Seq. No.

Seq. ID uC-gsflmaxxa091g05b1

Method BLASTX NCBI GI g4454471 BLAST score 145 E value 4.0e-09 Match length 58 % identity

NCBI Description (AC006234) putative G protein coupled receptor [Arabidopsis

thaliana]

Seq. No. 235972

Seq. ID uC-gsflmaxxa091g07b1

Method BLASTX NCBI GI g3608485 BLAST score 439 E value 2.0e-43 Match length 87

d

34186



% identity

NCBI Description

Seq. No. 235973 uC-gsflmaxxa091g11b1 Seq. ID Method BLASTX NCBI GI q1076663 BLAST score 262 E value 8.0e-23 Match length 54 % identity 96 NCBI Description H+-transporting ATPase (EC 3.6.1.35) (clone PHA2) - potato >gi\_435001\_emb\_CAA54045\_ (X76535) H(+)-transporting ATPase [Solanum tuberosum] 235974 Seq. No. Seq. ID uC-gsflmaxxa091h08b1 Method BLASTX NCBI GI g3135693 BLAST score 379 E value 2.0e-36 Match length 74 97 % identity NCBI Description (AF064201) glutathione S-transferase [Gossypium hirsutum] Seq. No. 235975 Seq. ID uC-gsflmaxxa091h11b1 Method BLASTX NCBI GI q2160692 BLAST score 513 E value 3.0e-52 Match length 125 % identity 72 NCBI Description (U73527) B' regulatory subunit of PP2A [Arabidopsis thaliana] Seq. No. 235976 Seq. ID uC-qsflmaxxa092a06b1 Method BLASTX NCBI GI q2651302 BLAST score 220 E value 3.0e-18 77 Match length % identity 52 NCBI Description (AC002336) hypothetical protein [Arabidopsis thaliana] Seq. No. Seq. ID 235977 uC-gsflmaxxa092c05b1 Method BLASTX NCBI GI q4263821 BLAST score 390 7.0e-38 E value Match length 122 70 % identity NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana] Seq. No. 235978

(AF088915) proteasome beta subunit [Petunia x hybrida]

Match length

% identity

35



```
uC-gsflmaxxa092g07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g220838
BLAST score
                   169
E value
                   3.0e-12
                   55
Match length
% identity
                   56
NCBI Description (D10655) dihydrolipoamide acetyltransferase [Rattus rattus]
                   235979
Seq. No.
Seq. ID
                   uC-gsflmaxxa092h07b1
Method
                   BLASTX
                   g1708236
NCBI GI
BLAST score
                   157
                   3.0e-24
E value
                   83
Match length
                   62
% identity
                 HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
NCBI Description
                   (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                   >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase
                   (EC 4.1.3.5) - Arabidopsis thaliana
                   >gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
                   >gi 1586548 prf 2204245A hydroxy methylglutaryl CoA
                   synthase [Arabidopsis thaliana]
                   235980
Seq. No.
Seq. ID
                   uC-gsflmaxxa092h08b1
Method
                   BLASTX
NCBI GI
                   g1666234
BLAST score
                   169
E value
                   2.0e-22
Match length
                   61
                   93
% identity
NCBI Description (U76193) actin [Pisum sativum] >gi 1724143 (U81049) actin
                   [Pisum sativum]
                   235981
Seq. No.
Seq. ID
                   uC-gsflmaxxa093h08b1
Method
                   BLASTX
NCBI GI
                   g4467096
BLAST score
                   189
E value
                   2.0e-14
Match length
                   106
% identity
                   42
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]
                   235982
Seq. No.
Seq. ID
                   uC-gsflmaxxa094b01b1
Method
                   BLASTX
NCBI GI
                   g1335862
BLAST score
                   165
E value
                   5.0e-12
```

NCBI Description (U42608) clathrin heavy chain [Glycine max]

NCBI Description

thaliana]



```
235983
Seq. No.
                   uC-gsflmaxxa094b03b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2499945
                   178
BLAST score
                   2.0e-13
E value
                   70
Match length
                   56
% identity
NCBI Description
                   URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE
                   PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE
                   DECARBOXYLASE >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) /
                   orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) -
                   Arabidopsis thaliana >gi 443818 emb CAA50686 (X71842).
                   pyrE-F [Arabidopsis thaliana]
                   235984
Seq. No.
                   uC-gsflmaxxa094c12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g217909
BLAST score
                   207
                   6.0e-17
E value
Match length
                   43
                   93
% identity
NCBI Description (D14044) glycolate oxidase [Cucurbita sp.]
Seq. No.
                   235985
                   uC-gsflmaxxa094d08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4220480
BLAST score
                   164
                   2.0e-11
E value
Match length
                   103
                   18
% identity
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                   235986
                   uC-qsflmaxxa094e06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4204695
BLAST score
                   145
E value
                   4.0e-09
Match length
                   106
% identity
                   42
                   (AF117062) putative inositol polyphosphate 5-phosphatase
NCBI Description
                   At5P1 [Arabidopsis thaliana]
Seq. No.
                   235987
                   uC-gsflmaxxa094g07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4580395
                   179
BLAST score
                   1.0e-13
E value
                   51
Match length
                   80
% identity
```

(AC007171) putative kinesin-related protein [Arabidopsis

NCBI GI

BLAST score

g2642157

559



```
235988
Seq. No.
                  uC-gsflmaxxa094h06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4415923
BLAST score
                  429
                  2.0e-42
E value
Match length
                  145
% identity
                  59
                   (AC006282) putative glucosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                   235989
Seq. No.
Seq. ID
                  uC-qsflmaxxa095b06b1
Method
                  BLASTX
NCBI GI
                  g1200205
BLAST score
                  147
E value
                   6.0e-10
Match length
                  43
% identity
                   70
NCBI Description (X95753) DAG [Antirrhinum majus]
Seq. No.
                   235990
                  uC-gsflmaxxa095b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q168424
BLAST score
                   140
E value
                   5.0e-09
                   35
Match length
% identity
                   86
NCBI Description (M59449) polypeptide chain-binding protein [Zea mays]
                   235991
Seq. No.
                   uC-gsflmaxxa095d11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3335375
                   177
BLAST score
                   2.0e-13
E value
                   35
Match length
% identity
                   91
NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]
                   235992
Seq. No.
Seq. ID
                   uC-gsflmaxxa095f10b1
Method
                   BLASTX
                   g3643603
NCBI GI
BLAST score
                   187
E value
                   3.0e-14
Match length
                   65
% identity
NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]
                   235993
Seq. No.
Seq. ID
                   uC-gsflmaxxa095h12b1
Method
                   BLASTX
```



```
1.0e-57
E value
Match length
                  123
                  82
% identity
                  (AC003000) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
                  235994
Seq. No.
                  uC-gsflmaxxa096a08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2980791
                  554
BLAST score
E value
                  5.0e-57
                  121
Match length
% identity
                  86
                  (AL022197) actin depolymerizing factor - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  235995
Seq. No.
                  uC-gsflmaxxa096a12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4512683
                  402
BLAST score
                   3.0e-39
E value
Match length
                   96
                   77
% identity
NCBI Description
                  (AC006931) putative lipase [Arabidopsis thaliana]
                   >qi 4559323 gb AAD22985.1 AC007087 4 (AC007087) putative
                  lipase [Arabidopsis thaliana]
                   235996
Seq. No.
                   uC-gsflmaxxa096b04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1174469
BLAST score
                   173
                   2.0e-12
E value
Match length
                   51
% identity
                   61
                  OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5)
NCBI Description
                   (INTEGRAL MEMBRANE PROTEIN 1) >gi_624704 (L38961) putative
                   transmembrane protein precursor [\overline{H}omo\ sapiens]
                   >gi 1588286 prf 2208301B integral membrane protein [Homo
                   sapiens] >gi_4504787_ref_NP_002210.1_pITM1_ integral
                   transmembrane protein
                   235997
Seq. No.
                   uC-gsflmaxxa096c07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3047108
                   157
BLAST score
E value
                   2.0e-10
```

130 Match length

NCBI Description (AF058919) No definition line found [Arabidopsis thaliana]

235998 Seq. No. uC-gsflmaxxa096d10b1 Seq. ID

Method BLASTX NCBI GI g508304

% identity



```
BLAST score
                  1.0e-28
E value
Match length
                  69
                  83
% identity
NCBI Description (L22305) corC [Medicago sativa]
                  235999
Seq. No.
Seq. ID
                  uC-gsflmaxxa096d12b1
Method
                  BLASTX
NCBI GI
                  q2558660
BLAST score
                  369
E value
                  3.0e - 35
                  157
Match length
                   50
% identity
NCBI Description (AC002354) No definition line found [Arabidopsis thaliana]
                   236000
Seq. No.
                  uC-gsflmaxxa096e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3850999
                  334
BLAST score
E value
                   3.0e-31
                  91
Match length
                   75
% identity
                   (AF069908) pyruvate dehydrogenase El beta subunit isoform 1
NCBI Description
                   [Zea mays]
                   236001
Seq. No.
Seq. ID
                   uC-gsflmaxxa096e07b1
Method
                  BLASTX
                  g2760839
NCBI GI
                   226
BLAST score
E value
                   1.0e-18
                  73
Match length
% identity
NCBI Description (AC003105) putative receptor kinase [Arabidopsis thaliana]
                   236002
Seq. No.
Seq. ID
                   uC-gsflmaxxa096e11b1
                   BLASTX
Method
NCBI GI
                   q4567249
BLAST score
                   499
E value
                   2.0e-50
Match length
                   133
% identity
NCBI Description (AC007070) hypothetical protein [Arabidopsis thaliana]
                   236003
Seq. No.
Seq. ID
                   uC-gsflmaxxa096g10b1
Method
                   BLASTX
NCBI GI
                   g2388580
                   753
```

Method BLASTX
NCBI GI g2388580
BLAST score 753
E value 3.0e-80
Match length 155
% identity 89

NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002

(gb\_1253956). [Arabidopsis thaliana]



```
236004
Seq. No.
Seq. ID
                   uC-qsflmaxxa096h01b1
Method
                   BLASTX
NCBI GI
                   g2244799
BLAST score
                   196
E value
                   3.0e-15
Match length
                   98
% identity
NCBI Description
                  (Z97336) carnitine racemase homolog [Arabidopsis thaliana]
Seq. No.
                   236005
Seq. ID
                   uC-qsflmaxxa096h04b1
Method
                   BLASTX
NCBI GI
                   q1483177
BLAST score
                   324
E value
                   6.0e-30
Match length
                   141
% identity
                   45
NCBI Description
                  (D86598) antifreeze-like protein (af70) [Picea abies]
Seq. No.
                   236006
Seq. ID
                   uC-qsflmaxxa097b10b1
Method
                   BLASTX
NCBI GI
                   q4063751
BLAST score
                   323
E value
                   6.0e-30
Match length
                   138
% identity
                   54
NCBI Description
                   (AC005851) putative white protein [Arabidopsis thaliana]
                   >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
                  protein [Arabidopsis thaliana]
Seq. No.
                   236007
Seq. ID
                   uC-gsflmaxxa097b12b1
Method
                   BLASTX
NCBI GI
                   q2708745
BLAST score
                   544
E value
                   6.0e-56
Match length
                   120
% identity
                   86
NCBI Description
                   (AC003952) putative calcium-dependent ser/thr protein
                   kinase [Arabidopsis thaliana]
Seq. No.
                   236008
Seq. ID
                   uC-gsflmaxxa097c11b1
Method
                   BLASTX
NCBI GI
                   g1707032
```

Method BLASTX
NCBI GI g1707032
BLAST score 148
E value 1.0e-09
Match length 83
% identity 43

NCBI Description

(U80445) coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA

yk65h8



```
Seq. No.
                  236009
Seq. ID
                  uC-gsflmaxxa097d10b1
Method
                  BLASTX
NCBI GI
                  g136739
BLAST score ·
                  231
E value
                  2.0e-19
                  58
Match length
                  79
% identity
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi_218001 dbj_BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
                  236010
Seq. No.
Seq. ID
                  uC-gsflmaxxa097d11b1
Method
                  BLASTX
NCBI GI
                  g3212877
BLAST score
                  284
E value
                  1.0e-25
Match length
                  66
                  77
% identity
                 (AC004005) Lea-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  236011
Seq. ID
                  uC-gsflmaxxa097e02b1
Method
                  BLASTX
NCBI GI
                  q3582333
BLAST score
                  199
E value
                  2.0e-15
Match length
                  127
% identity
                 (AC005496) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  236012
Seq. ID
                  uC-gsflmaxxa097e09b1
Method
                  BLASTX
NCBI GI
                  g2109293
BLAST score
                  386
E value
                  2.0e-37
Match length
                  106
% identity
NCBI Description
                  (U97568) serine/threonine protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  236013
Seq. ID
                  uC-gsflmaxxa097f03b1
Method
                  BLASTX
NCBI GI
                  g123554
BLAST score
                  364
```

E value 7.0e-35
Match length 125

% identity 58

NCBI Description 18.1 KD CLASS I HEAT SHOCK PROTEIN >gi 99978 pir S16248

heat shock protein 18 (clone pMsHsp18.1) - alfalfa (fragment) >gi\_19616\_emb\_CAA41546\_ (X58710) heat shock



## protein [Medicago sativa]

```
Seq. No.
                  236014
Seq. ID
                  uC-gsflmaxxa097f09b1
Method
                  BLASTX
NCBI GI
                  g3880922
BLAST score
                  248
E value
                  3.0e-21
Match length
                  113
% identity
                  42
                  (Z99271) similar to zinc metallopeptidase (M8 family); cDNA
NCBI Description
                  EST EMBL:C07771 comes from this gene; cDNA EST EMBL:C09261
                  comes from this gene; cDNA EST yk259c1.5 comes from this
                  gene [Caenorhabditis elegans]
```

Seq. No. 236015 Seq. ID uC-gsflmaxxa097h06b1 Method BLASTX NCBI GI g3228517 BLAST score

429 · E value 2.0e-42 Match length 133 % identity 63

NCBI Description (AF007788) ETTIN [Arabidopsis thaliana]

Seq. No. 236016

Seq. ID uC-gsflmaxxa097h10b1

Method BLASTX NCBI GI g3850816 BLAST score 454 E value 2.0e-45 Match length 86 % identity 93

NCBI Description (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza

sativa]

Seq. No. 236017

Seq. ID uC-gsflmaxxa098b02b1

Method BLASTX NCBI GI g3763917 BLAST score 452 E value 6.0e-45 Match length 129 % identity 71

NCBI Description (AC004450) hypothetical protein [Arabidopsis thaliana]

>gi\_4531438\_gb AAD22123.1 AC006224 5 (AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236018

Seq. ID uC-gsflmaxxa098b06b1

Method BLASTX NCBI GI g1705491 BLAST score 144 E value 6.0e-09 Match length 119 % identity

NCBI Description (U50068) C01G5.8 gene product [Caenorhabditis elegans]

```
Seq. No.
                   236019
 Seq. ID
                   uC-gsflmaxxa098b11b1
 Method
                   BLASTX
 NCBI GI
                   g82306
 BLAST score
                   605
 E value
                   7.0e-63
Match length
                   127
 % identity
                   87
NCBI Description myb protein 305 - garden snapdragon
 Seq. No.
                   236020
Seq. ID
                   uC-gsflmaxxa098b12b1
Method
                   BLASTX
NCBI GI
                   g4538926
BLAST score
                   276
E value
                   2.0e-24
Match length
                   94
% identity
                   56
NCBI Description (AL049483) putative phosphatidylserine decarboxylase
                   [Arabidopsis thaliana]
Seq. No.
                   236021
Seq. ID
                   uC-gsflmaxxa098c07b1
Method
                  BLASTX
NCBI GI
                   g2511693
BLAST score
                  270
E value
                   1.0e-23
Match length
                  71
% identity
                  73
NCBI Description (Z99954) cysteine proteinase precursor [Phaseolus vulgaris]
                   236022
Seq. No.
Seq. ID
                  uC-gsflmaxxa098c11b1
Method
                  BLASTX
NCBI GI
                  g120672
BLAST score
                  722
E value
                  1.0e-76
Match length
                  162
% identity
                  87
NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_66016_pir__DEPZG glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) - parsley
                  >gi_20549_emb_CAA42902 (X60344) glyceraldehyde 3-phosphate
                  dehydrogenase [Petroselinum crispum]
Seq. No.
                  236023
Seq. ID
                  uC-gsflmaxxa098d04b1
Method
                  BLASTX
NCBI GI
                  g1168537
BLAST score
                  338
E value
                  1.0e-31
Match length
                  132
% identity
                  51
NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
                  aspartic proteinase (EC 3.4.23.-) - rice
```

>gi\_218143\_dbj\_BAA02242\_ (D12777)..aspartic proteinase

Method

NCBI GI

BLASTX

q2342684



## [Oryza sativa]

```
Seq. No.
                  236024
Seq. ID
                  uC-gsflmaxxa098d11b1
Method
                  BLASTX
NCBI GI
                  g4544384
BLAST score
                  357
E value
                  8.0e-34
Match length
                  89
% identity
                  83
NCBI Description (AC007047) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236025
Seq. ID
                  uC-gsflmaxxa098f04b1
Method
                  BLASTX
NCBI GI
                  g4455199
BLAST score
                  206
E value
                  4.0e-16
Match length
                  129
% identity
                  39
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  236026
Seq. ID
                  uC-gsflmaxxa098g11b1
Method
                  BLASTX
NCBI GI
                  q4406767
BLAST score
                  362
E value
                  2.0e-34
Match length
                  153
% identity
                  49
                 (AC006836) putative flavonol sulfotransferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  236027
Seq. ID
                  uC-gsflmaxxa098h05b1
                  BLASTX
Method
NCBI GI
                  g2984147
BLAST score
                  172
E value
                  2.0e-12
Match length
                  90
% identity
                  41
NCBI Description (AE000760) hypothetical protein [Aquifex aeolicus]
Seq. No.
                  236028
Seq. ID
                  uC-gsflmaxxa098h09b1
Method
                  BLASTX
NCBI GI
                  g3201618
BLAST score
                  588
E value
                  7.0e-61
Match length
                  128
% identity
NCBI Description (AC004669) Sop2p-like protein [Arabidopsis thaliana]
Seq. No.
                  236029
Seq. ID
                  uC-gsflmaxxa098h11b1
```

NCBI GI

BLAST score

```
BLAST score
                   260
E value
                   1.0e-22
Match length
                   118
% identity
                   47
NCBI Description (AC000106) F7G19.14 [Arabidopsis thaliana]
Seq. No.
                   236030
Seq. ID
                   uC-gsflmaxxa098h12b1
Method
                   BLASTX
NCBI GI
                   g2507229
BLAST score
                   518
E value
                   9.0e-53
Match length
                   133
                   74
% identity
NCBI Description 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)
                   (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED
                   PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN)
                   >gi_423247_pir A46579 estrogen receptor-binding
                   cyclophilin - bovine >gi_393300 dbj BAA03159 (D14074)
                   cyclophilin [Bos taurus]
Seq. No.
                   236031
Seq. ID
                  uC-gsflmaxxa106c02b1
Method
                  BLASTX
NCBI GI
                   g4325341
BLAST score
                   216
E value
                   9.0e-18
Match length
                  53
% identity
                   79
NCBI Description
                  (AF128393) similar to the Drosophila DES-1 protein
                   (GB:X94180) [Arabidopsis thaliana]
Seq. No.
                  236032
Seq. ID
                  uC-gsflmaxxa107a01b1
Method
                  BLASTX
NCBI GI
                  g4049341
BLAST score
                  386
E value
                  2.0e-37
Match length
                  87
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
Seq. No.
                  236033
Seq. ID
                  uC-gsflmaxxa107a07b1
Method
                  BLASTX
NCBI GI
                  g3335375
BLAST score
                  278
E value
                  3.0e-25
Match length
                  61
% identity
                  85
NCBI Description (AC003028) putative amidase [Arabidopsis thaliana]
Seq. No.
                  236034
Seq. ID
                  uC-gsflmaxxa107b12b1
Method
                  BLASTX
```

34198

g3694872

394



```
E value
                  1.0e-38
Match length
                  89
% identity
                  83
NCBI Description
                  (AF092547) profilin [Ricinus communis]
Seq. No.
                  236035
Seq. ID
                  uC-gsflmaxxa107h12b1
Method
                  BLASTX
NCBI GI
                  g2088658
BLAST score
                  273
E value
                  4.0e-24
Match length
                  104
% identity
                  55
NCBI Description
                  (AF002109) unknown protein [Arabidopsis thaliana]
```

Seq. No. 236036

Seq. ID uC-gsflmaxxa119a04b1

Method BLASTX NCBI GI g3746059 BLAST score 407 E value 7.0e-40Match length 103 % identity 73

(AC005311) putative cysteinyl-tRNA synthetase [Arabidopsis NCBI Description

thaliana] >gi\_4432812\_gb\_AAD20662\_ (AC006593) putative

cysteinyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No. 236037

Seq. ID uC-gsflmaxxa119a09b1

Method BLASTX NCBI GI g125887 BLAST score 224 E value 1.0e-18 Match length 78 % identity 59

NCBI Description ANTHER SPECIFIC LAT52 PROTEIN PRECURSOR

> >gi\_82092 pir S04765 LAT52 protein precursor - tomato >gi 295812 emb CAA33854 (X15855) LAT52 [Lycopersicon

esculentum]

Seq. No. 236038

Seq. ID uC-gsflmaxxa119a11b1

Method BLASTX NCBI GI g1946371 BLAST score 158 E value 3.0e-11 Match length 37 % identity 76

NCBI Description (U93215) regulatory protein Viviparous-1 isolog

[Arabidopsis thaliana]

Seq. No. 236039

Seq. ID uC-gsflmaxxa119c01b1

Method BLASTX NCBI GI g1916292 BLAST score 198 E value 3.0e-15

Match length

% identity

76



```
Match length
                  93
                  39
% identity
                  (U89793) allergen Amb a VI [Ambrosia artemisiifolia]
NCBI Description
                  236040
Seq. No.
Seq. ID
                  uC-gsflmaxxa119c02b1
Method
                  BLASTX
NCBI GI
                  g1076511
BLAST score
                  145
E value
                  1.0e-09
                  31
Match length
                  90
% identity
                  H+-transporting ATPase (EC 3.6.1.35) - kidney bean
NCBI Description
                  >gi 758250 emb CAA59799 (X85804) H(+)-transporting ATPase
                  [Phaseolus vulgaris]
                  236041
Seq. No.
Seq. ID
                  uC-qsflmaxxa119c07b1
                  BLASTX
Method
NCBI GI
                  g1916292
BLAST score
                  157
                  1.0e-10
E value
                  65
Match length
                  42
% identity
NCBI Description (U89793) allergen Amb a VI [Ambrosia artemisiifolia]
Seq. No.
                  236042
Seq. ID
                  uC-gsflnu33B001a01b1
Method
                  BLASTX
NCBI GI
                  g2244898
BLAST score
                  364
E value
                  1.0e-34
                  150
Match length
                  46
% identity
NCBI Description
                  (Z97338) strong similarity to protein phosphatase 2A
                  regulatory chain, 74K [Arabidopsis thaliana]
                  236043
Seq. No.
Seq. ID
                  uC-gsflnu33B001b03b1
Method
                  BLASTX
NCBI GI
                  q2739168
BLAST score
                  179
E value
                   6.0e-16
Match length
                  87
% identity
                  56
                  (AF032386) aldose-1-epimerase-like protein [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  236044
                  uC-gsflnu33B001b05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1330401
BLAST score
                  133
E value
                  1.0e-08
```

34200

NCBI Description (U58762) T27F7.1 gene product [Caenorhabditis elegans]

```
Seq. No.
                   236045
Seq. ID
                   uC-gsflnu33B001b09b1
Method
                   BLASTX
NCBI GI
                   g3600052
BLAST score
                   275
E value
                   2.0e-24
Match length
                   94
% identity
                   56
NCBI Description
                   (AF080120) contains similarity to glycosyl hydrolases
                   family 9 (Pfam: glycosyl_hydro5.hmm, score: 88.03)
                   [Arabidopsis thaliana]
Seq. No.
                   236046
Seq. ID
                   uC-qsflnu33B001b11b1
Method
                   BLASTX
NCBI GI
                   g4322421
BLAST score
                   233
E value
                   2.0e-19
Match length
                   133
% identity
                   41
                  (AF085230) cadmium resistance factor 1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   236047
Seq. ID
                   uC-gsflnu33B001c09b1
Method
                   BLASTX
NCBI GI
                   g1184075
BLAST score
                   153
E value
                   5.0e-10
Match length
                   140
% identity
NCBI Description
                  (U42444) Cf-2.1 [Lycopersicon pimpinellifolium]
                   >gi_1587673_prf__2207203A Cf-2 gene [Lycopersicon
                   esculentum]
Seq. No.
                   236048
Seq. ID
                   uC-gsflnu33B001d05b1
Method
                  BLASTX
NCBI GI
                   g2982268
BLAST score
                   472
E value
                   2.0e-47
Match length
                   93
% identity
NCBI Description
                  (AF051217) probable 40S ribosomal protein S15 [Picea
                  mariana]
Seq. No.
                  236049
Seq. ID
                  uC-gsflnu33B001e09b1
Method
                  BLASTX
NCBI GI
                  g1816459
BLAST score
                  531
E value
                  3.0e-54
Match length
                  133 .
% identity
NCBI Description
                  (Y10750) DEFH125 protein [Antirrhinum majus]
```



```
236050
Seq. No.
                  uC-gsflnu33B001e11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4263787
BLAST score
                  548
                  3.0e-56
E value
                  145
Match length
                  77
% identity
                  (AC006068) unknown protein [Arabidopsis thaliana]
NCBI Description
                  236051
Seq. No.
                  uC-gsflnu33B001f04b1
Seq. ID
Method
                  BLASTX
                   q2739010
NCBI GI
BLAST score
                   551
                   1.0e-56
E value
                   146
Match length
                   68
% identity
                  (AF022464) CYP77A3p [Glycine max]
NCBI Description
                   236052
Seq. No.
                   uC-gsflnu33B001g10b1
Seq. ID
                   BLASTX
Method
                   g1352078
NCBI GI
BLAST score
                   535
                   9.0e-55
E value
Match length
                   105
                   84
% identity
                  BETA-GALACTOSIDASE PRECURSOR (LACTASE)
NCBI Description
                   (EXO-(1-->4)-BETA-D-GALACTANASE) >gi_507278 (L29451)
                   b-galactosidase-related protein; putative [Malus domestica]
                   236053
Seq. No.
                   uC-gsflnu33B002a11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4406770
BLAST score
                   335
                   1.0e-31
E value
                   93
Match length
                   71
% identity
NCBI Description (AC006836) unknown protein [Arabidopsis thaliana]
                   236054
Seq. No.
                   uC-qsflnu33B002e11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2109293
BLAST score
                   258
E value
                   2.0e-22
Match length
                   60
                   83
% identity
                   (U97568) serine/threonine protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   236055
Seq. No.
                   uC-gsflnu33B002f04b1
Seq. ID
```

BLASTX

g2501102

Method NCBI GI



BLAST score 236 E value 5.0e-34 Match length 93 % identity 82

NCBI Description SYNTAXIN-RELATED PROTEIN KNOLLE >gi\_1184165 (U39451) syntaxin-related [Arabidopsis thaliana] >gi\_1184167

(U39452) syntaxin-related [Arabidopsis thaliana] >gi\_3063443 (AC003981) F22013.4 [Arabidopsis thaliana]

>gi 1587182 prf 2206310A syntaxin-related protein

[Arabidopsis thaliana]

Seq. No. 236056

Seq. ID uC-gsflnu33B002f12b1

Method BLASTX
NCBI GI 94469025
BLAST score 179
E value 1.0e-13
Match length 61
% identity 37

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 236057

Seq. ID uC-gsflnu33B003a02b1

Method BLASTX
NCBI GI g4220480
BLAST score 167
E value 1.0e-11
Match length 97
% identity 36

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 236058

Seq. ID uC-gsflnu33B003a09b1

Method BLASTX
NCBI GI g2440044
BLAST score 533
E value 1.0e-54
Match length 111

Match length 111 % identity 89

NCBI Description (AJ001293) major intrinsic protein PIPB [Craterostigma

plantagineum]

Seq. No. 236059

Seq. ID uC-gsflnu33B003b06b1

Method BLASTX
NCBI GI g3172025
BLAST score 364
E value 6.0e-35
Match length 106
% identity 67

NCBI Description (AB005805) aldehyde oxidase [Arabidopsis thaliana]

Seq. No. 236060

Seq. ID uC-gsflnu33B003d04b1

Method BLASTX
NCBI GI g2960358
BLAST score 209



6.0e-17 E value Match length 40 97 % identity

(AJ224895) caffeoyl-CoA 3-O-methyltransferase [Populus NCBI Description balsamifera subsp. trichocarpa] >gi 2960360 emb CAA12200

(AJ224896) caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa] >gi\_3550590\_emb\_CAA11495\_ (AJ223620) caffeoyl CoA 3-O-methyltransferase [Populus

balsamifera subsp. trichocarpa]

236061 Seq. No.

Seq. ID uC-gsflnu33B003d09b1

BLASTX Method NCBI GI q3915037 279 BLAST score 3.0e-25 E value 57 Match length 91 % identity

SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) NCBI Description

>gi 2570067 emb CAA04512 (AJ001071) second sucrose

synthase [Pisum sativum]

236062 Seq. No.

uC-gsflnu33B004b04b1 Seq. ID

Method BLASTX NCBI GI q4314363 BLAST score 392 4.0e-38 E value Match length 129 % identity 58

NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.

Seq. ID uC-gsflnu33B004b06b1

236063

 ${\tt BLASTX}$ Method NCBI GI g3811293 BLAST score 213 5.0e-22 E value Match length 68 % identity 84

(AF032465) putative serine/threonine protein kinase NCBI Description

[Nicotiana tabacum] >gi\_4098172 (U73938) PK11-C1 [Nicotiana

tabacum]

Seq. No. 236064

uC-gsflnu33B004c02b1 Seq. ID

BLASTX Method NCBI GI g3193290 BLAST score 341 E value 3.0e-32 114 Match length 56 % identity

NCBI Description (AF069298) contains similarity to a protein kinase domain

(Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin\_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin legA.hmm, score: 16.72)

[Arabido



```
Seq. No.
                   236065
Seq. ID
                   uC-gsflnu33B004c05b1
Method
                   BLASTX
NCBI GI
                   q4467145
BLAST score
                   316
E value
                   4.0e-29
Match length
                   109
% identity
                   56
NCBI Description
                   (AL035540) farnesylated protein (ATFP6) [Arabidopsis
                   thaliana]
                   236066
Seq. No.
Seq. ID
                   uC-gsflnu33B004e02b1
Method
                   BLASTX
NCBI GI
                   q4557058
BLAST score
                   339
E value
                   4.0e-32
Match length
                   92
% identity
                   66
NCBI Description
                  (AC007154) aldehyde oxidase [Arabidopsis thaliana]
Seq. No.
                   236067
Seq. ID
                   uC-gsflnu33B004f03b1
Method
                   BLASTX
NCBI GI
                   q4263715
BLAST score
                   230
                   3.0e-22
E value
Match length
                   126
                   49
% identity
NCBI Description
                  (AC006223) putative alanine acetyl transferase [Arabidopsis
                   thaliana]
Seq. No.
                   236068
Seq. ID
                   uC-gsflnu33B004g04b1
Method
                   BLASTX
NCBI GI
                   g2462834
BLAST score
                   167
E value
                   8.0e-14
Match length
                   96
% identity
                   48
NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   236069
Seq. ID
                   uC-gsflnu33B004g07b1
Method
                   BLASTX
NCBI GI
                   g4454467
BLAST score
                   188
E value
                   4.0e-14
Match length
                   113
                   42
% identity
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                   236070
```

uC-gsflnu33B004h03b1

Method BLASTX NCBI GI g1922964

Seq. ID



```
BLAST score
                  417
                  6.0e-41
E value
Match length
                  89
% identity
                  (ACO00106) Similar to Schizosaccharomyces CCAAT-binding
NCBI Description
                  factor (gb_U88525). EST gb_T04310 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  236071
                  uC-gsflnu33B004h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2689720
BLAST score
                  432
                  2.0e-57
E value
Match length
                  159
                  73
% identity
NCBI Description (AF037168) DnaJ homologue [Arabidopsis thaliana]
                  236072
Seq. No.
                  uC-gsflnu33B005b12b1
Seq. ID
                  BLASTX
Method
                  q2245061
NCBI GI
BLAST score
                   307
E value
                   4.0e-28
                   68
Match length
% identity
                   87
NCBI Description (Z97342) Clp proteinase homolog [Arabidopsis thaliana]
                   236073
Seq. No.
Seq. ID
                  uC-gsflnu33B005d02b1
Method
                  BLASTX
NCBI GI
                   g3757521
BLAST score
                   470
E value
                   3.0e-47
Match length
                   132
% identity
                   64
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
                   236074
Seq. No.
Seq. ID
                   uC-gsflnu33B005d03b1
Method
                   BLASTX
NCBI GI
                   g1703446
                   497
BLAST score
                   2.0e-50
E value
                   130
Match length
% identity
                   78
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
                   >gi 1076292 pir S53127 asparaginase - Arabidopsis thaliana
                   >gi 735918 emb CAA84367 (Z34884) asparaginase [Arabidopsis
                   thaliana]
```

Seq. No. 236075

Seq. ID uC-gsflnu33B005d08b1

Method BLASTX
NCBI GI g3894393
BLAST score 185
E value 7.0e-14



59

% identity

```
Match length
% identity
NCBI Description
                  (AF053998) Hcr2-5D [Lycopersicon esculentum]
                  236076
Seq. No.
Seq. ID
                  uC-gsflnu33B005e03b1
Method
                  BLASTX
NCBI GI
                  q2252631
BLAST score
                  197
E value
                   3.0e-15
Match length
                  80
                  49
% identity
                  (U95973) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  236077
Seq. ID
                  uC-qsflnu33B005f03b1
Method
                  BLASTX
NCBI GI
                  q3063694
BLAST score
                  143
E value
                   7.0e-09
Match length
                  121
                   39
% identity
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
                  236078
Seq. No.
Seq. ID
                  uC-gsflnu33B005g01b1
Method
                  BLASTX
NCBI GI
                  q2507426
BLAST score
                  511
E value
                   4.0e-52
Match length
                  129
% identity
                   74
NCBI Description ALANYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR
                   (ALANINE--TRNA LIGASE) (ALARS) >gi_1673365_emb_CAA80380_
                   (Z22673) mitochondrial tRNA-Ala synthetase [Arabidopsis
                   thaliana]
                  236079
Seq. No.
Seq. ID
                  uC-gsflnu33B005g03b1
Method
                  BLASTX
NCBI GI
                  g2586123
BLAST score
                  343
E value
                   3.0e-32
Match length
                  102
% identity
                  60
NCBI Description
                 (U89511) b-keto acyl reductase [Allium porrum]
                  236080
Seq. No.
Seq. ID
                  uC-gsflnu33B005g10b1
Method
                  BLASTX
NCBI GI
                  g2129854
BLAST score
                  318
E value
                  1.0e-37
Match length
                  137
```

34207

NCBI Description early nodulin 8 precursor - alfalfa >gi\_304037 (L18899)

early nodulin [Medicago sativa]

Seq. No.



```
Seq. No.
                    236081
 Seq. ID
                    uC-gsflnu33B005h08b1
 Method
                    BLASTX
 NCBI GI
                    g3319882
 BLAST score
                    440
                    7.0e-44
 E value
 Match length
                    98
 % identity
                    87
                   (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
 NCBI Description
                    arietinum
 Seq. No.
                    236082
 Seq. ID
                    uC-qsflnu33B005h10b1
 Method
                    BLASTX
 NCBI GI
                    g1938227
 BLAST score
                    457
 E value
                    1.0e-45
 Match length
                    157
 % identity
                    58
NCBI Description (X93312) Carbonic anhydrase [Medicago sativa]
                    236083
 Seq. No.
 Seq. ID
                    uC-gsflnu33B005h12b1
 Method
                    BLASTX
 NCBI GI
                    g100347
 BLAST score
                    160
E value
                    2.0e-11
 Match length
                    36
 % identity
                    86
 NCBI Description
                    monosaccharide transport protein MST1 - common tobacco
                    >gi_19885_emb_CAA47324_ (X66856) monosaccharid transporter
                    [Nicotiana tabacum]
 Seq. No.
                    236084
 Seq. ID
                    uC-qsflnu33B006b09b1
 Method
                    BLASTX
 NCBI GI
                    g2130149
 BLAST score
                    425
 E value
                    4.0e-42
 Match length
                    90
                    90
 % identity
 NCBI Description translation elongation factor eEF-1 alpha chain - maize
                    (fragment)
                    236085
 Seq. No.
 Seq. ID
                    uC-gsflnu33B006b12b1
 Method
                    BLASTX
 NCBI GI
                    g4262167
 BLAST score
                    193
 E value
                    7.0e-24
 Match length
                    101
                    62
 % identity
 NCBI Description
                   (AC005275) putative LRR receptor-linked protein kinase
```

34208

[Arabidopsis thaliana]

236086

Seq. No.

236091



```
Seq. ID
                   uC-gsflnu33B006c02b1
Method
                   BLASTX
NCBI GI
                   g2961343
BLAST score
                   201
                   1.0e-15
E value
Match length
                   40
                   95
% identity
                   (AL022140) symbiosis-related like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   236087
                   uC-gsflnu33B006d02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4490305
BLAST score
                   407
                   9.0e-40
E value
Match length
                   147
% identity
                   54
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   236088
Seq. No.
                   uC-gsflnu33B006f04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120669
BLAST score
                   252
E value
                   8.0e-22
Match length
                   59
                   78
% identity
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                   236089
Seq. ID
                   uC-gsflnu33B006f06b1
Method
                   BLASTX
NCBI GI
                   g1076257
BLAST score
                   178
E value
                   1.0e-13
Match length
                   31
                   97
% identity
                   sucrose-proton symporter - beet >gi 633172 emb CAA58730_
NCBI Description
                   (X83850) sucrose/proton-symporter [Beta vulgaris]
Seq. No.
                   236090
Seq. ID
                   uC-gsflnu33B006g07b1
                   BLASTX
Method
NCBI GI
                   q2961390
BLAST score
                   347
E value
                   7.0e-33
                   84
Match length
                   74
% identity
                   (AL022141) beta-galactosidase like protein [Arabidopsis
NCBI Description
                   thaliana]
```



uC-gsflnu33B006g12b1 Seq. ID Method BLASTX g4115937 NCBI GI BLAST score 301 E value 7.0e-39 Match length 101 % identity 75 (AF118223) contains similarity to human PCF11p homolog NCBI Description (GB:AF046935) [Arabidopsis thaliana] 236092 Seq. No. Seq. ID uC-gsflnu33B006h10b1 Method BLASTX NCBI GI g2983537 BLAST score 147 E value 2.0e-09 Match length 55 % identity 53 NCBI Description (AE000720) phosphate transport ATP binding protein [Aquifex aeolicus] 236093 Seq. No. Seq. ID uC-gsflnu33B006h11b1 Method BLASTX NCBI GI g2583112 BLAST score 153 1.0e-10 E value Match length 42 % identity 67 NCBI Description (AC002387) putative PD1-like DNA-binding protein [Arabidopsis thaliana] Seq. No. 236094 Seq. ID uC-gsflnu33B008a04b1 Method BLASTX NCBI GI q4539401 BLAST score 289 E value 7.0e-26 Match length 109 % identity 61 NCBI Description (AL035526) putative protein [Arabidopsis thaliana] Seq. No. 236095 Seq. ID uC-gsflnu33B008b01b1 Method BLASTX NCBI GI g1706794 BLAST score 361 E value 3.0e - 34Match length 121 % identity 55 NCBI Description BIS(5'-ADENOSYL)-TRIPHOSPHATASE (DIADENOSINE 5',5'''-P1,P3-TRIPHOSPHATE HYDROLASE)

(DINUCLEOSIDETRIPHOSPHATASE) (AP3A HYDROLASE) (AP3AASE) (FRAGILE HISTIDINE TRIAD PROTEIN) >gi\_3114520\_pdb\_4FIT\_Fhit-Apo >gi\_3114524\_pdb\_6FIT\_Fhit-Transition State Analog >gi\_3318895\_pdb\_1FHI\_Substrate Analog (Ib2) Complex With The Fragile Histidine Triad Protein, Fhit



>gi\_1203836 (U46922) member of the histidine triad (HIT) gene family; similar to the S. pombe diadenosine 5',5'''-P1,P4-tetraphosphate asymmetrical hydrolase [Homo sapiens] >gi\_1945066 (U76272) diadenosine triphosphate (Ap3A) hydrolase [Homo sapiens] >gi\_4503719\_ref\_NP\_002003.1\_pFHIT\_ fragile histidine triad gene

Seq. No. 236096

Seq. ID uC-gsflnu33B008b07b1

Method BLASTX
NCBI GI g4160532
BLAST score 236
E value 7.0e-20
Match length 116
% identity 39

NCBI Description (AJ011304) sphingosine-1-phosphate lyase [Homo sapiens]

Seq. No. 236097

Seq. ID uC-gsflnu33B008b12b1

Method BLASTX
NCBI GI g1914685
BLAST score 283
E value 2.0e-25
Match length 113
% identity 54

NCBI Description (Y12014) RAD23 protein, isoform II [Daucus carota]

Seq. No. 236098

Seq. ID uC-gsflnu33B008c06b1

Method BLASTX
NCBI GI g3892059
BLAST score 276
E value 1.0e-24
Match length 99
% identity 17

NCBI Description (AC002330) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 236099

Seq. ID uC-gsflnu33B008c10b1

Method BLASTX
NCBI GI 94539373
BLAST score 142
E value 7.0e-09
Match length 84
% identity 38

NCBI Description (AL049525) putative retrotransposon polyprotein

[Arabidopsis thaliana]

Seq. No. 236100

Seq. ID uC-gsflnu33B008d11b1

Method BLASTX
NCBI GI g2342735
BLAST score 225
E value 9.0e-19
Match length 48



% identity NCBI Description (AC002341) unknown protein [Arabidopsis thaliana] Seq. No. 236101 Seq. ID uC-gsflnu33B008e09b1 Method BLASTX NCBI GI g2982309 BLAST score 167 E value 1.0e-23 Match length 98 % identity 50 (AF051239) probable ubiquitin activating enzyme 2 [Picea NCBI Description mariana] Seq. No. 236102 uC-gsflnu33B008f06b1 Seq. ID Method BLASTX NCBI GI g3420239 BLAST score 261 E value 3.0e-23Match length 49 100 % identity NCBI Description (AF059484) actin [Gossypium hirsutum] Seq. No. 236103 Seq. ID uC-qsflnu33B008f12b1 Method BLASTX NCBI GI q1174448 BLAST score 162 E value 4.0e-1175 Match length 49 % identity TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR NCBI Description (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi 547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana] 236104 Seq. No. Seq. ID uC-qsflnu33B008q12b1 Method BLASTX NCBI GI g4185143 BLAST score 246 E value 3.0e-21 72 Match length % identity 64 (AC005724) putative signal recognition particle receptor NCBI Description beta subunit [Arabidopsis thaliana] 236105 Seq. No. uC-gsflnu33B008h05b1 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g967125
BLAST score 444
E value 2.0e-44
Match length 91
% identity 95

NCBI Description (U08140) calcium dependent protein kinase [Vigna radiata]



```
Seq. No.
                  236106
Seq. ID
                  uC-qsflnu33B009a04b1
Method
                  BLASTX
NCBI GI
                  g2738949
BLAST score
                  406
                  2.0e-43
E value
Match length
                  98
% identity
                  90
NCBI Description
                  (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                  ananassa]
                  236107
Seq. No.
                  uC-qsflnu33B009b12b1
Seq. ID
Method
                  BLASTX
                  g2708741
NCBI GI
BLAST score
                  764
                  1.0e-81
E value
Match length
                  162
% identity
                  90
NCBI Description (AC003952) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  236108
Seq. ID
                  uC-gsflnu33B009c11b1
Method
                  BLASTX
NCBI GI
                  q2921334
BLAST score
                  374
E value
                  4.0e-36
                  70
Match length
% identity
                  97
NCBI Description (AF034131) MYB-like DNA-binding domain protein [Gossypium
                  hirsutum]
                  236109
Seq. No.
Seq. ID
                  uC-gsflnu33B009e01b1
Method
                  BLASTX
NCBI GI
                  g1518388
BLAST score
                  246
E value
                  5.0e-21
Match length
                  103
                  50
% identity
NCBI Description (X91172) korean-radish isoperoxidase [Raphanus sativus]
                  236110
Seq. No.
Seq. ID
                  uC-gsflnu33B009g01b1
Method
                  BLASTX
NCBI GI
                  q4249384
BLAST score
                  394
E value
                  2.0e-38
Match length
                  107
                   65
% identity
                  (AC005966) Similar to gi 4056506 F3G5.25 nodulin-like
NCBI Description
                  protein from Arabidopsis thaliana BAC gb AC005896.
                  [Arabidopsis thaliana]
```

Seq. No. 236111

Seq. ID uC-gsflnu33B009h09b1

Match length

% identity

56

71



```
Method
                  BLASTX
NCBI GI
                  g3335359
BLAST score
                  488
                  3.0e-49
E value
                  106
Match length
                  87
% identity
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236112
Seq. ID
                  uC-gsflnu33B009h11b1
                  BLASTX
Method
NCBI GI
                  g4432840
BLAST score
                  173
                  2.0e-12
E value
                  95
Match length
                  42
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236113
Seq. ID
                  uC-gsflnu33B011a02b1
Method
                  BLASTX
NCBI GI
                  g3080417
BLAST score
                  346
E value
                  9.0e-33
                  89
Match length
                  83
% identity
NCBI Description (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                  236114
Seq. ID
                  uC-gsflnu33B011b05b1
Method
                  BLASTX
NCBI GI
                  g2529670
BLAST score
                  236
E value
                  8.0e-20
                  79
Match length
% identity
                  61
NCBI Description (AC002535) ribosomal protein L18-like [Arabidopsis
                  thaliana]
                  236115
Seq. No.
Seq. ID
                  uC-gsflnu33B011d04b1
Method
                  BLASTX
NCBI GI
                  q3220021
BLAST score
                  224
                  3.0e-23
E value
                  125
Match length
% identity
                  46
NCBI Description (U57828) lipase homolog [Arabidopsis thaliana]
                  236116
Seq. No.
                  uC-gsflnu33B011d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4105633
BLAST score
                  204
E value
                  6.0e-16
```



```
(AF048982) putative ethylene receptor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  236117
                  uC-gsflnu33B011d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2842490
BLAST score
                  347
E value
                  8.0e-33
Match length
                  112
% identity
                  59
NCBI Description
                 (AL021749) heat-shock protein [Arabidopsis thaliana]
                  236118
Seq. No.
Seq. ID
                  uC-qsflnu33B011d12b1
Method
                  BLASTX
NCBI GI
                  q485514
BLAST score
                  389
E value
                  1.0e-37
Match length
                  79
                  91
% identity
NCBI Description
                  ADR11-2 protein - soybean (fragment)
                  >gi_296443_emb_CAA49341_ (X69640) auxin down regulated
                  [Glycine max]
Seq. No.
                  236119
Seq. ID
                  uC-qsflnu33B011e01b1
Method
                  BLASTX
NCBI GI
                  g3643611
BLAST score
                  573
E value
                  2.0e-59
Match length
                  122
% identity
                  83
NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]
Seq. No.
                  236120
Seq. ID
                  uC-gsflnu33B011e02b1
                  BLASTX
Method
NCBI GI
                  q3063465
BLAST score
                  164
E value
                  2.0e-23
Match length
                  88
% identity
                   68
NCBI Description (AC003981) F22013.27 [Arabidopsis thaliana]
Seq. No.
                  236121
Seq. ID
                  uC-gsflnu33B011e09b1
Method
                  BLASTX
NCBI GI
                  q3540195
BLAST score
                  396
```

Method BLASTX
NCBI GI g3540195
BLAST score 396
E value 1.0e-38
Match length 126
% identity 28

NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No. 236122

Seq. ID uC-gsflnu33B011g06b1



```
Method
                   BLASTX
NCBI GI
                   g1717744
BLAST score
                   222
E value
                   5.0e-18
Match length
                   108
% identity
                   42
NCBI Description
```

TOPOISOMERASE 1-RELATED PROTEIN TRF4

>gi\_1077298\_pir\_\_S51882 topoisomerase I-related protein

TRF4 - yeast (Saccharomyces cerevisiae)

>gi\_663237\_emb\_CAA88145\_ (Z48149) ORF [Saccharomyces cerevisiae] >gi\_950226 (U31355) Trf4p [Saccharomyces

cerevisiae] >gi\_1419987\_emb\_CAA99134\_ (Z74857) ORF YOL115w

[Saccharomyces cerevisiae]

Seq. No. Seq. ID uC-gsflnu33B011g09b1 Method BLASTX NCBI GI g2213600 BLAST score 161 E value 2.0e-11 Match length 80

46 % identity

NCBI Description (AC000348) T7N9.20 [Arabidopsis thaliana]

236124 Seq. No.

Seq. ID uC-qsflnu33B011h06b1

236123

Method BLASTX NCBI GI q3953470 BLAST score 149 E value 1.0e-09 Match length 80 % identity 49

NCBI Description (AC002328) F20N2.15 [Arabidopsis thaliana]

Seq. No. 236125

Seq. ID uC-gsflnu33B012c08b1

Method BLASTX NCBI GI g3832528 BLAST score 524 E value 1.0e-53 Match length 126 % identity 81

NCBI Description (AF100167) unknown [Glycine max]

Seq. No. 236126

Seq. ID uC-gsflnu33B012d01b1

Method BLASTX NCBI GI q3287693 BLAST score 434 E value 5.0e-43Match length 90 89 % identity

(AC003979) Similar to LIM17 gene product gb 1653769 from NCBI Description

the genome of Synechocystis sp. gb\_D90916. [Arabidopsis

thaliana]

Seq. No. 236127



uC-gsflnu33B012e08b1 Seq. ID Method BLASTX NCBI GI q2062170 BLAST score 272 E value 5.0e-24Match length 136 % identity 52 NCBI Description (AC001645) unknown protein [Arabidopsis thaliana] 236128 Seq. No. Seq. ID uC-gsflnu33B012g08b1 Method BLASTX NCBI GI q2244847 BLAST score 246 E value 5.0e-21 Match length 105 54 % identity NCBI Description (Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana] Seq. No. 236129 Seq. ID uC-gsflnu33B013a03b1 Method BLASTX NCBI GI q3647283 BLAST score 554 E value 5.0e-57 Match length 144 74 % identity NCBI Description (AJ011418) ubiquitin activating enzyme [Lycopersicon esculentum] Seq. No. 236130 Seq. ID uC-gsflnu33B013a06b1 Method BLASTX NCBI GI g1587206 BLAST score 363 E value 8.0e-56 Match length 148 80 % identity T complex protein [Cucumis sativus] NCBI Description Seq. No. 236131 Seq. ID uC-gsflnu33B013a07b1 Method BLASTX NCBI GI g4115377 BLAST score 196 E value 4.0e-15 Match length 94 % identity 43 (AC005967) unknown protein [Arabidopsis thaliana] NCBI Description

236132 Seq. No.

Seq. ID uC-gsflnu33B013a10b1

BLASTXMethod NCBI GI g2213626 BLAST score 239 E value 5.0e-20



Match length 120 % identity 42

NCBI Description (AC000103) F21J9.18 [Arabidopsis thaliana]

Seq. No. 236133

Seq. ID uC-gsflnu33B013b10b1

Method BLASTX
NCBI GI g2244759
BLAST score 542
E value 1.0e-55
Match length 137
% identity 72

NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No. 236134

Seq. ID uC-gsflnu33B013b11b1

Method BLASTX
NCBI GI g3928084
BLAST score 515
E value 2.0e-52
Match length 152
% identity 64

NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis

thaliana]

Seq. No. 236135

Seq. ID uC-gsflnu33B013f11b1

Method BLASTX
NCBI GI g1352186
BLAST score 523
E value 3.0e-53
Match length 123

% identity 77

NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)

(CYTOCHROME P450 74)  $>gi_404866$  (U00428) allene oxide

synthase [Linum usitatissimum]

Seq. No. 236136

Seq. ID uC-gsflnu33B013f12b1

Method BLASTX
NCBI GI 94567262
BLAST score 520
E value 6.0e-63
Match length 132
% identity 89

NCBI Description (AC006841) putative ubiquitin [Arabidopsis thaliana]

Seq. No. 236137

Seq. ID uC-gsflnu33B015a03b1

Method BLASTX
NCBI GI g4455340
BLAST score 466
E value 1.0e-46
Match length 131
% identity 66

NCBI Description (AL035522) putative protein [Arabidopsis thaliana]



Seq. No. 236138

Seq. ID uC-gsflnu33B015a04b1

Method BLASTX
NCBI GI g1723894
BLAST score 272
E value 7.0e-24
Match length 164
% identity 40

NCBI Description HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC

REGION >gi\_2131584\_pir\_\_\$64106 hypothetical protein YGL099w

- yeast (Saccharomyces cerevisiae)

>gi\_1322637\_emb\_CAA96805\_ (Z72621) ORF YGL099w

[Saccharomyces cerevisiae]

Seq. No. 236139

Seq. ID uC-gsflnu33B015a09b1

Method BLASTX
NCBI GI g464707
BLAST score 571
E value 4.0e-59
Match length 117
% identity 95

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi\_480908\_pir\_\_S37496 ribosomal

protein S18.A - Arabidopsis thaliana

>gi\_405613\_emb\_CAA80684\_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi\_434343\_emb\_CAA82273\_ (Z28701)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_434345\_emb\_CAA82274\_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi\_434906\_emb\_CAA82275\_ (Z28962)

S18 ribosomal protein [Arabidopsis thaliana]

>gi\_2505871\_emb\_CAA72909\_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi\_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb\_Z28701, DNA gb\_Z23165 from A. thaliana. ESTs gb\_T21121, gb\_Z17755, gb\_R64776 and gb\_R30430 come from this gene. [Arabidopsis thaliana] >gi\_4538910\_emb\_CAB39647.1\_ (AL049482) S18.A ribosomal

protein [Arabidopsis thaliana]

Seq. No. 236140

Seq. ID uC-qsflnu33B015b01b1

Method BLASTX
NCBI GI g3334157
BLAST score 516
E value 4.0e-70
Match length 155
% identity 82

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi 1220142 emb CAA59468 (X85185) cyclophilin

[Catharanthus roseus]

Seq. No. 236141

Seq. ID uC-gsflnu33B015b09b1

Method BLASTX
NCBI GI 94376203
BLAST score 343
E value 3.0e-32



Match length 158 % identity 40

NCBI Description (U35226) putative cytochrome P-450 [Nicotiana

plumbaginifolia]

Seq. No. 236142

Seq. ID uC-gsflnu33B015c08b1

Method BLASTX
NCBI GI g3342798
BLAST score 440
E value 2.0e-48
Match length 132
% identity 70

NCBI Description (AF061240) glutamine cyclotransferase precursor [Carica

papaya]

Seq. No. 236143

Seq. ID uC-gsflnu33B015d05b1

Method BLASTX
NCBI GI g464849
BLAST score 702
E value 2.0e-74
Match length 139
% identity 99

NCBI Description TUBULIN ALPHA CHAIN >gi\_486847\_pir\_\_S36232 tubulin alpha

chain - almond >gi\_20413\_emb\_CAA47635\_ (X67162)

alpha-tubulin [Prunus dulcis]

Seq. No. 236144

Seq. ID uC-gsflnu33B015e07b1

Method BLASTX
NCBI GI g2244834
BLAST score 199
E value 2.0e-28
Match length 105
% identity 64

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236145

Seq. ID uC-gsflnu33B015f11b1

Method BLASTX
NCBI GI g3337356
BLAST score 336
E value 7.0e-32
Match length 71
% identity 93

NCBI Description (AC004481) putative protein transport protein SEC61 alpha

subunit [Arabidopsis thaliana]

Seq. No. 236146

Seq. ID uC-gsflnu33B015g05b1

Method BLASTX
NCBI GI g1769901
BLAST score 164
E value 3.0e-11
Match length 41
% identity 71

34220



(X95737) proline transporter 1 [Arabidopsis thaliana] NCBI Description >gi 2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana] Seq. No. 236147 uC-gsflnu33B015g08b1 Seq. ID Method BLASTX g4309730 NCBI GI BLAST score 232 E value 4.0e-19 Match length 111 % identity 44 NCBI Description (AC006439) putative lipid transfer protein [Arabidopsis thaliana] 236148 Seq. No. uC-gsflnu33B015h09b1 Seq. ID Method BLASTX NCBI GI g4467096 BLAST score 526 E value 1.0e-53 Match length 152 47 % identity NCBI Description (AL035538) putative protein [Arabidopsis thaliana] Seq. No. 236149 uC-gsflnu33B016a06b1 Seq. ID Method BLASTX g3719211 NCBI GI BLAST score 209 E value 1.0e-16 Match length 44 % identity 89 NCBI Description (U97021) UIP2 [Arabidopsis thaliana] Seq. No. 236150 Seq. ID uC-gsflnu33B016a08b1 Method BLASTX NCBI GI q4468804 BLAST score 317 E value 3.0e-29 Match length 146 % identity 19 NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

236151 Seq. No.

Seq. ID uC-qsflnu33B016b10b1

Method BLASTX NCBI GI g231757 BLAST score 768 E value 5.0e-82Match length 167 % identity 88

CAFFEIC ACID 3-O-METHYLTRANSFERASE NCBI Description (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID

3-O-METHYLTRANSFERASE) (COMT) >gi 99653 pir S18568 lignin-bispecific O-methyltransferase (EC 2.1.1.-) -



quaking aspen >gi\_20951\_emb\_CAA44006\_ (X62096) lignin bispecific acid/5-hydroxyferulic acid methyltransferase [Populus tremuloides] >gi\_2226267 (U13171) caffeic acid/5-hydroxyferulic acid O-methyltransferase [Populus tremuloides]

Seq. No. 236152

Seq. ID uC-gsflnu33B016c08b1

Method BLASTX
NCBI GI g1173043
BLAST score 259
E value 2.0e-22
Match length 69
% identity 77

NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi 479441 pir S33899 ribosomal

protein L38 - tomato (cv. Moneymaker)

>gi 313027 emb CAA49599 (X69979) ribosomal protein L38

[Lycopersicon esculentum]

Seq. No. 236153

Seq. ID uC-gsflnu33B016c12b1

Method BLASTX
NCBI GI g401189
BLAST score 146
E value 1.0e-09
Match length 40
% identity 78

NCBI Description WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP)

(TURGOR-RESPONSIVE PROTEIN 7A) >gi\_485511\_pir\_\_S33617 trg-31 protein - garden pea >gi\_20426\_emb\_CAA79159\_

(Z18288) trg-31 [Pisum sativum]

Seq. No. 236154

Seq. ID uC-gsflnu33B016d11b1

Method BLASTX
NCBI GI g2462834
BLAST score 325
E value 4.0e-30
Match length 151
% identity 42

NCBI Description (AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236155

Seq. ID uC-gsflnu33B016e04b1

Method BLASTX
NCBI GI g3941480
BLAST score 356
E value 1.0e-33
Match length 164
% identity 48

NCBI Description (AF062894) putative transcription factor [Arabidopsis

thaliana]

Seq. No. 236156

Seq. ID uC-gsflnu33B016f11b1

Method BLASTX NCBI GI g3377822



```
BLAST score
                    6.0e-29
E value
Match length
                    76
% identity
                    83
                   (AF076275) contains similarity to Caenorhabditis elegans
NCBI Description
                   MEL-26 (GB:U67737) [Arabidopsis thaliana]
                    236157
Seq. No.
Seq. ID
                   uC-gsflnu33B016f12b1
Method
                   BLASTX
NCBI GI
                    q2809246
BLAST score
                    347
                    8.0e-33
E value
Match length
                    123
% identity
                    59
                  (AC002560) F2401.15 [Arabidopsis thaliana]
NCBI Description
                    236158
Seq. No.
                   uC-gsflnu33B016g05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                    q1480012
                    157
BLAST score
E value
                    7.0e-11
Match length
                    30
                    93
% identity
NCBI Description
                   (D78492) putative ubiquitin extension protein [Brassica
                    rapa]
                    236159
Seq. No.
Seq. ID
                    uC-gsflnu33B016g06b1
Method
                    BLASTX
NCBI GI
                    q585628
BLAST score
                    164
E value
                    2.0e-11
Match length
                    40
% identity
                    78
                    SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-1 CATALYTIC
NCBI Description
                    SUBUNIT >gi_418779_pir__S31162 phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain (clone EP14a) -
                    Arabidopsis thaliana >gi_166823 (M96733) protein
                    phosphatase [Arabidopsis thaliana]
Seq. No.
                    236160
Seq. ID
                    uC-gsflnu33B016g09b1
Method
                    BLASTX
NCBI GI
                    g132935
BLAST score
                    214
                    2.0e-17 ·
E value
Match length
                    65
% identity
                    60
                    60S RIBOSOMAL PROTEIN L37A (YL37) (RP47)
NCBI Description
                    >gi_101568_pir__S18431 ribosomal protein L35a.e.c16 - yeast
```

>g1\_101568\_pir\_\_S18431 ribosomal protein L35a.e.c16 - yeast
(Saccharomyces cerevisiae) >gi 4392 emb CAA41035 (X57969)

ribosomal protein L37a [Saccharomyces cerevisiae] >gi\_1244773 (U43703) Lpi4p [Saccharomyces cerevisiae]

>gi\_1370305\_emb\_CAA97847\_ (Z73499) ORF YPL143w

[Saccharomyces cerevisiae]



```
236161
Seq. No.
                  uC-gsflnu33B018b04b1
Seq. ID
Method
                  BLASTX
                   g4204304
NCBI GI
                   144
BLAST score
                   4.0e-09
E value
                   30
Match length
                   83
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   236162
Seq. No.
                   uC-qsflnu33B018b06b1
Seq. ID
Method
                   BLASTX
                   g2737926
NCBI GI
                   402
BLAST score
                   3.0e-39
E value
                   110
Match length
                   76
% identity
                  (U77673) fimbrin-like protein AtFim2 [Arabidopsis thaliana]
NCBI Description
                   236163
Seq. No.
                   uC-gsflnu33B018b08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2982259
                   155
BLAST score
                   7.0e-11
E value
                   35
Match length
                   89
% identity
                   (AF051212) probable 60s ribosomal protein L13a [Picea
NCBI Description
                   mariana]
                   236164
Seq. No.
                   uC-gsflnu33B018b10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4545262
BLAST score
                   159
E value
                   1.0e-10
Match length
                   44
% identity
                   (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                   hirsutum]
                   236165
Seq. No.
Seq. ID
                   uC-gsflnu33B018b12b1
Method
                   BLASTX
                   q4467157
NCBI GI
                   142
BLAST score
                   8.0e-09
E value
                   65
Match length
% identity
                   48
                   (AL035540) disease resistance response like protein
NCBI Description
                   [Arabidopsis thaliana]
```

34224

236166

uC-gsflnu33B018c02b1

Seq. No.

Seq. ID



```
BLASTX
Method
NCBI GI
                  q2213627
                  287
BLAST score
                  1.0e-25
E value
                  135
Match length
                  38
% identity
                  (AC000103) F21J9.19 [Arabidopsis thaliana]
NCBI Description
                  236167
Seq. No.
                  uC-gsflnu33B018c11b1
Seq. ID
Method
                  BLASTX
                  q2827084
NCBI GI
BLAST score
                   243
                  1.0e-20
E value
                   60
Match length
% identity
                   80
                  (AF020273) malate dehydrogenase precursor [Medicago sativa]
NCBI Description
                   236168
Seq. No.
                   uC-gsflnu33B018d02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2642448
BLAST score
                   368
                   3.0e - 35
E value
Match length
                   112
                   27
% identity
                  (AC002391) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3169187 (AC004401) hypothetical protein [Arabidopsis
                   thaliana]
                   236169
Seq. No.
                   uC-gsflnu33B018d06b1
Seq. ID
                   BLASTX
Method
                   q2398525
NCBI GI
                   274
BLAST score
E value
                   2.0e-24
Match length
                   98
% identity
NCBI Description (Y13722) Transcription factor [Arabidopsis thaliana]
                   236170
Seq. No.
Seq. ID
                   uC-gsflnu33B018d09b1
Method
                   BLASTX
NCBI GI
                   g4567200
BLAST score
                   472
E value
                   2.0e-47
Match length
                   109
% identity
                   73
NCBI Description (AC007168) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   236171
Seq. ID
                   uC-gsflnu33B018e12b1
Method
                   BLASTX
```

Method BLASTX NCBI GI g2191150 BLAST score 669 E value 2.0e-70 Match length 164

```
% identity
NCBI Description
                   (AF007269) similar to mitochondrial carrier family
                   [Arabidopsis thaliana]
Seq. No.
                   236172
Seq. ID
                   uC-gsflnu33B018f07b1
Method
                  BLASTX
NCBI GI
                   g534982
BLAST score
                   214
                   8.0e-18
E value
Match length
                   71
% identity
                   61
NCBI Description (X75898) phosphoglucomutase [Spinacia oleracea]
Seq. No.
                   236173
Seq. ID
                  uC-gsflnu33B018f10b1
Method
                  BLASTX
NCBI GI
                  g1246823
BLAST score
                   572
E value
                   5.0e-59
Match length
                   166
% identity
                   72
NCBI Description (X89865) unknown [Phoenix dactylifera]
Seq. No.
                   236174
Seq. ID
                  uC-qsflnu33B018q02b1
Method
                  BLASTX
NCBI GI
                   q2497539
BLAST score
                   175
E value
                   1.0e-12
Match length
                   120
% identity
                   46
NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >qi 169703
                   (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]
Seq. No.
                  236175
Seq. ID
                  uC-gsflnu33B018g12b1
Method
                  BLASTX
NCBI GI
                  q3335359
BLAST score
                  565
E value
                   3.0e-58
Match length
                  170
% identity
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236176
Seq. ID
                  uC-gsflnu33B018h06b1
Method
                  BLASTX
NCBI GI
                  g1706082
BLAST score
                  288
E value
                  8.0e-26
Match length
                  139
```

% identity NCBI Description SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)

47

>gi\_629787\_pir\_\_S44191 serine-type carboxypeptidase (EC

3.4.16.1) II-3 - barley >gi\_619350\_bbs\_153536

CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,



```
>gi 474392_emb CAA55478_ (X78877) serine carboxylase II-3
                    [Hordeum vulgare]
 Seq. No.
                    236177
 Seq. ID
                    uC-gsflnu33B018h08b1
 Method
                    BLASTX
 NCBI GI
                    g4417304
 BLAST score
                    379
 E value
                    1.0e-36
                    100
 Match length
 % identity
                    63
 NCBI Description
                    (AC006446) putative beta-1,4-mannosyl-glycoprotein
                    beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis
                    thaliana]
 Seq. No.
                    236178
 Seq. ID
                    uC-gsflnu33B019a02b1
 Method
                    BLASTX
 NCBI GI
                    g3776084
 BLAST score
                    223
-E value
                    4.0e-18
 Match length
                    83
 % identity
                    48
 NCBI Description (Y18251) NtN2 [Medicago truncatula]
 Seq. No.
                    236179
 Seq. ID
                    uC-gsflnu33B019b01b1
 Method
                    BLASTX
 NCBI GI
                    g4558673
 BLAST score
                    311
 E value
                    1.0e-28
 Match length
                    134
 % identity
                    37
 NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    236180
                    uC-gsflnu33B019b10b1
 Method
                    BLASTX
```

cv. Alexis, aleurone, Peptide, 516 aa]

Seq. ID

NCBI GI g3004565 BLAST score 259 E value 1.0e-22 Match length 94 % identity

NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 236181

Seq. ID uC-gsflnu33B019c05b1

Method BLASTX NCBI GI g4185819 BLAST score 192 E value 9.0e-15 Match length 47 % identity 68

NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea

batatas]



```
236182
  Seq. No.
  Seq. ID
                     uC-gsflnu33B019c12b1
Method
                     BLASTX
  NCBI GI
                     g2244834
  BLAST score
                     156
                     2.0e-10
  E value
  Match length
                     137
  % identity
                     39
  NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                     236183
  Seq. ID
                     uC-gsflnu33B019d04b1
  Method
                     BLASTX
  NCBI GI
                     q4249390
  BLAST score
                     346
  E value
                     1.0e-32
  Match length
                     106
  % identity
                     61
  NCBI Description
                    (AC005966) Similar to gb_AF039182 probable aldo-keto
                     reductase from Fragaria x ananassa. This gene may be cut
                     off. EST gb_U74151 comes from this gene. [Arabidopsis
                     thaliana]
 Seq. No.
                     236184
  Seq. ID
                    uC-qsflnu33B019d07b1
  Method
                    BLASTX
  NCBI GI
                     q3127031
  BLAST score
                     251
  E value
                     5.0e-22
  Match length
                     70
  % identity
                     63
  NCBI Description (AF014802) (S)-N-methylcoclaurine 3'-hydroxylase
                     [Eschscholzia californica]
  Seq. No.
                     236185
  Seq. ID
                    uC-gsflnu33B019d08b1
  Method
                    BLASTX
  NCBI GI
                     q3414938
  BLAST score
                    158
  E value
                     1.0e-10
  Match length
                    45
  % identity
  NCBI Description (AF076603) GgtA [Dictyostelium discoideum]
  Seq. No.
                     236186
  Seq. ID
                    uC-gsflnu33B019e09b1
  Method
                    BLASTX
  NCBI GI
                    g2443878
  BLAST score
                    186
  E value
                     6.0e-14
  Match length
                    80
  % identity
                     60
  NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]
```

Seq. No. 236187

Seq. ID uC-gsflnu33B019e10b1

Method BLASTX



```
q3367523
NCBI GI
BLAST score
                   185
E value
                  1.0e-23
Match length
                  74
% identity
                   69
NCBI Description
                  (AC004392) ESTs gb AA728658 and gb N95943 come from this
                  gene. [Arabidopsis thaliana]
                  236188
Seq. No.
Seq. ID
                  uC-gsflnu33B019h06b1
Method
                  BLASTX
NCBI GI
                  g2980641
BLAST score
                  194
                  3.0e-20
E value
                  89
Match length
% identity
                   44
                 (Y11250) multi resistance protein [Arabidopsis thaliana]
NCBI Description
                   236189
Seq. No.
                  uC-gsflnu33B019h09b1
Seq. ID
Method
                  BLASTX
                  g2213610
NCBI GI
BLAST score
                   377
                   3.0e-36
E value
Match length
                  105
                   27
% identity
NCBI Description
                 (AC000103) F21J9.4 [Arabidopsis thaliana]
                  236190
Seq. No.
                  uC-gsflnu33B019h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2623309
BLAST score
                   313
                   8.0e-29
E value
Match length
                  130
% identity
                   52
NCBI Description
                   (AC002409) similar to tgacg-specific DNA-binding protein
                   [Arabidopsis thaliana]
                  236191
Seq. No.
Seq. ID
                  uC-gsflnu33B022a12b1
Method
                  BLASTX
NCBI GI
                   g4204259
BLAST score
                   333
E value
                   4.0e-31
Match length
                   108
% identity
                   68
NCBI Description (AC005223) 18074 [Arabidopsis thaliana]
Seq. No.
                  236192
Seq. ID
                  uC-qsflnu33B022b03b1
```

Method BLASTX NCBI GI q4539660 BLAST score 388 E value 1.0e-37 Match length 107 % identity 66



```
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
                  236193
Seq. No.
                  uC-gsflnu33B022b06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3880625
BLAST score
                  248
                  4.0e-21
E value
                  82
Match length
                  54
% identity
                  (Z93785) predicted using Genefinder; similar to RNA
NCBI Description
                  recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST
                  EMBL:T01682 comes from this gene; cDNA EST EMBL:M75823
                  comes from this gene; cDNA EST EMBL: D27559 comes from this
                  ge
                  236194
Seq. No.
                  uC-gsflnu33B022f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2262099
BLAST score
                  466
E value
                  7.0e-47
                  99
Match length
                  79
% identity
NCBI Description (AC002343) thaumatin isolog [Arabidopsis thaliana]
Seq. No.
                  236195
                  uC-gsflnu33B022g04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2507442
BLAST score
                  147
E value
                   2.0e-09
Match length
                  29
                  93
% identity
NCBI Description
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                  >gi 1419685 emb_CAA67207_ (X98618) TCTP-like protein
                   [Medicago sativa]
Seq. No.
                   236196
Seq. ID
                  uC-qsflnu33B023a10b1
Method
                  BLASTX
NCBI GI
                  g913227
BLAST score
                  209
E value
                   3.0e-17
Match length
                  59
% identity
                  68
NCBI Description
                  transcription factor XlDP-1 [Xenopus laevis, embryos,
                  Peptide, 409 aa]
                   236197
Seq. No.
```

Seq. No. 236197
Seq. ID uC-gsflnu33B023a11b1
Method BLASTX
NCBI GI g3892047
BLAST score 158
E value 1.0e-10

Match length 107 % identity 37



(AC002330) putative bZIP-like DNA binding protein NCBI Description [Arabidopsis thaliana] 236198 Seq. No. uC-gsflnu33B023d05b1 Seq. ID Method BLASTX NCBI GI q1296816 377 BLAST score E value 3.0e-36 Match length 88 % identity 84 NCBI Description (X94995) naringenin-chalcone synthase [Juglans sp.] 236199 Seq. No. Seq. ID uC-qsflnu33B023f01b1 BLASTX Method q1076620 NCBI GI 334 BLAST score 2.0e-31 E value Match length 92 % identity 67 cyclin - common tobacco >gi\_599933\_emb\_CAA86032\_ (Z37978) NCBI Description Cyclin [Nicotiana tabacum] 236200 Seq. No. Seq. ID uC-qsflnu33B023f04b1 Method BLASTX q2462925 NCBI GI BLAST score 138 E value 1.0e-08 Match length 33 % identity NCBI Description (AJ000053) GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis thaliana] 236201 Seq. No. Seq. ID uC-gsflnu33B023f12b1 BLASTX Method NCBI GI g1532167 BLAST score 147 E value 2.0e-09 Match length 48 % identity 52 (U63815) localized according to blastn similarity to EST NCBI Description sequences; therefore, the coding span corresponds only to

an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No. 236202

Seq. ID uC-gsflnu33B023g01b1

Method BLASTX g4154352 NCBI GI BLAST score 174 E value 1.0e-12 91 Match length

% identity

NCBI Description

68

thaliana]



```
% identity
NCBI Description
                  (AF110333) PrMC3 [Pinus radiata]
                   236203
Seq. No.
Seq. ID
                  uC-gsflnu33B023h04b1
Method
                  BLASTX
                  g2618689
NCBI GI
BLAST score
                   672
E value
                   7.0e-71
Match length
                  149
% identity
                   88
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
                  236204
Seq. No.
Seq. ID
                  uC-gsflnu33B023h11b1
Method
                  BLASTX
                  g4309759
NCBI GI
                   327
BLAST score
                   8.0e-31
E value
Match length
                  86
% identity
                   78
NCBI Description
                  (AC006217) unknown protein with Src homology 3 (SH3) domain
                  profile (PDOC50002) [Arabidopsis thaliana]
Seq. No.
                  236205
Seq. ID
                  uC-gsflnu33B024d09b1
Method
                  BLASTX
NCBI GI
                  q3776573
BLAST score
                   259
                   5.0e-23
E value
Match length
                   63
                   71
% identity
                   (AC005388) Similar to nodulins and lipase homolog F14J9.5
NCBI Description
                   gi_3482914 from Arabidopsis thaliana BAC gb_AC003970.
                  Alternate first exon from 72258 to 72509. [Arabidopsis
                   thaliana]
                   236206
Seq. No.
Seq. ID
                  uC-gsflnu33B024g09b1
Method
                  BLASTX
NCBI GI
                  q2832632
BLAST score
                  146
E value
                   2.0e-09
Match length
                  52
% identity
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  236207
Seq. ID
                  uC-qsflnu33B025b07b1
Method
                  BLASTX
NCBI GI
                  g4415924
BLAST score
                  218
E value
                  3.0e-18
                  53
Match length
```

34232

(AC006282) putative glucosyl transferase [Arabidopsis

Seq. No.

Seq. ID



```
236208
Seq. No.
                  uC-gsflnu33B025b11b1
Seq. ID
Method .
                  BLASTX
NCBI GI
                  q3169719
BLAST score
                  355
                  3.0e-34
E value
Match length
                  77
% identity
NCBI Description
                 (AF007109) similar to yeast dcp1 [Arabidopsis thaliana]
                  236209
Seq. No.
                  uC-gsflnu33B025g07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q401189
BLAST score
                  281
                  1.0e-25
E value
Match length
                  59
                  88
% identity
NCBI Description
                  WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP)
                   (TURGOR-RESPONSIVE PROTEIN 7A) >gi_485511_pir__S33617
                  trg-31 protein - garden pea >gi_20426_emb_CAA79159_
                   (Z18288) trg-31 [Pisum sativum]
                  236210
Seq. No.
Seq. ID
                  uC-gsflnu33B025g11b1
Method
                  BLASTX
NCBI GI
                  g633110
BLAST score
                  157
E value
                  5.0e-11
Match length
                  34
% identity
                  100
NCBI Description (D31843) plasma membrane H+-ATPase [Oryza sativa]
                  236211
Seq. No.
Seq. ID
                  uC-gsflnu33B026a02b1
Method
                  BLASTX
NCBI GI
                  g4406819
BLAST score
                  193
E value
                  1.0e-14
Match length
                  81
% identity
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236212
Seq. ID
                  uC-gsflnu33B026b10b1
Method
                  BLASTX
NCBI GI
                  q3005576
BLAST score
                  642
E value
                  2.0e-67
Match length
                  134
                  53
% identity
                  (AF047718) putative high affinity nitrate transporter;
NCBI Description
```

GmNRT2 [Glycine max]

uC-gsflnu33B026d04b1

236213



```
BLASTX
Method
NCBI GI
                   g2739374
                   288
BLAST score
E value
                    9.0e-26
                   139
Match length
                   17
% identity
                   (AC002505) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   236214
Seq. No.
                   uC-gsflnu33B026e01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                    q3080415
BLAST score
                    648
                    5.0e-68
E value
                    158
Match length
                    72
% identity
                    (AL022604) cysteine proteinase - like protein [Arabidopsis
NCBI Description
                    thaliana]
                    236215
Seq. No.
Seq. ID
                   uC-gsflnu33B026e08b1
                    BLASTX
Method
                    g1502430
NCBI GI
BLAST score
                    505
E value
                    3.0e-63
                    145
Match length
% identity
                    82
NCBI Description
                    (U62331) phosphate transporter [Arabidopsis thaliana]
                    >qi 2564661 (AF022872) phosphate transporter [Arabidopsis
                   thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate
Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770)
                    phosphate transporter, AtPT2 [Arabidopsis thaliana]
                    236216
Seq. No.
                    uC-gsflnu33B026e10b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3702327
                    272
BLAST score
                    5.0e-24
E value
Match length
                    104
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                    236217
Seq. No.
Seq. ID
                    uC-qsflnu33B026f04b1
Method
                    BLASTX
NCBI GI
                    g3193284
BLAST score
                    277
```

E value 1.0e-24 Match length 141 % identity

NCBI Description (AF069298) No definition line found [Arabidopsis thaliana]

Seq. No. 236218

uC-gsflnu33B026h07b1 Seq. ID

Method BLASTX NCBI GI g2894596



BLAST score 502 E value 6.0e-51 Match length 130 % identity 75

NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No.

Seq. ID uC-gsflnu33B026h10b1

236219

Method BLASTX
NCBI GI g4101564
BLAST score 244
E value 1.0e-20
Match length 122
% identity 46

NCBI Description (AF004556) IFA-binding protein [Arabidopsis thaliana]

Seq. No.

Seq. ID uC-gsflnu33B027a01b1

236220

Method BLASTX
NCBI GI g2245096
BLAST score 216
E value 1.0e-17
Match length 78
% identity 62

NCBI Description (Z97343) inositol 2-dehydrogenase homolog [Arabidopsis

thaliana]

Seq. No. 236221

Seq. ID uC-gsflnu33B027a02b1

Method BLASTX
NCBI GI g4539301
BLAST score 219
E value 8.0e-18
Match length 114
% identity 38

NCBI Description (AL049480) putative mitochondrial protein [Arabidopsis

thaliana],

Seq. No. 236222

Seq. ID uC-qsflnu33B027a09b1

Method BLASTX
NCBI GI g3367534
BLAST score 526
E value 9.0e-54
Match length 139
% identity 76

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb\_U24105 from Homo sapiens. [Arabidopsis

thaliana]

Seq. No. 236223

Seq. ID uC-gsflnu33B027b12b1

Method BLASTX
NCBI GI g1621467
BLAST score 633
E value 3.0e-66
Match length 161



% identity

NCBI Description (U73106) laccase [Liriodendron tulipifera]

Seq. No.

236224

Seq. ID

uC-gsflnu33B027c06b1

Method NCBI GI BLASTX g4163997

BLAST score E value

423 8.0e-42

Match length

103 75

% identity

NCBI Description (AF087483) alpha-xylosidase precursor [Arabidopsis

thaliana]

Seq. No.

236225

Seq. ID

uC-gsflnu33B027c09b1

Method NCBI GI BLASTX g2851508

BLAST score E value

219 4.0e-20

Match length % identity

55 82

NCBI Description

60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to

ribosomal protein L21 (gb\_L38826). ESTs

gb\_AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 (AC003970) Putative ribosomal protein

L21 [Arabidopsis thaliana]

Seq. No.

236226

Seq. ID

uC-gsflnu33B027e01b1

Method NCBI GI BLASTX g3522952

BLAST score E value

304 6.0e-28

Match length

90

61

% identity

NCBI Description (AC004411) putative alcohol dehydrogenase [Arabidopsis

thaliana]

Seq. No.

236227

Seq. ID

uC-gsflnu33B027f06b1

Method

BLASTX

NCBI GI

g3875112

BLAST score

217

E value

9.0e-18

Match length

82

% identity

NCBI Description

54 (Z68882) Similarity to Bovine inorganic pyrophosphatase

(SW:IPYR BOVIN); cDNA EST EMBL:D66533 comes from this gene;

cDNA EST EMBL:D70345 comes from this gene; cDNA EST

yk338a8.3 comes from this gene; cDNA EST yk338a8.5 comes fr

Seq. No.

236228

Seq. ID

uC-gsflnu33B027f09b1

Method NCBI GI BLAST score BLASTX q1076662

495



Method BLASTX

NCBI GI g1171978

BLAST score 278

E value 3.0e-25

Match length 80
% identity 18

NCBI Description POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)

(PABP 2) >gi\_304109 (L19418) poly(A)-binding protein

[Arabidopsis thaliana] >gi\_2911051\_emb\_CAA17561 (AL021961)

poly(A)-binding protein [Arabidopsis thaliana]

 Seq. No.
 236230

 Seq. ID
 uC-gsflnu33B027h04b1

 Method
 BLASTX

 NCBI GI
 g3850818

 BLAST score
 390

 E value
 7.0e-38

 Match length
 90

Match length 90
% identity 77

NCBI Description (Y18349) U2 snRNP auxiliary factor, small subunit [Oryza

sativa]

Seq. No. 236231

Seq. ID uC-gsflnu33B028a04b1

Method BLASTX
NCBI GI g2781362
BLAST score 200
E value 7.0e-16
Match length 89
% identity 23

NCBI Description (AC003113) F2401.18 [Arabidopsis thaliana]

Seq. No. 236232

Seq. ID uC-gsflnu33B028b04b1

Method BLASTX
NCBI GI g3142292
BLAST score 543
E value 1.0e-55
Match length 125
% identity 79

NCBI Description (AC002411) Contains similarity to tetratricopeptide repeat

protein gb\_U46571 from home sapiens. EST gb\_Z47802 and gb\_Z48402 come from this gene. [Arabidopsis thaliana]

Seq. No. 236233

Seq. ID uC-gsflnu33B028b08b1

Method BLASTX NCBI GI g1076510



BLAST score 269 E value 1.0e-23 Match length 63 % identity 79

NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp - kidney bean >gi 829119 emb\_CAA52414\_ (X74403) cyclophilin [Phaseolus

vulgaris]

Seq. No. 236234

Seq. ID uC-gsflnu33B028e11b1

Method BLASTX
NCBI GI g3879472
BLAST score 205
E value 4.0e-16
Match length 89
% identity 46

NCBI Description (Z69885) Similarity to Yeast protein kinase YAK1

(SW:YAK1\_YEAST); cDNA EST EMBL:D27831 comes from this gene;

cDNA EST EMBL:M75800 comes from this gene; cDNA EST EMBL:D27832 comes from this gene; cDNA EST EMBL:D69493

comes from

Seq. No. 236235

Seq. ID uC-gsflnu33B028f03b1

Method BLASTX
NCBI GI g2894440
BLAST score 210
E value 7.0e-17
Match length 106
% identity 45

NCBI Description (Y14366) lipase 1 [Drosophila melanogaster]

Seq. No. 236236

Seq. ID uC-gsflnu33B029b09b1

Method BLASTX
NCBI GI g3927825
BLAST score 263
E value 7.0e-23
Match length 55
% identity 89

NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase

[Arabidopsis thaliana]

Seq. No. 236237

Seq. ID uC-gsflnu33B029e02b1

Method BLASTX
NCBI GI g2827552
BLAST score 218
E value 1.0e-17
Match length 123
% identity 40

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

Seq. No. 236238

Seq. ID uC-gsflnu33B029f02b1

Method BLASTX NCBI GI g4239879



```
BLAST score
                  332
                   4.0e-31
E value
Match length
                  124
% identity
                  51
                  (AB016780) Glutamine:fructose-6-phosphate amidotransferase
NCBI Description
                  2 [Mus musculus]
                  236239
Seq. No.
                  uC-gsflnu33B029g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023419
BLAST score
                   304
E value
                  7.0e-28
                  61
Match length
                  93
% identity
                  CAFFEOYL-COA O-METHYLTRANSFERASE (TRANS-CAFFEOYL-COA
NCBI Description
                  3-O-METHYLTRANSFERASE) (CCOAMT) (CCOAOMT)
                  >gi_1934859_emb_CAA72911_ (Y12228) caffeoyl-CoA
                  O-methyltransferase [Eucalyptus gunnii]
Seq. No.
                  236240
                  uC-gsflnu33B029h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3033392
BLAST score
                   225
E value
                   4.0e-19
Match length
                   62
                   66
% identity
                   (AC004238) putative translation initiation factor
NCBI Description
                  EIF-2B-epsilon subunit [Arabidopsis thaliana]
                   236241
Seq. No.
                  uC-gsflnu33B031a01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3269291
BLAST score
                   568
E value
                   2.0e-58
Match length
                   151
% identity
                   (AL030978) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   236242
Seq. ID
                   uC-gsflnu33B031a02b1
Method
                   BLASTX
NCBI GI
                   g3204129
BLAST score
                   473
E value
                   2.0e-47
                  134
```

Match length 72 % identity

NCBI Description (AJ006768) histone H2A [Cicer arietinum]

Seq. No. 236243

uC-gsflnu33B031b02b1 Seq. ID

Method BLASTX NCBI GI g3861214 BLAST score 216



```
E value
                    2.0e-17
 Match length
                    118
 % identity
                    41
                    (AJ235272) unknown [Rickettsia prowazekii]
 NCBI Description
                    236244
 Seq. No.
 Seq. ID
                    uC-gsflnu33B031b04b1
 Method
                    BLASTX
 NCBI GI
                    q3413707
 BLAST score
                    645
 E value
                    1.0e-67
 Match length
                    142
                    48
 % identity
NCBI Description
                    (AC004747) hypothetical protein [Arabidopsis thaliana]
                    236245
 Seq. No.
                    uC-gsflnu33B031b05b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2959781
 BLAST score
                    261
 E value
                    9.0e-23
 Match length
                    73
 % identity
                    74
 NCBI Description
                   (AJ223508) Zwille protein [Arabidopsis thaliana]
 Seq. No.
                    236246
                    uC-qsflnu33B031f09b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2244806
 BLAST score
                    384
 E value
                    3.0e-37
 Match length
                    117
 % identity
 NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    236247
 Seq. ID
                    uC-qsflnu33B031q03b1
 Method
                    BLASTX
 NCBI GI
                    q3287695
 BLAST score
                    211
 E value
                    1.0e-16
                    93
 Match length
 % identity
                    48
                    (AC003979) Similar to hypothetical protein C34B7.2
 NCBI Description
                    gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis
                    thaliana]
                    236248
 Seq. No.
 Seq. ID
                    uC-gsflnu33B031g10b1
                    BLASTX
 Method
 NCBI GI
                    q3176709
 BLAST score
                    187
 E value
                    6.0e-14
```

% identity 46
NCBI Description (AC002392) putative anthranilate

74

Match length % identity

N-hydroxycinnamoyl/benzoyltransferase [Arabidopsis



## thaliana]

Seq. No. 236249 Seq. ID uC-gsflnu33B035a08b1 Method BLASTX NCBI GI g2829918 BLAST score 312 E value 1.0e-28 Match length 123 % identity 54 NCBI Description (AC002291) similar to "tub" protein gp\_U82468\_2072162 [Arabidopsis thaliana] 236250 Seq. No. Seq. ID uC-gsflnu33B035a12b1 Method BLASTX NCBI GI g2281449 BLAST score 224 E value 2.0e-18 Match length 86 % identity 55 NCBI Description (U90214) leucine zipper transcription factor TGA2.1 [Nicotiana tabacum] Seq. No. 236251 Seq. ID uC-gsflnu33B035b05b1 Method BLASTX NCBI GI q2583108 BLAST score 243 E value 4.0e-21 70 Match length % identity 70 NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana] Seq. No. 236252 Seq. ID uC-gsflnu33B035c07b1 Method BLASTX NCBI GI g3738316 BLAST score 363 E value 1.0e-34 106 Match length % identity 67 NCBI Description (AC005170) unknown protein [Arabidopsis thaliana] Seq. No. 236253 Seq. ID uC-gsflnu33B035d07b1 Method BLASTX NCBI GI g2270994 BLAST score 134 E value 3.0e-10 99 Match length % identity 42 NCBI Description (AF004809) Ca+2-binding EF hand protein [Glycine max]

Seq. No. 236254

Seq. ID uC-gsflnu33B035d12b1

Method BLASTX



```
NCBI GI
                   q3598861
BLAST score
                   162
E value
                   4.0e-11
Match length
                   67
% identity
                   45
NCBI Description
                   (AF072449) short-chain alcohol dehydrogenase [Ipomoea
                   trifida]
Seq. No.
                   236255
Seq. ID
                   uC-gsflnu33B035f10b1
Method
                   BLASTX
NCBI GI
                   g1468969
BLAST score
                   347
E value
                   8.0e-33
                   109
Match length
% identity
                   59
NCBI Description (D30666) brain acyl-CoA synthtase II [Rattus norvegicus]
Seq. No.
                   236256
Seq. ID
                   uC-qsflnu33B036a03b1
Method
                   BLASTX
NCBI GI
                   g3046694
BLAST score
                   325
E value
                   4.0e-30
Match length
                   99
% identity
                   57
NCBI Description (AL022224) vacuolar sorting receptor-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   236257
Seq. ID
                   uC-gsflnu33B036b03b1
Method
                   BLASTX
NCBI GI
                   q417499
BLAST score
                   500
E value
                   1.0e-50
Match length
                   159
% identity
                   61
NCBI Description AUTOANTIGEN PM-SCL >gi_284357_pir__A43920 nucleolar 100K polymyositis-scleroderma protein 2 - human >gi_179283
                   (L01457) PM-Scl autoantigen [Homo sapiens]
                   >gi 4505917 ref NP 002676.1 pPMSCL2 autoantigen PM-SCL
                   236258
Seq. No.
Seq. ID
                   uC-gsflnu33B036b12b1
Method
                   BLASTX
NCBI GI
                   g1408471
BLAST score ·
                   612
E value
                   9.0e-64
Match length
                   139
                   81
% identity
NCBI Description
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
```

Seq. No. 236259

Seq. ID uC-gsflnu33B036d01b1

Method BLASTX

```
NCBI GI
                  g1663724
BLAST score
                  548
E value
                  3.0e-56
Match length
                  150
% identity
                  72
NCBI Description (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
                  236260
Seq. No.
Seq. ID
                  uC-gsflnu33B036g08b1
Method
                  BLASTX
NCBI GI
                  q2213591
BLAST score
                  229
E value
                  5.0e-19
Match length
                  59
% identity
                  81
NCBI Description (AC000348) T7N9.11 [Arabidopsis thaliana]
                  236261
Seq. No.
Seq. ID
                  uC-gsflnu33B036h04b1
Method
                  BLASTX
NCBI GI
                  q2398531
BLAST score
                  242
E value
                  2.0e-20
Match length
                  100
% identity
                  58
NCBI Description (Y13726) Transcription factor [Arabidopsis thaliana]
                  236262
Seq. No.
Seq. ID
                  uC-gsflnu33B037a05b1
Method
                  BLASTX
NCBI GI
                  g1871177
BLAST score
                  388
E value
                  1.0e-37
                  99
Match length
% identity
                  78
NCBI Description (U90439) unknown protein [Arabidopsis thaliana]
                  236263
```

Seq. No.

Seq. ID uC-gsflnu33B037b07b1

Method BLASTX NCBI GI g584711 BLAST score 288 E value 1.0e-25 75 Match length % identity 76

NCBI Description 1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE)

(ETHYLENE-FORMING ENZYME) (EFE) >gi\_629707\_pir\_S42561 1-aminocyclopropane-1-carboxylate oxidase - garden petunia >gi 347417 (L21978) 1-aminocyclopropane-1-carboxylate

oxidase [Petunia hybrida]

Seq. No. 236264

Seq. ID uC-gsflnu33B037c11b1

Method BLASTX -NCBI GI g2252836 BLAST score 205 E value 1.0e-16



Match length 58 % identity 62

NCBI Description (AF013293) contains weak similarity to S. cerevisiae BOB1

protein (PIR:S45444) [Arabidopsis thaliana]

Seq. No. 236265

uC-gsflnu33B037d06b1 Seq. ID

Method BLASTX NCBI GI g2342725 BLAST score 309 E value 3.0e-28Match length 141 % identity

NCBI Description (AC002341) hypothetical protein [Arabidopsis thaliana]

236266 Seq. No.

Seq. ID uC-gsflnu33B037e11b1

Method BLASTX NCBI GI q4262228 BLAST score 368 E value 2.0e-35 Match length 111 % identity

NCBI Description (AC006200) putative receptor protein kinase [Arabidopsis

thaliana]

236267 Seq. No.

Seq. ID uC-gsflnu33B037f01b1

Method BLASTX NCBI GI g3024516 BLAST score 317 E value 8.0e-45

Match length 118 % identity

RAS-RELATED PROTEIN RAB11C >gi\_2160157 (AC000132) Strong similarity to A. thaliana ara-2 (gb\_ATHARA2). ESTs NCBI Description

gb\_ATTS2483,gb\_ATTS2484,gb\_AA042159 come from this gene.
[Arabidopsis thaliana] >gi\_2231303 (U74669) ras-related

small GTPase [Arabidopsis thaliana]

Seq. No. 236268

Seq. ID uC-gsflnu33B037h09b1

Method BLASTX NCBI GI g2281090 BLAST score 307 E value 1.0e-28 75 Match length % identity

NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236269

Seq. ID uC-gsflnu33B046a09b1

Method BLASTX NCBI GI g4455323 BLAST score 143 E value 4.0e-09 Match length 63

E value

Match length % identity

3.0e-33 93

77



```
% identity
NCBI Description
                   (AL035525) aminopeptidase-like protein [Arabidopsis
                  thalianal
                   236270
Seq. No.
Seq. ID
                  uC-gsflnu33B046a12b1
Method
                  BLASTX
NCBI GI
                   q2281633
BLAST score
                   317
E value
                  2.0e-29
Match length
                  107
% identity
                   60
NCBI Description
                  (AF003097) AP2 domain containing protein RAP2.4
                   [Arabidopsis thaliana]
                  236271
Seq. No.
Seq. ID
                  uC-gsflnu33B046b02b1
Method
                  BLASTX
NCBI GI
                  q1619321
BLAST score
                  282
E value
                   4.0e-25
Match length
                  97
% identity
                   55
NCBI Description (Y07563) hin1 [Nicotiana tabacum]
Seq. No.
                  236272
Seq. ID
                  uC-gsflnu33B046b03b1
Method
                  BLASTX
NCBI GI
                  g1711381
BLAST score
                  269
E value
                  7.0e-24
Match length
                  97
% identity
                  57
NCBI Description
                  PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
                  >gi_1256204_dbj_BAA12206_ (D84061) phosphoserine
                  aminotransferase [Spinacia oleracea]
Seq. No.
                  236273
Seq. ID
                  uC-gsflnu33B046c02b1
Method
                  BLASTX
NCBI GI
                  g2407800
BLAST score
                  339
E value
                  7.0e-32
Match length
                  97
% identity
                  73
NCBI Description (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
Seq. No.
                  236274
Seq. ID
                  uC-gsflnu33B046f06b1
Method
                  BLASTX
NCBI GI
                  g3021485
BLAST score
                  349
```

34245

NCBI Description (AJ224932) histone H2B-3 [Lycopersicon esculentum]



```
Seq. No.
                   236275
Seq. ID
                  uC-gsflnu33B046f08b1
Method
                  BLASTX
NCBI GI
                   g4039153
BLAST score
                  159
E value
                   4.0e-11
Match length
                  51
                   57
% identity
NCBI Description
                   (AF104221) low temperature and salt responsive protein
                  LTI6A [Arabidopsis thaliana] >gi_4325217_gb_AAD17302_
                   (AF122005) hydrophobic protein [Arabidopsis thaliana]
                  236276
Seq. No.
Seq. ID
                  uC-gsflnu33B046f09b1
Method
                  BLASTX
NCBI GI
                   q2708749
BLAST score
                   271
E value
                   5.0e-24
Match length
                  106
% identity
                   50
                  (AC003952) putative senescence-assoc. rhodanese-like
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  236277
                  uC-gsflnu33B046g10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   a435039
BLAST score
                   154
E value
                   3.0e-10
Match length
                   31
% identity
NCBI Description
                   (L17308) proline-rich cell wall protein [Gossypium
                  hirsutum]
Seq. No.
                   236278
Seq. ID
                  uC-gsflnu33B049a01b1
Method
                  BLASTX
NCBI GI
                   g2967452
BLAST score
                   496
E value
                   4.0e-50
Match length
                  154
% identity
                   65
                  (AB010882) hSNF2H [Homo sapiens]
NCBI Description
                   >gi_4507075_ref_NP_003592.1_pSMARCA5_ SWI/SNF related,
                   matrix associated, actin dependent regulator of chromatin,
                   subfamily a, member
                   236279
Seq. No.
Seq. ID
                  uC-qsflnu33B049c06b1
Method
                  BLASTX
NCBI GI
                  g1706918
BLAST score
                   228
E value
                   2.0e-19
```

71 Match length 56 % identity

NCBI Description FLAVONOL SULFOTRANSFERASE-LIKE >gi 498647 (U10277) sulfotransferase-like flavonol [Flaveria bidentis]



Seq. No. 236280

Seq. ID uC-qsflnu33B049d04b1

Method BLASTX NCBI GI g464981 BLAST score 393 E value 4.0e-38 Match length 74 % identity 99

UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762)

ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No. 236281

Seq. ID uC-qsflnu33B049e06b1

Method BLASTX NCBI GI q416641 BLAST score 229 E value 2.0e-19 Match length 48 % identity 85

NCBI Description INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG4

>gi\_287568\_dbj\_BAA03309\_ (D14413) ORF [Vigna radiata]

Seq. No. 236282

Seq. ID uC-gsflnu33B049e08b1

Method BLASTX NCBI GI q4100433 BLAST score 240 E value 2.0e-20 Match length 72 % identity

NCBI Description (AF000378) beta-glucosidase [Glycine max]

Seq. No. 236283

Seq. ID uC-gsflnu33B049f01b1 Method

BLASTX

NCBI GI g1707015 BLAST score 345 E value 9.0e-33 Match length 101 % identity 65

NCBI Description (U78721) protein phosphatase 2C isolog [Arabidopsis

thaliana]

Seq. No. 236284

Seq. ID uC-gsflnu33B049f09b1

Method BLASTX NCBI GI q3789940 BLAST score 216 E value 5.0e-18 47 Match length 23 % identity

NCBI Description (AF093504) tetra-ubiquitin [Saccharum hybrid cultivar

H32-8560]

Seq. No. 236285

Seq. No.

Seq. ID

236290

uC-gsflnu33B050d11b1



```
uC-gsflnu33B049f12b1
  Seq. ID
  Method
                     BLASTX
                     q3608263
  NCBI GI
  BLAST score
                     359
  E value
                     3.0e - 34
                     108
  Match length
                     65
  % identity
                    (AB017565) Dof zinc finger protein [Arabidopsis thaliana]
  NCBI Description
                     236286
  Seq. No.
                     uC-gsflnu33B049h08b1
  Seq. ID
  Method
                     BLASTX
                     g3738298
  NCBI GI
  BLAST score
                     148
                     1.0e-09
  E value
  Match length
                     103
                     41
 % identity
                     (AC005309) unknown protein [Arabidopsis thaliana]
  NCBI Description
                     >gi 4249394 (AC006072) unknown protein [Arabidopsis
                     thaliana]
  Seq. No.
                     236287
                     uC-gsflnu33B050a08b1
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g2829899
  BLAST score
                     324
  E value
                     5.0e - 30
                     133
  Match length
                     47
  % identity
                     (AC002311) similar to ripening-induced protein,
  NCBI Description
                     gp AJ001449 2465015 and major#latex protein,
                     gp X91961 1107495 [Arabidopsis thaliana]
                     236288
  Seq. No.
                     uC-gsflnu33B050b05b1
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     a2980784
... BLAST score
                     500
                     9.0e-51
  E value
  Match length
                     132
  % identity
  NCBI Description
                    (AL022198) puative protein [Arabidopsis thaliana]
                     236289
  Seq. No.
  Seq. ID
                     uC-gsflnu33B050c01b1
  Method
                     BLASTX
  NCBI GI
                     q2288981
  BLAST score
                     300
  E value
                     3.0e-27
  Match length
                     89
  % identity
                     39
  NCBI Description
                     (AC002335) calcium binding protein isolog [Arabidopsis
                     thaliana] >gi 3763938 (AC004450) putative calcium binding
                     protein [Arabidopsis thaliana]
```



```
Method
                  BLASTX
NCBI GI
                  g3341694
                  372
BLAST score
                   6.0e-52
E value
Match length
                  135
                  76
% identity
NCBI Description (AC003672) PREG-like protein [Arabidopsis thaliana]
Seq. No.
                  236291
Seq. ID
                  uC-gsflnu33B050e09b1
Method
                  BLASTX
NCBI GI
                  g3158474
BLAST score
                  644
E value
                  1.0e-67
Match length
                  136
                   91
% identity
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
Seq. No.
                  236292
Seq. ID
                  uC-gsflnu33B050e12b1
Method
                  BLASTX
NCBI GI
                  g3033392
BLAST score
                  178
E value
                   5.0e-13
Match length
                  122
% identity
                   40
                  (AC004238) putative translation initiation factor
NCBI Description
                  EIF-2B-epsilon subunit [Arabidopsis thaliana]
Seq. No.
                   236293
Seq. ID
                  uC-gsflnu33B050g06b1
Method
                  BLASTX
NCBI GI
                  q4104058
BLAST score
                  176
E value
                  3.0e-13
                  70
Match length
% identity
                   44
                  (AF031195) blue copper-binding protein homolog [Triticum
NCBI Description
                  aestivum]
                  236294
Seq. No.
Seq. ID
                  uC-gsflnu33B050g08b1
Method
                  BLASTX
NCBI GI
                  g4467157
BLAST score
                  248
E value
                   4.0e-21
                  100
Match length
                   49
% identity
NCBI Description (AL035540) disease resistance response like protein
                   [Arabidopsis thaliana]
                  236295
Seq. No.
```

Seq. ID

uC-gsflnu33B050g09b1

Method BLASTX NCBI GI q3292823 BLAST score 319 E value 2.0e-29

```
Match length
                  137
% identity
NCBI Description
                  (AL031018) putative protein [Arabidopsis thaliana]
                  236296
Seq. No.
                  uC-gsflnu33B051a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2104536
BLAST score
                  458
E value
                  9.0e-46
Match length
                  99
% identity
                  77
                  (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                  thaliana]
```

236297 Seq. No. Seq. ID uC-gsflnu33B051a08b1 Method BLASTX NCBI GI g3913724 329

BLAST score E value 5.0e - 31Match length 74 % identity 88

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-2 SUBUNIT

(GP-ALPHA-2) >gi\_1834453\_emb\_CAA64834\_ (X95582) G protein

[Glycine max]

236298 Seq. No.

Seq. ID uC-qsflnu33B051b04b1

Method BLASTX NCBI GI g553111 BLAST score 143 E value 1.0e-08 Match length 91 % identity 11

NCBI Description (J03625) hydroproline-rich protein [Glycine max]

Seq. No. 236299

Seq. ID uC-gsflnu33B051c02b1

Method BLASTX NCBI GI g3935171 BLAST score 252 E value 1.0e-21 Match length 55 % identity 84

NCBI Description (AC004557) F17L21.14 [Arabidopsis thaliana]

Seq. No. 236300

Seq. ID uC-gsflnu33B051e02b1

Method BLASTX NCBI GI g3413697 BLAST score 200 E value 2.0e-15 Match length 150 % identity 39

NCBI Description (AC004747) SF16-like protein, 5' partial [Arabidopsis

thalianal

NCBI Description

thaliana]

```
Seq. No.
                   236301
                   uC-gsflnu33B051f03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3914430
BLAST score
                   205
E value
                   2.0e-16
                   64
Match length
                   61
% identity
                   PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
NCBI Description
                   CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                   >gi 2285800 dbj BAA21650 (D78172) 26S proteasome beta
                   subunit [Spinacia oleracea]
Seq. No.
                   236302
                   uC-gsflnu33B051g02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g548441
BLAST score
                   250
                   5.0e-22
E value
                   45
Match length
                   98
% identity
NCBI Description
                   SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT
                   >gi_486805_pir__S35502 phosphoprotein phosphatase (EC
                   3.1.3.16) ZA - alfalfa >gi 287811 emb CAA49849 (X70399)
                   phosphoprotein phosphatase type 2A [Medicago sativa]
Seq. No.
                   236303
                   uC-gsflnu33B051g07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g538067
BLAST score
                   164
E value
                   1.0e-11
                   90
Match length
                   44
% identity
NCBI Description (M77661) putative pol polyprotein [Magnaporthe grisea]
Seq. No.
                   236304
                   uC-gsflnu33B051h12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1076402
BLAST score
                   159
E value
                   9.0e-11
Match length
                   112
                   38
% identity
NCBI Description S-like ribonuclease RNS2 - Arabidopsis thaliana
Seq. No.
                   236305
Seq. ID
                   uC-gsflnu33B055a06b1
Method
                   BLASTX
NCBI GI
                   g2104536
BLAST score
                   263
E value
                   4.0e-23
Match length
                   65
% identity
                   69
```

(AF001308) predicted glycosyl transferase [Arabidopsis

Seq. ID

Method



```
236306
Seq. No.
Seq. ID
                   uC-gsflnu33B055a12b1
Method
                   BLASTX
NCBI GI
                   g2623304
BLAST score
                   229
E value
                   6.0e-19
Match length
                   131
% identity
                   39
NCBI Description
                   (AC002409) similar to Medicago nodulin N21 [Arabidopsis
                   thaliana]
Seq. No.
                   236307
Seq. ID
                   uC-gsflnu33B055c02b1
Method
                   BLASTX
NCBI GI
                   q4206209
BLAST score
                   531
E value
                   3.0e-54
Match length
                   155
                   67
% identity
NCBI Description
                   (AF071527) putative glucan synthase component [Arabidopsis
                   thaliana] >gi_4263042 gb AAD15311 (AC005142) putative
                   glucan synthase component [Arabidopsis thaliana]
Seq. No.
                   236308
Seq. ID
                  uC-gsflnu33B055c10b1
Method
                  BLASTX
                  g3402672
NCBI GI
BLAST score
                   396
E value
                  1.0e-38
Match length
                  106
% identity
                   71
NCBI Description
                  (AC004697) putative white protein [Arabidopsis thaliana]
Seq. No.
                  236309
Seq. ID
                  uC-gsflnu33B055e08b1
Method
                  BLASTX
NCBI GI
                  g1542941
BLAST score
                  244
E value
                  1.0e-20
Match length
                  59
% identity
                  (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
NCBI Description
Seq. No.
                  236310
Seq. ID
                  uC-gsflnu33B055g04b1
Method
                  BLASTX
NCBI GI
                  g113217
BLAST score
                  183
E value
                  6.0e-14
Match length
                  37
% identity
                  95
NCBI Description ACTIN 1 > gi 100149 pir S07002 actin 1 - carrot
Seq. No.
                  236311
```

34252

uC-gsflnu33B055g06b1

BLASTX



```
NCBI GI
                   q3249099
BLAST score
                   381
                   8.0e-37
E value
Match length
                   111
                   67
% identity
NCBI Description
```

(ACOO3114) EST gb T21244 comes from this gene. [Arabidopsis

thaliana] >gi\_4220616\_dbj\_BAA74591\_ (AB021936)

nicotianamine synthase [Arabidopsis thaliana]

Seq. No.

Seq. ID uC-gsflnu33B055g08b1

BLASTX Method NCBI GI q2388943 BLAST score 194 E value 4.0e-15 Match length 55 % identity 64

(Z98978) SPAC27E2.03c, putative gtp-binding protein, NCBI Description

len:392a a, similar eg. to YBR025C, YBN5\_YEAST, P38219, hypothetica 1 44.2 kd protein, (394aa), fasta scores, opt:1664, E():0, (63.7% identity in 391 aa overlap), also

Seq. No. 236313

uC-gsflnu33B056a12b1 Seq. ID

Method BLASTX NCBI GI q2244818 215 BLAST score 9.0e-18 E value Match length 63 % identity

NCBI Description (Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.

Seq. ID uC-gsflnu33B056b01b1

Method BLASTX q2145356 NCBI GI 206 BLAST score E value 2.0e-16 Match length 53

74 % identity

(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi\_3132474 NCBI Description

(AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

236315 Seq. No.

Seq. ID uC-gsflnu33B056b11b1

Method BLASTX NCBI GI g4049502 BLAST score 189 E value 4.0e-14 136 Match length 35 % identity

(AL034563) transcription initiation factor iif, beta NCBI Description

subunit [Schizosaccharomyces pombe]

Seq. No. 236316

Seq. ID uC-gsflnu33B056e09b1



```
Method BLASTX
NCBI GI 94263646
BLAST score 179
E value 5.0e-13
Match length 128
% identity 34
NCBI Description (AC00613
[Arabido
```

ICBI Description (AC006136) putative TA1-like reverse transcriptase [Arabidopsis thaliana]

Seq. No. 236317 Seq. ID uC-gsflnu33B056e11b1

Method BLASTX
NCBI GI g116527
BLAST score 235
E value 6.0e-20
Match length 49
% identity 96

NCBI Description PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196)

>gi\_1143166 (U32397) ClpP protease [Nicotiana tabacum]

>gi\_2924270 emb\_CAA77422 (Z00044) ATP-dependent protease

proteolytic subuni [Nicotiana tabacum]

Seq. No. 236318

Seq. ID uC-gsflnu33B056h01b1

Method BLASTX
NCBI GI g3915961
BLAST score 505
E value 2.0e-51
Match length 112
% identity 88

NCBI Description HYPOTHETICAL 267 KD PROTEIN (ORF 2280)

>gi\_2924274\_emb\_CAA77427\_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi\_2924285\_emb\_CAA77438\_ (Z00044) hypothetical

protein [Nicotiana tabacum]

Seq. No. 236319

Seq. ID uC-gsflnu33B057a02b1

Method BLASTX
NCBI GI g4335754
BLAST score 413
E value 2.0e-40
Match length 135
% identity 60

NCBI Description (AC006284) putative acid phophatase (contains

metallo-phosphoesterase motif, prosite: QDOC50185)

[Arabidopsis thaliana]

Seq. No. 236320

Seq. ID uC-gsflnu33B057c02b1

Method BLASTX
NCBI GI g3810596
BLAST score 214
E value 2.0e-26
Match length 126
% identity 49

NCBI Description (AC005398) reverse-transcriptase-like protein [Arabidopsis

thaliana]



Seq. No. 236321 UC-gsfl

uC-gsflnu33B057d04b1

Method BLASTX
NCBI GI g127041
BLAST score 189
E value 2.0e-14
Match length 34
% identity 94

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi\_81647\_pir\_\_JN0131 methionine adenosyltransferase (EC
2.5.1.6) - Arabidopsis thaliana >gi\_166872 (M55077)
S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No. 236322

Seq. ID uC-gsflnu33B057d10b1

Method BLASTX
NCBI GI g3122765
BLAST score 246
E value 6.0e-21
Match length 73
% identity 63

NCBI Description DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (RPC155)

>qi 2460208 (AF021351) RNA polymerase III largest subunit

[Homo sapiens]

Seq. No. 236323

Seq. ID uC-gsflnu33B057e03b1

Method BLASTX
NCBI GI g4406777
BLAST score 300
E value 3.0e-27
Match length 104
% identity 63

NCBI Description (AC006532) putative zinc-finger protein [Arabidopsis

thaliana]

Seq. No. 236324

Seq. ID uC-gsflnu33B057f04b1

Method BLASTX
NCBI GI g629693
BLAST score 337
E value 1.0e-31
Match length 113
% identity 57

NCBI Description probable integrase - common tobacco (fragment)

>gi\_530742\_emb\_CAA56791\_ (X80830) integrase [Nicotiana

tabacum]

Seq. No. 236325

Seq. ID uC-gsflnu33B057f12b1

Method BLASTX
NCBI GI g2914701
BLAST score 306
E value 7.0e-28
Match length 119



% identity 49

NCBI Description (AC003974) putative cytochrome b5 [Arabidopsis thaliana]

Seq. No. 2

Seq. ID uC-gsflnu33B057h05b1

Method BLASTX
NCBI GI g3881189
BLAST score 210
E value 1.0e-16
Match length 71
% identity 54

NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337

comes from this gene; cDNA EST EMBL: C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No. 236327

Seq. ID uC-gsflnu33B057h11b1

Method BLASTX
NCBI GI g2190542
BLAST score 416
E value 7.0e-41
Match length 139
% identity 61

NCBI Description (AC001229) F5I14.5 gene product [Arabidopsis thaliana]

Seq. No. 236328

Seq. ID uC-qsflnu33B058a04b1

Method BLASTX
NCBI GI g2462741
BLAST score 179
E value 1.0e-13
Match length 38
% identity 87

NCBI Description (AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No. 236329

Seq. ID uC-gsflnu33B058a09b1

Method BLASTX
NCBI GI g3800878
BLAST score 357
E value 3.0e-34
Match length 90
% identity 80

NCBI Description (AF096281) threonine dehydratase/deaminase [Arabidopsis

thaliana]

Seq. No. 236330

Seq. ID uC-gsflnu33B058d01b1

Method BLASTX
NCBI GI g3892059
BLAST score 190
E value 3.0e-14
Match length 67
% identity 63

NCBI Description (AC002330) predicted protein of unknown function



## [Arabidopsis thaliana]

```
Seq. No.
                    236331
Seq. ID
                    uC-gsflnu33B058d06b1
Method
                    BLASTX
NCBI GI
                    g123551
BLAST score
                    246
E value
                    4.0e-21
Match length
                    81
% identity
                    69
NCBI Description 18.2 KD CLASS I HEAT SHOCK PROTEIN (HSP 18.2)
                    >gi_81640_pir__JQ0352 heat shock protein 18 - Arabidopsis thaliana >gi_16344_emb_CAA35183_ (X17295) heat shock
                    protein (AA 1 - 161) [Arabidopsis thaliana]
                    236332
Seq. No.
                    uC-gsflnu33B058d10b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4104931
BLAST score
                    459
E value
                    6.0e-46
Match length
                    114
% identity
                    78
NCBI Description (AF042196) auxin response factor 8 [Arabidopsis thaliana]
Seq. No.
                    236333
Seq. ID
                    uC-qsflnu33B058e02b1
Method
                    BLASTX
NCBI GI
                    g3608150
```

BLAST score 278 E value 5.0e-25 Match length 89 % identity 63

NCBI Description (AC005314) putative peroxidase [Arabidopsis thaliana]

Seq. No. 236334

uC-gsflnu33B058e03b1 Seq. ID

Method BLASTX NCBI GI q986969 BLAST score 424 E value 9.0e-42 Match length 113 73 % identity

NCBI Description (L28005) TGACG-motif-binding protein [Glycine max]

Seq. No. 236335

Seq. ID uC-gsflnu33B058f12b1

 ${\tt BLASTX}$ Method NCBI GI g3327868 BLAST score 158 E value 2.0e-10 Match length 68 57 % identity

(AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis NCBI Description

thaliana]

Seq. No. 236336

34257



Seq. ID uC-gsflnu33B058g07b1 BLASTX Method NCBI GI g1705826 BLAST score 250 E value 2.0e-21 Match length 54 % identity 89 CHALCONE SYNTHASE 1 (NARINGENIN-CHALCONE SYNTHASE 1) NCBI Description >gi 437708 (M91193) chalcone synthase [Trifolium subterraneum] >gi 741008\_prf\_\_2006270A chalcone synthase [Trifolium subterraneum] Seq. No. 236337 Seq. ID uC-gsflnu33B058g12b1 BLASTX Method NCBI GI g3879775 BLAST score 185 E value 1.0e-13 115 Match length 38 % identity NCBI Description (Z68752) Similarity to Serpentwood strictosidine synthase precursor (SW:STSY RAUSE); cDNA EST yk364d8.3 comes from this gene; cDNA EST yk364d8.5 comes from this gene [Caenorhabditis elegans] 236338 Seq. No. Seq. ID uC-gsflnu33B058h02b1 BLASTX Method NCBI GI g2160692 BLAST score 339 2.0e-32 E value Match length 74 84 % identity NCBI Description (U73527) B' regulatory subunit of PP2A [Arabidopsis thaliana] 236339 Seq. No. Seq. ID uC-gsflnu33B059a02b1 Method BLASTX NCBI GI g266410 BLAST score 210 E value 1.0e-16 Match length 69 % identity NCBI Description CDC2+/CDC28-RELATED PROTEIN KINASE R2 >gi 82507 pir S13934 protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog rice >gi 20194 emb CAA41172 (X58194) cdc2+/CDC28-related protein kinase [Oryza sativa] 236340 Seq. No. uC-gsflnu33B059b12b1 Seq. ID

Method BLASTX
NCBI GI g3450842
BLAST score 187
E value 3.0e-14
Match length 91
% identity 43



```
(AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                  satival
                  236341
Seq. No.
                  uC-gsflnu33B059c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2842493
BLAST score
                  346
                  1.0e-32
E value
Match length
                  105
                  64
% identity
                  (AL021749) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  236342
                  uC-gsflnu33B059d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3242077
                  504
BLAST score
                  4.0e-51
E value
Match length
                  140
% identity
                  69
                  (AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
NCBI Description
                  236343
Seq. No.
                  uC-gsflnu33B059e11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  a2558962
BLAST score
                  422
                  2.0e-41
E value
                  86
Match length
% identity
                  100
NCBI Description (AF025667) histone H2B1 [Gossypium hirsutum]
                  236344
Seq. No.
Seq. ID
                  uC-qsflnu33B059f03b1
Method
                  BLASTX
NCBI GI
                  g3249070
                  475
BLAST score
E value
                  1.0e-47
Match length
                  144
% identity
                  73
                  (AC004473) Contains similarity to siah binding protein 1
NCBI Description
                   (SiahBP1) gb U51586 from Homo sapiens. ESTs gb_T43314,
                  gb T43315 and gb R90521, gb_T75905 [Arabidopsis thaliana]
Seq. No.
                   236345
                  uC-gsflnu33B059f07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1076746
                  457
BLAST score
E value
                  1.0e-45
Match length
                  112
                  81
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi 763160_emb_CAA47948_ (X67711) heat shock protein 70
```

[Oryza sativa]

Seq. ID

Method

NCBI GI



```
Seq. No.
                    uC-gsflnu33B059f09b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1345642
BLAST score
                    250
                    1.0e-21
E value
Match length
                    64
                    78
% identity
                    FLAVONOID 3',5'-HYDROXYLASE 1 (F3'5'H) (CYTOCHROME P450
NCBI Description
                    75A1) (CYPLXXVA1) >gi_629710_pir__S38985 flavonoid 3',5'-hydroxylase Hf1 - garden petunia >gi_311656_emb_CAA80266_ (Z22545) flavonoid
                    3',5'-hydroxylase [Petunia x hybrida]
                    >gi_1853972_dbj_BAA03438_ (D14588)
flavonoid-3',5'-hydroxylase [Petunia x hybrida] >gi_3426337
                    (AF081575) flavonoid 3',5'-hydroxylase [Petunia x hybrida]
                    >gi 738772 prf 2001426B flavonoid 3',5'-hydroxylase
                    [Petunia x hybrida]
Seq. No.
                    236347
Seq. ID
                    uC-gsflnu33B059f10b1
Method
                    BLASTX
NCBI GI
                    q127041
BLAST score
                    283
                    3.0e-25
E value
Match length
                    53
                    92
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                    ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                    >gi_81647_pir__JN0131 methionine adenosyltransferase (EC
                    2.5.1.6) - Arabidopsis thaliana >gi 166872 (M55077)
                    S-adenosylmethionine synthetase [Arabidopsis thaliana]
Seq. No.
                    236348
Seq. ID
                    uC-gsflnu33B059g03b1
Method
                    BLASTX
                    g872116
NCBI GI
BLAST score
                    341
E value
                    3.0e-32
                    74
Match length
% identity
                    46
NCBI Description (X79770) sti (stress inducible protein) [Glycine max]
                    236349
Seq. No.
Seq. ID
                    uC-gsflnu33B059g04b1
Method
                    BLASTX
                    g3668089
NCBI GI
BLAST score
                    474
                    1.0e-47
E value
Match length
                    134
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                    236350
```

34260

uC-gsflnu33B060a08b1

BLASTX

g4063748



```
BLAST score
                   277
E value
                   1.0e-24
Match length
                  77
% identity
                   62
NCBI Description (AC005851) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236351
Seq. ID
                  uC-gsflnu33B060b02b1
Method
                  BLASTX
NCBI GI
                   q541951
BLAST score
                  318
E value
                   2.0e-29
Match length
                   66
                   49
% identity
NCBI Description
                  SPCP2 protein - soybean >gi 310578 (L12258) nodulin-26
                   [Glycine max]
                  236352
Seq. No.
Seq. ID
                  uC-gsflnu33B060b12b1
Method
                  BLASTX
NCBI GI
                   g1076662
BLAST score
                   506
E value
                   2.0e-51
Match length
                  125
                   83
% identity
NCBI Description
                  H+-transporting ATPase (EC 3.6.1.35) (clone PHA1) - potato
                  >gi 435003 emb CAA54046 (X76536) H(+)-transporting ATPase
                   [Solanum tuberosum]
Seq. No.
                   236353
Seq. ID
                  uC-gsflnu33B060d04b1
Method
                  BLASTX
NCBI GI
                  g2392769
BLAST score
                  197
E value
                  2.0e-15
Match length
                  83
                   52
% identity
                  (AC002534) putative histone deacetylase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  236354
Seq. ID
                  uC-gsflnu33B060f06b1
Method
                  BLASTX
NCBI GI
                  g2245038
BLAST score
                  155
E value
                  3.0e-10
                  98
Match length
                  39
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  236355
Seq. ID
                  uC-gsflnu33B060f10b1
```

Method BLASTX
NCBI GI g4455217
BLAST score 459
E value 5.0e-46
Match length 122

% identity NCBI Description (AL035440) Avr9 elicitor response like protein [Arabidopsis thaliana] Seq. No. 236356 Seq. ID uC-gsflnu33B060f12b1 Method BLASTX NCBI GI g167367 BLAST score 227 E value 7.0e-19 Match length 44 % identity 100 NCBI Description (L08199) peroxidase [Gossypium hirsutum] Seq. No. 236357 Seq. ID uC-gsflnu33B060g10b1

Method BLASTX NCBI GI g4105696 BLAST score 576 E value 1.0e-59 Match length 116 % identity 93

NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]

Seq. No. 236358 Seq. ID uC-qsflnu33B060h07b1 Method BLASTX NCBI GI g130972 BLAST score 138 E value 7.0e-09

Match length 61 % identity 49

NCBI Description PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi\_99952 pir S10186 pyrroline-5-carboxylate reductase (EC

1.5.1.2) - soybean >gi\_18724\_emb\_CAA34401\_ (X16352)

pyrroline-5-carboxylate reductase (AA 1- 274) [Glycine max]

236359 Seq. No.

Seq. ID uC-gsflnu33B061a07b1

BLASTX Method NCBI GI g1915974 BLAST score 254 E value 3.0e-22 Match length 58 % identity 84

NCBI Description (U62329) fructokinase [Lycopersicon esculentum] >gi 2102693

(U64818) fructokinase [Lycopersicon esculentum]

Seq. No. 236360

uC-gsflnu33B061b12b1 Seq. ID

Method BLASTX NCBI GI g135915 BLAST score 224 E value 1.0e-18 Match length 76 % identity

NCBI Description PATHOGENESIS-RELATED PROTEIN 5 PRECURSOR (PR-5)

Match length

% identity

168

43



>gi\_322559\_pir\_\_JQ1695 pathogenesis-related protein 5
precursor - Arabidopsis thaliana >gi\_166865 (M90510)
thaumatin-like protein [Arabidopsis thaliana] >gi\_1448919
(L78079) thaumatin-like protein [Arabidopsis thaliana]

Seq. No. 236361 Seq. ID uC-gsflnu33B061c02b1 BLASTX Method NCBI GI g3482919 BLAST score 115 2.0e-11 E value Match length 84 % identity 48 NCBI Description (AC003970) Putative protein kinase [Arabidopsis thaliana] 236362 Seq. No. Seq. ID uC-gsflnu33B061c07b1 BLASTX Method NCBI GI g2342679 BLAST score 484 E value 9.0e-49 138 Match length 72 % identity (AC000106) Similar to Vicia sativa ENBP1 (gb X95995). NCBI Description [Arabidopsis thaliana] 236363 Seq. No. uC-gsflnu33B061c11b1 Seq. ID Method BLASTX NCBI GI g4490736 BLAST score 233 E value 5.0e-20 Match length 53 % identity 81 NCBI Description (AL035708) putative protein [Arabidopsis thaliana] 236364 Seq. No. Seq. ID uC-gsflnu33B061d07b1 BLASTX Method NCBI GI q3776005 BLAST score 459 E value 7.0e-46Match length 128 % identity 75 NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana] 236365 Seq. No. Seq. ID uC-gsflnu33B061d09b1 Method BLASTX NCBI GI g1706588 BLAST score 317 E value 4.0e-29

NCBI Description PROBABLE ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA)

>gi\_3876061\_emb\_CAA96631\_ (Z72507) similar to elongation factor 1-gamma; cDNA EST EMBL:M75877 comes from this gene;

NCBI GI

E value

BLAST score



cDNA EST EMBL:M88933 comes from this gene; cDNA EST EMBL:D34157 comes from this gene; cDNA EST EMBL:D37196 comes from this gene; cDNA EST

236366 Seq. No. uC-gsflnu33B061e04b1 Seq. ID BLASTX Method NCBI GI g1170938 BLAST score 431 2.0e-42 E value Match length 86 91 % identity S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi\_481566\_pir\_\_S38875 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi\_429106\_emb\_CAA80866\_ (Z24742) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum] 236367 Seq. No. uC-gsflnu33B061f04b1 Seq. ID Method BLASTX NCBI GI q3122914 BLAST score 611 E value 1.0e-63 135 Match length % identity 84 VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) NCBI Description >qi 1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana] 236368 Seq. No. uC-gsflnu33B061g05b1 Seq. ID Method BLASTX NCBI GI q1652217 BLAST score 186 E value 8.0e-14 Match length 67 % identity NCBI Description (D90903) hypothetical protein [Synechocystis sp.] Seq. No. Seq. ID uC-gsflnu33B061h11b1 Method BLASTX NCBI GI q2160166 BLAST score 318 E value 3.0e-29 Match length 143 % identity 50 NCBI Description (AC000132) No definition line found [Arabidopsis thaliana] 236370 Seq. No. uC-qsflnu33B062a06b1 Seq. ID Method BLASTX

g3941480

236 7.0e-20



```
104
Match length
% identity
                  53
                  (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                  236371
Seq. No.
                  uC-gsflnu33B062a11b1
Seq. ID
                  BLASTX
Method
                  g3941480
NCBI GI
                  361
BLAST score
                  6.0e - 35
E value
                  71
Match length
% identity
                  93
                  (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                  236372
Seq. No.
                  uC-gsflnu33B062b02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2583110
BLAST score
                  162
E value
                  4.0e-11
                  62
Match length
                  60
% identity
                  (AC002387) unknown protein [Arabidopsis thaliana]
NCBI Description
                  236373
Seq. No.
                  uC-gsflnu33B062b07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539292
                   337
BLAST score
                   7.0e-32
E value
                  71
Match length
                  86
% identity
                  (AL049480) putative ribosomal protein S10 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   236374
                  uC-gsflnu33B062b10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q544075
BLAST score
                   304
E value
                   1.0e-42
Match length
                  111
                   53
% identity
                  COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
NCBI Description
                   (P102) >gi_486768_pir__S35312 coatomer complex chain beta'
                   - bovine >gi_312732_emb_CAA51285_ (X72756) beta prime cop
                   [Bos taurus]
Seq. No.
                   236375
```

Seq. ID uC-gsflnu33B062c12b1

Method BLASTX
NCBI GI g860712
BLAST score 193
E value 6.0e-30
Match length 86



% identity (U28735) coded for by C. elegans cDNA cm06e4; coded for by NCBI Description C. elegans cDNA CEESP39F; coded for by C. elegans cDNA CEESR26F; coded for by C. elegans cDNA CEESX83F; coded for by C. elegans cDNA yk16e9.3; coded for by C. elegans cDNA yk16e9.5; c 236376 Seq. No. uC-gsflnu33B062d01b1 Seq. ID Method BLASTX NCBI GI q3415126 BLAST score 181 1.0e-13 E value Match length 91 41 % identity (AF081678) phenylcoumaran benzylic ether reductase [Pinus NCBI Description taedal 236377 Seq. No. uC-gsflnu33B062e01b1 Seq. ID Method BLASTX NCBI GI g1050849 BLAST score 204 E value 4.0e-16 Match length 110 40 % identity (X83742) MAP kinase phosphatase [Xenopus laevis] NCBI Description 236378 Seq. No. uC-qsflnu33B062f02b1 Seq. ID Method BLASTX NCBI GI g4263522 261 BLAST score 6.0e-23 E value Match length 97 % identity 25 NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana] Seq. No. 236379 Seq. ID uC-qsflnu33B062f04b1 Method BLASTX NCBI GI g2369714 BLAST score 143 E value 5.0e-09 Match length 36 % identity NCBI Description (Z97178) elongation factor 2 [Beta vulgaris] Seq. No. 236380 Seq. ID uC-gsflnu33B062h01b1 Method BLASTX NCBI GI g3005576 BLAST score 176

E value 7.0e-28 Match length 89 % identity

NCBI Description (AF047718) putative high affinity nitrate transporter;



```
GmNRT2 [Glycine max]
Seq. No.
                  236381
Seq. ID
                  uC-gsflnu33B062h07b1
Method
                  BLASTX
NCBI GI
                  g4559380
BLAST score
                  349
                  3.0e-33
E value
Match length
                  99
% identity
                  63
NCBI Description (AC006526) putative auxin-responsive GH3 protein
                  [Arabidopsis thaliana]
                  236382
Seq. No.
Seq. ID
                  uC-gsflnu33B063a04b1
Method
                  BLASTX
NCBI GI
                  g3152585
BLAST score
                  224
E value
                  2.0e-18
Match length
                  97
                  55
% identity
```

NCBI Description (AC002986) Contains similarity to auxin-induced protein TM018A10.6 from A. thaliana BAC gb AF013294. [Arabidopsis

thaliana]

Seq. No. 236383

Seq. ID uC-gsflnu33B063b10b1

Method BLASTX
NCBI GI g3250675
BLAST score 368
E value 9.0e-42
Match length 124
% identity 65

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 236384

Seq. ID uC-gsflnu33B063c05b1

Method BLASTX
NCBI GI g1174199
BLAST score 189
E value 3.0e-14
Match length 76
% identity 55

NCBI Description (U44760) S25-PR6 [Nicotiana tabacum]

Seq. No. 236385

Seq. ID uC-qsflnu33B063e03b1

Method BLASTX
NCBI GI g1402912
BLAST score 470
E value 4.0e-47
Match length 121
% identity 74

NCBI Description (X98317) peroxidase [Arabidopsis thaliana]

Seq. No. 236386

Seq. ID uC-qsflnu33B063f11b1

E value

Match length

% identity

1.0e-12

63

54



```
Method
                  BLASTX
NCBI GI
                  g4454025
BLAST score
                  327
E value
                  2.0e-30
                  125
Match length
% identity
                  48
NCBI Description (AL035394) putative cellulase [Arabidopsis thaliana]
Seq. No.
                  236387
Seq. ID
                  uC-gsflnu33B063f12b1
Method
                  BLASTX
NCBI GI
                  g4522005
BLAST score
                  180
E value
                   4.0e-13
Match length
                  136
% identity
                  33
NCBI Description (AC007069) putative reverse transcriptase [Arabidopsis
                  thaliana]
                  236388
Seq. No.
Seq. ID
                  uC-gsflnu33B063g02b1
Method
                  BLASTX
NCBI GI
                  g4097579
BLAST score
                  257
E value
                  2.0e-22
                  72
Match length
% identity
                   68
NCBI Description (U64922) NTGP1 [Nicotiana tabacum]
Seq. No.
                  236389
Seq. ID
                  uC-gsflnu33B063g10b1
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  203
E value
                  6.0e-16
Match length
                  46
                  80
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236390
Seq. ID
                  uC-gsflnu33B063h02b1
Method
                  BLASTX
NCBI GI
                  g166410
BLAST score
                  164
E value
                  3.0e-19
Match length
                  64
% identity
                  69
NCBI Description (L07291) Alfin-1 [Medicago sativa]
Seq. No.
                  236391
Seq. ID
                  uC-gsflnu33B063h03b1
Method
                  BLASTX
NCBI GI
                  g4263517
BLAST score
                  146
```

(AC004044) similar to PHZF, catalyzing the hydroxylation of NCBI Description phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana] 236392 Seq. No. uC-gsflnu33B064b01b1 Seq. ID Method BLASTX NCBI GI q3805956 BLAST score 266 E value 3.0e-29 Match length 72 89 % identity (Y13769) laccase [Populus balsamifera subsp. trichocarpa] NCBI Description 236393 Seq. No. uC-gsflnu33B064b09b1

Seq. ID BLASTX Method g2980795 NCBI GI BLAST score 262 E value 4.0e-23

86 Match length 58 % identity

(AL022197) putative protein [Arabidopsis thaliana] NCBI Description

236394 Seq. No.

uC-gsflnu33B064c01b1 Seq. ID

Method BLASTX NCBI GI q2459440 BLAST score 434 E value 5.0e-43

129 Match length % identity 64

(AC002332) putative receptor kinase [Arabidopsis thaliana] NCBI Description

Seq. No. 236395

Seq. ID uC-qsflnu33B064d12b1

Method BLASTX NCBI GI q4371285 BLAST score 194 E value 6.0e-15 Match length 95 % identity 48

(AC006260) hypothetical protein [Arabidopsis thaliana] NCBI Description

236396 Seq. No.

Seq. ID uC-gsflnu33B064e01b1

Method BLASTX NCBI GI q3249105 BLAST score 237 E value 2.0e-20 Match length 68 % identity 69

(AC003114) Contains similarity to protein phosphatase 2C NCBI Description (ABI1) gb\_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 236397

NCBI Description



```
uC-qsflnu33B064e07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2738982
BLAST score
                  421
E value
                  2.0e-41
Match length
                  137
% identity
                  61
NCBI Description
                 (AF022157) CYP71A10 [Glycine max]
Seq. No.
                  236398
Seq. ID
                  uC-qsflnu33B064f01b1
                  BLASTX
Method
NCBI GI
                  g2911067
BLAST score
                  446
E value
                  2.0e-44
Match length
                  100
% identity
                  86
                  (AL021960) UV-damaged DNA-binding protein-like
NCBI Description
                  [Arabidopsis thaliana]
                  236399
Seq. No.
Seq. ID
                  uC-gsflnu33B064g04b1
                  BLASTX
Method
NCBI GI
                  q1488255
                  323
BLAST score
                  1.0e-30
E value
                  75
Match length
% identity
                  88
                  (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
NCBI Description
                  >gi 2961381_emb_CAA18128_ (AL022141) ferulate-5-hydroxylase
                  (FAH1) [Arabidopsis thaliana] >gi_3925365 (AF068574)
                  ferulate-5-hydroxylase [Arabidopsis thaliana]
                  236400
Seq. No.
Seq. ID
                  uC-qsflnu33B064g07b1
                  BLASTX
Method
NCBI GI
                  q1730057
BLAST score
                  173
E value
                  2.0e-12
Match length
                  41
                  73
% identity
                 PROBABLE SERINE/THREONINE-PROTEIN KINASE YNR047W
NCBI Description
                  >gi 2131975 pir S63378 hypothetical protein YNR047w -
                  yeast (Saccharomyces cerevisiae) >gi 1302558 emb CAA96328_
                  (Z71662) ORF YNR047w [Saccharomyces cerevisiae]
                  236401
Seq. No.
Seq. ID
                  uC-gsflnu33B064g11b1
Method
                  BLASTX
NCBI GI
                  g2388994
BLAST score
                  401
E value
                  3.0e-39
Match length
                  118
% identity
```

[Schizosaccharomyces pombe]

(Z98981) hypothetical gtp-binding protein associated



```
Seq. No.
                  236402
                  uC-gsflnu33B064h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501182
BLAST score
                  349
E value
                  2.0e-40
Match length
                  111
% identity
                  65
                  OSMOTIN-LIKE PROTEIN PRECURSOR >gi 2129934 pir JC5237
NCBI Description
                  osmotin-like protein - tomato >gi 1220537 (L76632)
                  osmotin-like protein [Lycopersicon esculentum]
                  236403
Seq. No.
                  uC-gsflnu33B066b08b1
```

Seq. ID

Method BLASTX NCBI GI g129692 BLAST score 695 E value 1.0e-73 Match length 145 95 % identity

NCBI Description PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN)

Seq. No. Seq. ID uC-gsflnu33B066c07b1 BLASTX Method NCBI GI q4263782 BLAST score 152 E value 7.0e-10 47 Match length 57 % identity

NCBI Description (AC006068) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236405 Seq. ID

uC-gsflnu33B066c12b1

236404

BLASTX Method NCBI GI q2137308 BLAST score 377 E value 2.0e-36 Match length 102 % identity 36

NCBI Description G protein beta subuit like - mouse >gi 475012 dbj BAA06185

(D29802) G protein beta subuit like [Mus musculus]

Seq. No. 236406

uC-gsflnu33B066d03b1 Seq. ID

BLASTX Method q1076634 NCBI GI BLAST score 287 E value 3.0e-26 Match length 76 % identity 68

NCBI Description protein-serine/threonine kinase NPK15 - common tobacco

>gi 505146 dbj BAA06538 (D31737) protein-serine/threonine

kinase [Nicotiana tabacum]

236407 Seq. No.

Seq. ID uC-gsflnu33B066d04b1

BLAST score

Match length

E value

249

53

3.0e-21



```
Method
                    BLASTX
 NCBI GI
                    g4512670
 BLAST score
                    216
                    2.0e-17
 E value
                   77
 Match length
                    44
 % identity
 NCBI Description (AC006931) putative cytochrome P450 [Arabidopsis thaliana]
                    236408
 Seq. No.
 Seq. ID
                   uC-gsflnu33B066e05b1
                   BLASTX
 Method
 NCBI GI
                    g2398523
 BLAST score
                   220
 E value
                    6.0e-18
 Match length
                    88
                    61
 % identity
 NCBI Description (Y13721) Transcription factor [Arabidopsis thaliana]
                    236409
 Seq. No.
 Seq. ID
                   uC-gsflnu33B066f02b1
Method
                   BLASTX
 NCBI GI
                    q3355780
 BLAST score
                   150
 E value
                    8.0e-10
                   28
 Match length
                    86
 % identity
 NCBI Description (AJ004997) expansin18 [Lycopersicon esculentum]
 Seq. No.
                    236410
 Seq. ID
                    uC-gsflnu33B066f08b1
 Method
                    BLASTX
 NCBI GI
                    g2522227
 BLAST score
                    149
 E value
                    2.0e-09
 Match length
                   79
                    43
 % identity
 NCBI Description (AB007466) retrotransposon-like gene; the first amino acid
                    was determined to be glycine [Vicia faba]
 Seq. No.
                    236411
 Seq. ID
                    uC-gsflnu33B066g12b1
 Method
                    BLASTX
 NCBI GI
                    g4539292
 BLAST score
                    452
 E value
                    4.0e-45
 Match length
                    96
% identity
 NCBI Description
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
                    thaliana]
 Seq. No.
                    236412
 Seq. ID
                    uC-gsflnu33B066h01b1
 Method
                    BLASTX
 NCBI GI
                    g3947719
```



% identity NCBI Description (AJ012653) ribosomal protein S28 [Prunus persica] >gi 3947721 emb CAA10102 (AJ012654) ribosomal protein S28 [Prunus persica] >gi 3947723 emb CAA10103 (AJ012655) ribosomal protein S28 [Prunus persica] Seq. No. 236413 uC-gsflnu33B066h08b1 Seq. ID BLASTXMethod NCBI GI g3250697 BLAST score 252 7.0e-22 E value 56 Match length 82 % identity NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

236414 Seq. No. Seq. ID uC-gsflnu33B066h09b1 Method BLASTX NCBI GI g3335347 BLAST score 479 2.0e-48 E value

Match length 104 % identity 77

NCBI Description (AC004512) Contains similarity to ARI, RING finger protein gb X98309 from Drosophila melanogaster. ESTs gb T44383, gb W43120, gb N65868, gb H36013, gb AA042241, gb T76869 and gb\_AA042359 come from this gene. [Arabidopsis thaliana]

Seq. No. 236415

Seq. ID uC-gsflnu33B068e01b1

Method BLASTX NCBI GI g1518540 BLAST score 615 E value 3.0e-64 Match length 124 % identity 89

NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

236416 Seq. No.

uC-gsflnu33B068e12b1 Seq. ID

Method BLASTX NCBI GI g584893 BLAST score 182 E value 5.0e-14 Match length 50 % identity 66 -

SERINE CARBOXYPEPTIDASE III PRECURSOR NCBI Description

>gi 283002 pir S22530 carboxypeptidase III (EC 3.4.16.-) -

rice >gi\_218153\_dbj\_BAA01757\_ (D10985) serine

carboxypeptidase III [Oryza sativa]

Seq. No. 236417

Seq. ID uC-gsflnu33B068f01b1

Method BLASTX NCBI GI g710626 BLAST score 149



E value 1.0e-09 Match length 47 % identity 55

NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi\_3241941

(AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis

thaliana]

Seq. No. 236418

Seq. ID uC-gsflnu33B068g09b1

Method BLASTX
NCBI GI g2564249
BLAST score 208
E value 2.0e-16
Match length 84
% identity 50

NCBI Description (Y08686) serine palmitoyltransferase, subunit II [Homo

sapiens] >gi\_3043576\_dbj\_BAA25452\_ (AB011098) KIAA0526
protein [Homo sapiens] >gi\_4186182 (AF111168) serine
palmitoyl transferase, subunit II [Homo sapiens]

Seq. No. 236419

Seq. ID uC-gsflnu33B070c07b1

Method BLASTX
NCBI GI g3063442
BLAST score 180
E value 3.0e-13
Match length 77
% identity 52

NCBI Description (AC003981) F22013.6 [Arabidopsis thaliana]

Seq. No. 236420

Seq. ID uC-gsflnu33B070d10b1

Method BLASTX
NCBI GI 9464863
BLAST score 303
E value 3.0e-28
Match length 65
% identity 94

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 8 (TAT-BINDING PROTEIN

<code>HOMOLOG 10) >gi\_422297\_pir\_\_ JN0610</code> probable transcription factor <code>DdTBP10 - slime mold (Dictyostelium discoideum) (fragment) >gi\_290057 (L16579) HIV1 TAT-binding protein</code>

[Dictyostelium discoideum]

Seq. No. 236421

Seq. ID uC-gsflnu33B070f12b1

Method BLASTX
NCBI GI g3980407
BLAST score 192
E value 9.0e-23
Match length 122
% identity 48

NCBI Description (AC004561) putative receptor-like protein kinase

[Arabidopsis thaliana]

Seq. No. 236422



```
uC-gsflnu33B070g06b1
  Seq. ID
                    BLASTX
 Method
                    g3335366
 NCBI GI
                    245
 BLAST score
                    5.0e-21
 E value
                    69
 Match length
                    68
  % identity
 NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    236423
                    uC-gsflnu33B071a03b1
 Seq. ID
                    {\tt BLASTX}
 Method
 NCBI GI
                    g2623304
  BLAST score
                    285
  E value
                    2.0e-25
 Match length
                    163
  % identity
                    39
                    (AC002409) similar to Medicago nodulin N21 [Arabidopsis
 NCBI Description
                    thaliana]
  Seq. No.
                    236424
  Seq. ID
                    uC-gsflnu33B071b01b1
 Method
                    BLASTX
  NCBI GI
                    g2760832

→ BLAST score

                    483
  E value
                    1.0e-48
 Match length
                    150
  % identity
                     61
  NCBI Description (AC003105) similar to barley ids-4 gene product
                     [Arabidopsis thaliana]
                     236425
  Seq. No.
                    uC-gsflnu33B071b10b1
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                    q4102600
                    190
  BLAST score
                    2.0e-14
  E value
                    54
  Match length
  % identity
                     67
  NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]
                     236426
  Seq. No.
  Seq. ID
                    uC-gsflnu33B071b11b1
                    BLASTX
  Method
  NCBI GI
                     g4455182
  BLAST score
                     423
                     1.0e-41
  E value
                    142
  Match length
                     58
  % identity
  NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
                     236427
  Seq. No.
  Seq. ID
                     uC-gsflnu33B071c01b1
  Method
                    BLASTX
  NCBI GI
                     g3043432
```

34275

180

1.0e-13

BLAST score

E value



```
Match length
                  35
% identity
NCBI Description (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]
                  236428
Seq. No.
                  uC-gsflnu33B071d08b1
Seq. ID.
                  BLASTX
Method
NCBI GI
                  q4102839
BLAST score
                  240
E value
                  3.0e-27
Match length
                  148
                  47
% identity
NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]
                  236429
Seq. No.
                  uC-gsflnu33B071e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g531389
                  138
BLAST score
E value
                  2.0e-10
Match length
                  70
% identity
                  51
NCBI Description (U12626) copia-like retrotransposon Hopscotch polyprotein
                  [Zea mays]
                  236430
Seq. No.
Seq. ID
                  uC-gsflnu33B071f01b1
                  BLASTX
Method
NCBI GI
                  g3452263
                  155
BLAST score
E value
                  3.0e-10
                  31
Match length
                  90
% identity
NCBI Description (AF035936) phosphatidylinositol 4-kinase; PI4K [Arabidopsis
                  thaliana]
                  236431
Seq. No.
                  uC-gsflnu33B071h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2541876
BLAST score
                  177
                  6.0e-13
E value
Match length
                  92
% identity
                  45
NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein
                  [Nicotiana tabacum]
                  236432
Seq. No.
Seq. ID
                  uC-gsflnu33B071h10b1
                  BLASTX
Method
NCBI GI
                  q3492806
BLAST score
                  403
E value
                  2.0e-39
Match length
                  103
% identity
                  77
                  (AJ225045) adventitious rooting related oxygenase [Malus
NCBI Description
```

domestica]



```
236433
Seq. No.
Seq. ID
                  uC-gsflnu33B072a01b1
Method
                  BLASTX
NCBI GI
                  g2982434
BLAST score
                  509
E value
                  8.0e-52
Match length
                  128
                  70
% identity
NCBI Description
                 (AL022224) putative protein [Arabidopsis thaliana]
                  236434
Seq. No.
Seq. ID
                  uC-qsflnu33B072b09b1
Method
                  BLASTX
NCBI GI
                  g3986289
BLAST score
                  638
E value
                  6.0e-67
Match length
                  132
% identity
                  86
NCBI Description
                  (AB017357) L-Galactono-1,4-lactone dehydrogenase [Ipomoea
                  batatas]
Seq. No.
                  236435
Seq. ID
                  uC-gsflnu33B072c05b1
Method
                  BLASTX
NCBI GI
                  q2194119
BLAST score
                  441
E value
                  7.0e-44
Match length
                  110
% identity
                  65
NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]
Seq. No.
                  236436
Seq. ID
                  uC-gsflnu33B072d06b1
Method
                  BLASTX
NCBI GI
                  g2443320
BLAST score
                  297
E value
                  6.0e-27
Match length
                  125
% identity
                  51
NCBI Description (D85597) polyprotein [Oryza australiensis]
Seq. No.
                  236437
Seq. ID
                  uC-gsflnu33B072g01b1
Method
                  BLASTX
NCBI GI
                  g3450889
BLAST score
                  196
E value
                  1.0e-15
Match length
                  72
% identity
                  62
NCBI Description
                 (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
Seq. No.
                  236438
```

Seq. ID uC-gsflnu33B073a09b1

Method BLASTX
NCBI GI g2749943
BLAST score 191



```
E value
                  4.0e-15
Match length
                  38
% identity
NCBI Description
                  (U71244) pathogenesis-related group 5 protein [Brassica
                  rapa]
                  236439
Seq. No.
Seq. ID
                  uC-gsflnu33B073c07b1
Method
                  {\tt BLASTX}
NCBI GI
                  g4193388
BLAST score
                  210
E value
                  2.0e-17
Match length
                  45
                  89
% identity
                 (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                  brasiliensis]
                  236440
Seq. No.
Seq. ID
                  uC-gsflnu33B073f06b1
Method
                  BLASTX
NCBI GI
                  q4531434
BLAST score
                  160
E value
                  2.0e-11
Match length
                  40
% identity
NCBI Description (AC006224) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236441
Seq. ID
                  uC-gsflnu33B074d05b1
Method
                  BLASTX
NCBI GI
                  g2129597
BLAST score
                  457
E value
                  9.0e-46
Match length
                  93
% identity
                  92
                  glutamate dehydrogenase 1 - Arabidopsis thaliana
NCBI Description
                  >gi 1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis
                  thaliana] >gi 1293095 (U53527) glutamate dehydrogenase 1
                  [Arabidopsis thaliana]
Seq. No.
                  236442
                  uC-gsflnu33B074d11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432855
BLAST score
                  197
                  2.0e-15
E value
Match length
                  102
% identity
NCBI Description
                 (AC006300) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236443
```

Seq. ID uC-gsflnu33B074e06b1

Method BLASTX NCBI GI g2708743 BLAST score 144 E value 6.0e-09 Match length 139



```
% identity
                   (AC003952) putative Tal-1-like reverse transcriptase
NCBI Description
                   [Arabidopsis thaliana]
                   236444
Seq. No.
Seq. ID
                   uC-gsflnu33B074e07b1
                   BLASTX
Method
NCBI GI
                   g4539452
BLAST score
                   518
E value
                   6.0e-53
Match length
                   119
                   75
% identity
                  (AL049500) putative phosphoribosylanthranilate transferase
NCBI Description
                   [Arabidopsis thaliana]
                   236445
Seq. No.
Seq. ID
                   uC-gsflnu33B074g03b1
Method
                   BLASTX
NCBI GI
                   g2842478
BLAST score
                   356
                   5.0e-34
E value
Match length
                   112
% identity
                   65
                   (AL021749) receptor protein kinase like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No. Seq. ID
                   236446
                   uC-gsflnu33B074h01b1
                   BLASTX
Method
NCBI GI
                   g553111
BLAST score
                   146
E value
                   2.0e-09
Match length
                   112
% identity
                   24
NCBI Description (J03625) hydroproline-rich protein [Glycine max]
                   236447
Seq. No.
Seq. ID
                   uC-gsflnu33B074h03b1
Method
                   BLASTX
NCBI GI
                   g1666236
BLAST score
                   233
                   2.0e-19
E value
                   117
Match length
                   38
% identity
NCBI Description (U76261) unknown [Hordeum vulgare]
                   236448
Seq. No.
Seq. ID
                   uC-gsflnu33B074h05b1
Method
                   BLASTX
NCBI GI
                   q2618698
BLAST score
                   319
```

1.0e-29 E value Match length 124 % identity 53

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

236449 Seq. No.



```
uC-qsflnu33B074h07b1
Seq. ID
                  BLASTX
Method
                  g3695059
NCBI GI
                  283
BLAST score
                  3.0e-25
E value
Match length
                  81
                  73
% identity
                  (AF064787) rac GTPase activating protein 1 [Lotus .
NCBI Description
                  japonicus]
                  236450
Seq. No.
Seq. ID
                  uC-qsflnu33B074h12b1
                  BLASTX
Method
NCBI GI
                  q2760835
BLAST score
                  622
                  5.0e-65
E value
Match length
                  148
% identity
                  80
NCBI Description (AC003105) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236451
Seq. ID
                  uC-gsflnu33B075b03b1
Method
                  BLASTX
NCBI GI
                  q1707955
BLAST score
                  477
                  4.0e-48
E value
Match length
                  96
% identity
                  92
NCBI Description GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME 1
                   (GLUTAMATE--AMMONIA LIGASE) >gi 1134896_emb_CAA63981_
                   (X94320) glutamine synthetase [Vitis vinifera]
Seq. No.
                  236452
                  uC-gsflnu33B075b04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1361983
BLAST score
                  365
E value
                  4.0e-35
                  105
Match length
                  70
% identity
NCBI Description ARP protein - Arabidopsis thaliana >gi_886434 emb_CAA89858
                   (Z49776) ARP protein [Arabidopsis thaliana]
                  236453
Seq. No.
Seq. ID
                  uC-gsflnu33B075c06b1
                  BLASTX
Method
NCBI GI
                  g3142296
BLAST score
                  252
                  6.0e-22
E value
Match length
                  86
% identity
                   56
                  (AC002411) Contains similarity to hypothetical
NCBI Description
                  mitochondrial import receptor subunit gb_Z98597 from S.
                  pombe. ESTs gb T45575 and gb Z26435 and gb AA394576 come
```

Seq. No. 236454

from this gene. [Arabidopsis thaliana]



```
Seq. ID
                   uC-qsflnu33B075c08b1
Method
                   BLASTX
NCBI GI
                   q404688
BLAST score
                   154
E value
                   1.0e-10
Match length
                   58
                   47
% identity
NCBI Description
                  (L19074) cytochrome P450 [Catharanthus roseus]
                   236455
Seq. No.
Seq. ID
                   uC-gsflnu33B075c09b1
Method
                   BLASTX
NCBI GI
                   q3831438
BLAST score
                   138
E value
                   1.0e-08
Match length
                   47
% identity
                   64
                   (AC005819) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4415944_gb_AAD20174_ (AC006418) hypothetical protein
                   [Arabidopsis thaliana]
                   236456
Seq. No.
Seq. ID
                   uC-gsflnu33B075d11b1
Method
                   BLASTX
NCBI GI
                   q3776005
BLAST score
                   151
                   9.0e-10
E value
Match length
                  82
% identity
                   48
NCBI Description
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
                   236457
Seq. No.
Seq. ID
                   uC-gsflnu33B075e02b1
Method
                   BLASTX
NCBI GI
                   g140285
BLAST score
                   525
E value
                   1.0e-53
Match length
                   102
% identity
                   98
NCBI Description
                  HYPOTHETICAL 19 KD PROTEIN (ORF 168)
                   >gi 2924263 emb CAA77415 (Z00044) Ycf3 protein [Nicotiana
                   tabacum]
                   236458
Seq. No.
Seq. ID
                   uC-gsflnu33B075e11b1
Method
                   BLASTX
NCBI GI
                   g2129473
BLAST score
                   197
E value
                   1.0e-15
                  71
Match length
                   49
% identity
NCBI Description
                  arabinogalactan-like protein - loblolly pine >gi 607774
                   (U09556) arabinogalactan-like protein [Pinus taeda]
```

34281

236459

BLASTX

uC-gsflnu33B075f08b1

Seq. No. Seq. ID

Method

Method

NCBI GI

BLAST score

BLASTX

176

g3132475



```
NCBI GI
                  q2642428
BLAST score
                  298
                  5.0e-27
E value
Match length
                  118
% identity
                  48
                  (AC002391) unknown protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
                  236460
Seq. No.
                  uC-gsflnu33B075g04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2454629
                  272
BLAST score
                  1.0e-24
E value
Match length
                 62
% identity
                  82
NCBI Description
                  (AF019559) cytosolic glutamine synthetase; GS1 [Daucus
                  carota]
                  236461
Seq. No.
Seq. ID
                  uC-gsflnu33B075g09b1
Method
                  BLASTX
NCBI GI
                  g4539437
BLAST score
                  195
E value
                  5.0e-15
Match length
                  42
% identity
                  83
                  (AL049523) putative protein [Arabidopsis thaliana]
NCBI Description
                  236462
Seq. No.
                  uC-gsflnu33B075h04b1
Seq. ID
Method
                  BLASTX
                  g3250680
NCBI GI
BLAST score
                  513
E value
                  3.0e-52
Match length
                  121
% identity
                  82
NCBI Description
                  (AL024486) aspartate kinase-homoserine dehydrogenase - like
                  protein [Arabidopsis thaliana]
Seq. No.
                  236463
Seq. ID
                  uC-gsflnu33B076e06b1
Method
                  BLASTX
NCBI GI
                  g1408471
BLAST score
                  181
E value
                   3.0e-13
Match length
                  40
% identity
                  (U48938) actin depolymerizing factor 1 [Arabidopsis
NCBI Description
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                  factor 1 [Arabidopsis thaliana]
                  236464
Seq. No.
Seq. ID
                  uC-gsflnu33B076e12b1
```



```
E value
                  1.0e-12
Match length
                  51
                  63
% identity
NCBI Description
                 (AC003096) similar to proline-rich protein [Arabidopsis
                  thaliana]
Seq. No.
                  236465
Seq. ID
                  uC-gsflnu33B076g05b1
                  BLASTX
Method
NCBI GI
                  g3935187
BLAST score
                  316
E value
                  1.0e-29
                  77
Match length
% identity
                  51
NCBI Description (AC004557) F17L21.30 [Arabidopsis thaliana]
Seq. No.
                  236466
Seq. ID
                  uC-gsflnu33B077h06b1
Method
                  BLASTX
NCBI GI
                  g1518540
BLAST score
                  359
E value
                  2.0e-34
Match length
                  77
% identity
                  88
NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                  236467
Seq. ID
                  uC-gsflnu33B078a02b1
Method
                  BLASTX
NCBI GI
                  g3914361
BLAST score
                  366
                  6.0e-35
E value
Match length
                  94
% identity
                  73
NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi_2281951_emb CAB06620 (Z84822) phospholipase D
                  [Nicotiana tabacum] -
Seq. No.
                  236468
Seq. ID
                  uC-gsflnu33B078a04b1
Method
                  BLASTX
NCBI GI
                  g3033375
BLAST score
                  223
E value
                  2.0e-18
Match length
                  89
% identity
NCBI Description
                  thaliana]
```

(AC004238) putative berberine bridge enzyme [Arabidopsis

Seq. No. 236469

Seq. ID uC-gsflnu33B078b03b1

Method BLASTX NCBI GI g3158474 BLAST score 618 E value 2.0e-64 Match length 134



% identity

NCBI Description (AF067184) aquaporin 1 [Samanea saman]

Seq. No.

236470

Seq. ID

uC-gsflnu33B078d02b1

Method NCBI GI BLASTX g2462762

BLAST score

292

E value Match length 2.0e-26 115

% identity

56

NCBI Description

(AC002292) Highly similar to auxin-induced protein

(aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.

236471

Seq. ID

uC-gsflnu33B078d04b1

Method NCBI GI BLASTX g731086

BLAST score

159

E value Match length

1.0e-10 115

% identity

37

NCBI Description UV-INDUCED PROTEIN UVI22 >gi\_629909\_pir S47147 uvi22 protein - fission yeast (Schizosaccharomyces pombe)

>qi 1076930 pir JC2442 UV inducible protein, UV122 -

fission yeast (Schizosaccharomyces pombe) >gi 499199 emb CAA84069 (Z34299) uvi22

[Schizosaccharomyces pombe] >gi 3184086\_emb\_CAA19342 (AL023781) uv-induced protein uvi22 [Schizosaccharomyces

pombe]

Seq. No.

236472

Seq. ID uC-gsflnu33B078d07b1

67

Method BLASTX NCBI GI q1709804 BLAST score 496 E value 4.0e-50 Match length 140

% identity

NCBI Description 26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44) >gi 1045497 (U36395) conserved

ATPase domain protein 44 [Spermophilus tridecemlineatus] >gi 2213932 (AF006305) 26S proteasome regulatory subunit

[Homo sapiens]

Seq. No.

236473

Seq. ID

uC-gsflnu33B078e09b1 BLASTX

Method NCBI GI

q2909781

BLAST score

139

E value

6.0e-17

Match length % identity

78

62

NCBI Description

(AF020288) MgATP-energized glutathione S-conjugate pump

[Arabidopsis thaliana]

Seq. No.



```
uC-gsflnu33B078e10b1
Seq. ID
                  BLASTX
Method
                  g4056479
NCBI GI
                  302
BLAST score
                  2.0e-27
E value
                  71
Match length
                  77
% identity
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236475
                  uC-gsflnu33B078f02b1
Seq. ID
Method
                  BLASTX
                  g3776559
NCBI GI
BLAST score
                  513
                  3.0e-52
E value
Match length
                  129
% identity
                  71
                  (AC005388) Strong similarity to gene F14J9.26 gi_3482933
NCBI Description
                  cdc2 protein kinase homolog from A. thaliana BAC
                  gb AC003970. ESTs gb Z35332 and gb_F19907 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  236476
                  uC-gsflnu33B078f12b1
Seq. ID
                  BLASTX
Method
                  g3915826
NCBI GI
BLAST score
                  154
                  3.0e-10
E value
                  41
Match length
                  76
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
                  236477
Seq. No.
Seq. ID
                  uC-gsflnu33B078g03b1
Method
                  BLASTX
                  g3868758
NCBI GI
BLAST score
                  467
E value
                  8.0e-47
                  131
Match length
% identity
                  63
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                  236478
Seq. No.
Seq. ID
                  uC-gsflnu33B078g12b1
Method
                  BLASTX
NCBI GI
                  g1703380
BLAST score
                  243
E value
                  1.0e-20
                  45
Match length
                  100
% identity
NCBI Description ADP-RIBOSYLATION FACTOR >gi_1132483 dbj_BAA04607 (D17760)
                  ADP-ribosylation factor [Oryza sativa]
```

236479 Seq. No.

Seq. ID uC-gsflnu33B078h07b1

BLASTX Method NCBI GI g4468986

NCBI Description



```
BLAST score
                    2.0e-23
 E value
Match length
                    106
                    53
 % identity
 NCBI Description (AL035605) putative protein [Arabidopsis thaliana]
 Seq. No.
                    236480
                    uC-gsflnu33B078h10b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3559811
 BLAST score
                    246
 E value
                    7.0e-21
                    60
 Match length
                    78
 % identity
 NCBI Description (AJ010735) grl-protein [Arabidopsis thaliana]
 Seq. No.
                    236481
                    uC-gsflnu33B079d01b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2586123
 BLAST score
                    463
                    2.0e-46
 E value
 Match length
                    100
                    87
 % identity
 NCBI Description (U89511) b-keto acyl reductase [Allium porrum]
                    236482
 Seq. No.
                    uC-gsflnu33B079d05b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4580461
 BLAST score
                    286
 E value
                    3.0e-26
 Match length
                    59
 % identity
                    92
 NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
                    236483
 Seq. No.
 Seq. ID
                    uC-gsflnu33B079e06b1
 Method
                    BLASTX
 NCBI GI
                    g117188
 BLAST score
                    411
                    2.0e-40
 E value
 Match length
                    127
 % identity
                    57
 NCBI Description CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2)
                    >gi 81423 pir A35867 cytochrome P450 71A1 - avocado
                    236484
 Seq. No.
 Seq. ID
                    uC-gsflnu33B079f03b1
 Method
                    BLASTX
 NCBI GI
                    q123554
 BLAST score
                    142
 E value
                    3.0e-09
 Match length
                    33
 % identity
                    79
```

34286

18.1 KD CLASS I HEAT SHOCK PROTEIN >gi 99978 pir S16248

heat shock protein 18 (clone pMsHsp18.1) - alfalfa



(fragment) >gi\_19616\_emb\_CAA41546\_ (X58710) heat shock
protein [Medicago sativa]

Seq. No. 236485

Seq. ID uC-gsflnu33B080c08b1

Method BLASTX
NCBI GI g3123745
BLAST score 280
E value 8.0e-25
Match length 132
% identity 42

NCBI Description (AB013447) aluminum-induced [Brassica napus]

Seq. No. 236486

Seq. ID uC-gsflnu33B080c09b1

Method BLASTX
NCBI GI g3334299
BLAST score 267
E value 1.0e-23
Match length 63
% identity 87

NCBI Description PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE

COMPLEX ALPHA SUBUNIT) >gi\_2315211\_emb\_CAA74725\_ (Y14339)

proteasome alpha subunit [Lycopersicon esculentum]

Seq. No. 236487

Seq. ID uC-gsflnu33B080e12b1

Method BLASTX
NCBI GI g2253010
BLAST score 282
E value 9.0e-26
Match length 68

Match length 68 % identity 76

NCBI Description (Y14199) MAP3K delta-1 protein kinase [Arabidopsis

thaliana]

Seq. No. 236488

Seq. ID uC-qsflnu33B081b04b1

Method BLASTX
NCBI GI g2129675
BLAST score 545
E value 5.0e-56
Match length 127
% identity 81

NCBI Description probable chlorophyll synthetase G4 - Arabidopsis thaliana

>gi\_972938 (U19382) putative chlorophyll synthetase
[Arabidopsis thaliana] >gi\_3068709 (AF049236) putative

chlorophyll synthetase [Arabidopsis thaliana]

Seq. No. 236489

Seq. ID uC-gsflnu33B081c08b1

Method BLASTX
NCBI GI g3242717
BLAST score 238
E value 5.0e-20
Match length 98
% identity 56



NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana]

Seq. No. 236490

Seq. ID uC-gsflnu33B081e05b1

Method BLASTX
NCBI GI g2649749
BLAST score 160
E value 9.0e-11
Match length 131
% identity 36

NCBI Description (AE001045) proliferating-cell nucleolar antigen P120,

putative [Archaeoglobus fulgidus]

Seq. No. 236491

Seq. ID uC-gsflnu33B081f10b1

Method BLASTX
NCBI GI 94204278
BLAST score 179
E value 4.0e-13
Match length 122
% identity 35

NCBI Description (AC004146) putative Cytochrome P450 protein [Arabidopsis

thaliana]

Seq. No. 236492

Seq. ID uC-gsflnu33B081g08b1

Method BLASTX
NCBI GI g3080416
BLAST score 215
E value 3.0e-17
Match length 53
% identity 83

NCBI Description (AL022604) UDP-galactose transporter - like protein

[Arabidopsis thaliana]

Seq. No. 236493

Seq. ID uC-gsflnu33B081h05b1

Method BLASTX
NCBI GI g4115383
BLAST score 168
E value 3.0e-12
Match length 71
% identity 45

NCBI Description (AC005967) receptor-like protein kinase [Arabidopsis

thaliana]

Seq. No. 236494

Seq. ID uC-gsflnu33B082a08b1

Method BLASTX
NCBI GI g416641
BLAST score 253
E value 1.0e-21
Match length 52
% identity 85

NCBI Description INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG4

>gi\_287568\_dbj\_BAA03309 (D14413) ORF [Vigna radiata]

Seq. ID Method

NCBI GI



```
Seq. No.
                     236495
  Seq. ID
                     uC-gsflnu33B082a11b1
 Method
                     BLASTX
 NCBI GI
                     g1076387
 BLAST score
                     338
 E value
                     8.0e-32
 Match length
                     89
 % identity
                     69
 NCBI Description protein kinase homolog - Arabidopsis thaliana >gi_717180_emb_CAA55866_ (X79279) protein kinase homologous
                     to shaggy and glycogen synthase kinase-3 [Arabidopsis
                     thaliana]
                     236496
 Seq. No.
 Seq. ID
                     uC-gsflnu33B082c08b1
 Method
                     BLASTX
 NCBI GI
                     g1755166
 BLAST score
                     381
 E value
                     9.0e-37
 Match length
                     102
 % identity
                     74
 NCBI Description (U75194) germin-like protein [Arabidopsis thaliana]
 Seq. No.
                     236497
" Seq. ID
                     uC-gsflnu33B082d11b1
 Method
                     BLASTX
 NCBI GI
                     g1171579
 BLAST score
                     386
 E value
                     1.0e-46
 Match length
                     129
                     71
 % identity
 NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]
 Seq. No.
                     236498
 Seq. ID
                     uC-gsflnu33B082e10b1
 Method
                     BLASTX
 NCBI GI
                     q3337361
 BLAST score
                     431
 E value
                     8.0e-43
 Match length
                     99
 % identity
 NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
 Seq. No.
                     236499
 Seq. ID
                    uC-gsflnu33B082f11b1
 Method
                    BLASTX
 NCBI GI
                    q4220527
 BLAST score
                     611
 E value
                    1.0e-63
 Match length
                    131
 % identity
 NCBI Description
                    (AL035356) putative protein [Arabidopsis thaliana]
 Seq. No.
                    236500
```

34289

uC-gsflnu33B082g10b1

BLASTX

g2827548



BLAST score 222 E value 5.0e-28 Match length 137 % identity 50

NCBI Description (AL021635) cytochrome P450 - like protein [Arabidopsis

thaliana]

Seq. No. 236501

Seq. ID uC-gsflnu33B082g11b1

Method BLASTX
NCBI GI g1749596
BLAST score 169
E value 8.0e-12
Match length 42
% identity 69

NCBI Description (D89194) similar to Rat ATP citrate-lyase, SWISS-PROT

Accession Number P16638 [Schizosaccharomyces pombe]

Seq. No. 236502

Seq. ID uC-gsflnu33B082h02b1

Method BLASTX
NCBI GI g4539350
BLAST score 266
E value 3.0e-38
Match length 113
% identity 71

NCBI Description (AL035539) putative pectinesterase [Arabidopsis thaliana]

Seq. No. 236503

Seq. ID uC-gsflnu33B083a02b1

Method BLASTX
NCBI GI g4337189
BLAST score 237
E value 6.0e-20
Match length 74
% identity 55

NCBI Description (AC006403) putative calmodulin-binding protein [Arabidopsis

thaliana]

Seq. No. 236504

Seq. ID uC-gsflnu33B083a04b1

Method BLASTX
NCBI GI g2842477
BLAST score 237
E value 4.0e-20
Match length 72
% identity 65

NCBI Description (AL021749) copper-binding protein-like [Arabidopsis

thaliana]

Seq. No. 236505

Seq. ID uC-gsflnu33B083b03b1

Method BLASTX
NCBI GI g1076708
BLAST score 375
E value 4.0e-36
Match length 75



```
% identity
NCBI Description
                     seed tetraubiquitin - common sunflower
                     >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max]
>gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max]
>gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin
[Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092)
                     Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044)
                     putative polyubiquitin [Arabidopsis thaliana]
                     >gi_1096513_prf__2111434A tetraubiquitin [Helianthus
                     annuus]
                     236506
Seq. No.
Seq. ID
                     uC-qsflnu33B083b05b1
Method
                     BLASTX
NCBI GI
                     q1814401
BLAST score
                     402
                     2.0e-39
E value
Match length
                     100
                     69
% identity
                    (U84888) phosphoglucomutase [Mesembryanthemum crystallinum]
NCBI Description
                     236507
Seq. No.
Seq. ID
                     uC-qsflnu33B083e08b1
Method
                     BLASTX
NCBI GI
                     q3688170
BLAST score
                     278
                     8.0e-25
E value
Match length
                     92
% identity
NCBI Description (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                     236508
                     uC-gsflnu33B083e09b1
Seq. ID
Method
                     BLASTX
NCBI GI
                     q3668089
BLAST score
                     229
E value
                     5.0e-19
Match length
                     78
% identity
NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]
                     236509
Seq. No.
Seq. ID
                     uC-gsflnu33B084b09b1
                     BLASTX
Method
NCBI GI
                     g2459417
BLAST score
                     365
E value
                     9.0e-35
Match length
                     139
                     53
% identity
NCBI Description
                    (AC002332) putative pre-mRNA splicing factor PRP19
                     [Arabidopsis thaliana]
                     236510
Seq. No.
```

Seq. ID uC-gsflnu33B084c02b1

Method BLASTX NCBI GI g2245028 BLAST score 176



```
4.0e-13
E value
Match length
                     60
% identity
                     52
                    (Z97341) limonene cyclase [Arabidopsis thaliana]
NCBI Description
                     236511
Seq. No.
                     uC-gsflnu33B084c10b1
Seq. ID
Method
                     BLASTX
NCBI GI
                     g730645
BLAST score
                     516
E value
                     1.0e-52
Match length
                     111
                     90
% identity
                    40S RIBOSOMAL PROTEIN S15 >gi 629556 pir S43412 ribosomal
NCBI Description
                     protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_
                     (Z23161) ribosomal protein S15 [Arabidopsis thaliana]
                     >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs
                     gb R29788, gb ATTS0365 come from this gene. [Arabidopsis
                     thaliana]
Seq. No.
                     236512
                     uC-qsflnu33B084d03b1
Seq. ID
Method
                     BLASTX
NCBI GI
                     q4218011
BLAST score
                     150
E value
                     1.0e-09
Match length
                     53
% identity
                     (AC006135) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                     >gi_4309721_gb_AAD15491_ (AC006439) putative
serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.
                     236513
                     uC-qsflnu33B084e03b1
Seq. ID
                     BLASTX
Method
NCBI GI
                     q2739381
BLAST score
                     339
                     7.0e-32
E value
Match length
                     112
% identity
                     60
NCBI Description (AC002505) putative patatin [Arabidopsis thaliana]
                     236514
Seq. No.
Seq. ID
                     uC-gsflnu33B084e11b1
Method
                     BLASTX
NCBI GI
                     g2618684
BLAST score
                     309
                     3.0e-28
E value
                     95
Match length
% identity
                     62
```

(AC002510) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase [Arabidopsis

NCBI Description

thaliana] >gi\_3241947 (AC004625) putative UDP-N-acetylglucosamine--dolichyl-phosphate

% identity



N-acetylglucosaminephosphotransferase [Arabidopsis thaliana]

```
236515
Seq. No.
                  uC-gsflnu33B084f05b1
Seq. ID
                  BLASTX
Method
                  q4415938
NCBI GI
BLAST score
                  192
E value
                  4.0e-27
                  83
Match length
                  72
% identity
NCBI Description (AC006418) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236516
                  uC-gsflnu33B084f09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3759177
BLAST score
                  161
E value
                  6.0e-11
Match length
                  47
                  72
% identity
                  (AB018408) 3-phosphoserine phosphatase [Arabidopsis
NCBI Description
                  thaliana] >gi 3759179 dbj BAA33807_ (AB018409)
                  3-phosphoserin phosphatase [Arabidopsis thaliana]
                  236517
Seq. No.
                  uC-qsflnu33B084h06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3252815
BLAST score
                  290
                  4.0e-26
E value
                  74
Match length
                  78
% identity
NCBI Description (AC004705) vacuolar sorting receptor-like protein
                   [Arabidopsis thaliana] >gi 3810588 (AC005398) vacuolar
                  sorting receptor-like protein [Arabidopsis thaliana]
                  236518
Seq. No.
Seq. ID
                  uC-qsflnu33B085d05b1
Method
                  BLASTX
                  g4580461
NCBI GI
BLAST score
                  286
E value
                   3.0e-26
Match length
                  59
% identity
NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]
                  236519
Seq. No.
Seq. ID
                  uC-gsflnu33B085h03b1
                  BLASTX
Method
                  g3080447
NCBI GI
                  161
BLAST score
E value
                   5.0e-20
                  117
Match length
```

NCBI Description (AL022605) putative protein [Arabidopsis thaliana]



```
236520
Seq. No.
                  uC-gsflnu33B085h07b1
Seq. ID
Method
                  BLASTX
                  g3935168
NCBI GI
BLAST score
                   250
E value
                   2.0e-21
                  96
Match length
% identity
                   58
NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]
Seq. No.
                   236521
                  uC-gsflnu33B088a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3176684
BLAST score
                   360
E value
                   2.0e-34
Match length
                   107
% identity
                   67
NCBI Description
                  (AC003671) Contains similarity to equilibratiave nucleoside
                   transporter 1 gb U81375 from Homo sapiens. ESTs gb N65317,
                   gb T20785, gb AA586285 and gb AA712578 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   236522
Seq. ID
                  uC-gsflnu33B088a05b1
Method
                  BLASTX
NCBI GI
                   g3540219
BLAST score
                   187
E value
                   2.0e-14
Match length
                  52
% identity
                   62
NCBI Description (D87686) KIAA0017 protein [Homo sapiens]
Seq. No.
                   236523
Seq. ID
                  uC-gsflnu33B088b05b1
Method
                  BLASTX
NCBI GI
                  g1946279
BLAST score
                   287
E value
                   7.0e-26
Match length
                  102
% identity
                   47
                  (Y12433) polyprotein; reverse transcriptase, RNase H
NCBI Description
                   [pineapple bacilliform virus]
Seq. No.
                   236524
Seq. ID
                  uC-qsflnu33B088b11b1
Method
                  BLASTX
NCBI GI
                  g3915601
BLAST score
                  257
```

E value 1.0e-22 78 Match length 63 % identity

NCBI Description ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD

SUBUNIT) (A1 38 KD SUBUNIT) (RF-C 38 KD SUBUNIT) (RFC38) >gi\_1498259 (L07541) replication factor C, 38-kDa subunit

[Homo sapiens] >gi\_4506489\_ref\_NP\_002906.1\_pRFC3\_ replication factor C (activator 1) 3 (38kD)



```
236525
Seq. No.
                  uC-gsflnu33B088c02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g407942
BLAST score
                  218
E value
                  1.0e-17
                  53
Match length
                  70
% identity
NCBI Description (U02496) epoxide hydrolase [Solanum tuberosum]
                  236526
Seq. No.
                  uC-gsflnu33B088d05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3461820
BLAST score
                  270
E value
                  2.0e-24
                  60
Match length
                  73
% identity
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
                  236527
Seq. No.
                  uC-gsflnu33B088d06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3702321
BLAST score
                  447
                  9.0e-45
E value
Match length
                  98
                  50
% identity
NCBI Description (AC005397) putative TGF-beta receptor interacting protein
                  [Arabidopsis thaliana]
Seq. No.
                  236528
                  uC-qsflnu33B088e10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3757515
BLAST score
                  189
E value
                  2.0e-14
Match length
                  66
                  59
% identity
NCBI Description (AC005167) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  236529
Seq. ID
                  uC-qsflnu33B088e12b1
Method
                  BLASTX
NCBI GI
                  g231757
BLAST score
                  625
E value
                  3.0e-65
Match length
                  146
% identity
                  84
NCBI Description CAFFEIC ACID 3-O-METHYLTRANSFERASE
                  (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                  3-O-METHYLTRANSFERASE) (COMT) >gi 99653 pir S18568
                  lignin-bispecific O-methyltransferase (EC 2.1.1.-) -
                  quaking aspen >gi 20951 emb CAA44006 (X62096) lignin
```

bispecific acid/5-hydroxyferulic acid methyltransferase

[Populus tremuloides] >gi 2226267 (U13171) caffeic

Match length

NCBI Description

% identity

86

84



acid/5-hydroxyferulic acid O-methyltransferase [Populus tremuloides]

Seq. No. 236530 Seq. ID uC-gsflnu33B088f07b1 Method BLASTX NCBI GI g3135274 BLAST score 196 E value 3.0e-15Match length 45 % identity NCBI Description (AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana] Seq. No. 236531 Seq. ID uC-gsflnu33B088f08b1 Method BLASTX NCBI GI g3600048 BLAST score 409 E value 5.0e-45Match length 115 77 % identity (AF080120) similar to hypothetical proteins in NCBI Description Schizosaccharomyces pombe (GB:Z98533) and C. elegans (GB:Z48334 and Z78419) [Arabidopsis thaliana] Seq. No. 236532 Seq. ID uC-gsflnu33B088g07b1 Method BLASTX NCBI GI g3643604 BLAST score 225 E value 8.0e-19Match length 81 % identity 56 NCBI Description (AC005395) receptor-like protein kinase [Arabidopsis thaliana] 236533 Seq. No. Seq. ID uC-gsflnu33B088h03b1 Method BLASTX NCBI GI g3702334 BLAST score 185 E value 7.0e-14 Match length 116 % identity 41 NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana] Seq. No. 236534 Seq. ID uC-gsflnu33B088h04b1 BLASTX Method NCBI GI g4193382 BLAST score 392 E value 4.0e-38

(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi\_4193384 (AF083337) ribosomal protein S27 [Arabidopsis

Seq. ID



## thaliana]

```
236535
Seq. No.
Seq. ID
                  uC-gsflnu33B089a12b1
                  BLASTX
Method
NCBI GI
                  g4455190
                  266
BLAST score
E value
                  2.0e-23
Match length
                  69
% identity
                  80
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
                  236536
Seq. No.
                  uC-gsflnu33B089b01b1
Seq. ID
                  BLASTX
Method
NCBI GI'
                  g3746060
BLAST score
                  463
E value
                  2.0e-46
Match length
                  116
                  78
% identity
NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]
                  236537
Seq. No.
                  uC-gsflnu33B089b04b1
Seq. ID
Method
                  BLASTX
                  q2465923
NCBI GI
BLAST score
                  181
                  7.0e-14
E value
Match length
                   47
% identity
                   68
NCBI Description (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
                  236538
Seq. No.
Seq. ID
                  uC-gsflnu33B089b06b1
Method
                  BLASTX
NCBI GI
                  q1762939
BLAST score
                  136
E value
                  1.0e-08
Match length
                  35
                   69
% identity
NCBI Description (U66266) ORF; able to induce HR-like lesions [Nicotiana
                   tabacum]
Seq. No.
                   236539
Seq. ID
                   uC-gsflnu33B089b09b1
                   BLASTX
Method
                   q3080452
NCBI GI
BLAST score
                   321
                   4.0e-30
E value
                   88
Match length
% identity
                  (AL022605) putative L-ascorbate oxidase [Arabidopsis
NCBI Description
                   thaliana]
                   236540
Seq. No.
```

uC-qsflnu33B089c05b1



```
Method
                  BLASTX
NCBI GI
                  g1169782
BLAST score
                  506
E value
                  1.0e-51
Match length
                  112
% identity
                  88
NCBI Description FUSCA PROTEIN FUS6 >gi 432446 (L26498) FUS6 [Arabidopsis
                  thaliana]
Seq. No.
                  236541
                  uC-gsflnu33B089c12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3935148
BLAST score
                  190
E value
                  2.0e-14
                  57
Match length
% identity
                   68
NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]
Seq. No.
                   236542
                  uC-gsflnu33B089d05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3212863
BLAST score
                  182
E value
                   5.0e-14
Match length
                   42
% identity
                   83
NCBI Description (AC004005) putative translation initiation factor
                   [Arabidopsis thaliana]
                   236543
Seq. No.
Seq. ID
                   uC-gsflnu33B089d12b1
                  BLASTX
Method
NCBI GI
                   q130181
BLAST score
                   180
E value
                   2.0e-13
                   37
Match length
                   86
% identity
NCBI Description PHYTOCHROME A TYPE 3 (AP3) >gi 82335 pir S00096
                  phytochrome 3 - oat >gi_16111_emb CAA26999 (X03242)
                  phytochrome type 3 (aa 1-1129) [Avena sativa]
                   236544
Seq. No.
Seq. ID
                   uC-gsflnu33B089e04b1
Method
                  BLASTX
                   g1663722
NCBI GI
BLAST score
                   321
                   6.0e-30
E value
                   81
Match length
                   70
% identity
NCBI Description (U50845) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
Seq. No.
                   236545
Seq. ID
                   uC-gsflnu33B089f04b1
```

Method BLASTX NCBI GI g167367 BLAST score 153



1.0e-10 E value 49 Match length

61 % identity

NCBI Description (L08199) peroxidase [Gossypium hirsutum]

236546 Seq. No.

uC-gsflnu33B089g03b1 Seq. ID

Method BLASTX NCBI GI g2642215 BLAST score 136 1.0e-08 E value Match length 24 % identity 100

(AF030386) NOI protein [Arabidopsis thaliana] NCBI Description

236547 Seq. No.

Seq. ID uC-gsflnu33B089h12b1

Method BLASTX NCBI GI q3241943 BLAST score 140 E value 1.0e-08 34 Match length

76 % identity

NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]

236548 Seq. No.

Seq. ID uC-qsflnu33B090a07b1

Method BLASTX NCBI GI q3292816 BLAST score 580 E value 4.0e-60 Match length 134

33 % identity

NCBI Description (AL031018) putative fizzy-related protein [Arabidopsis

thaliana]

Seq. No. 236549

uC-gsflnu33B090b08b1 Seq. ID

Method BLASTX NCBI GI q2129677 170 BLAST score E value 1.0e-12 Match length 45 67 % identity

probablel N-acetyltransferase hookless 1 - Arabidopsis NCBI Description

thaliana >gi\_1277090 (U50399) putative N-acetyltransferase

hookless1 [Arabidopsis thaliana] >gi\_1277092 (U50400) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi\_4468983\_emb\_CAB38297\_ (AL035605) probable N-acetyltransferase hookless 1 [Arabidopsis thaliana]

236550 Seq. No.

Seq. ID uC-gsflnu33B090b12b1

Method BLASTX NCBI GI g3355468 BLAST score 150 E value 3.0e-10

NCBI GI

E value

BLAST score

g1773330

9.0e-60

577



```
Match length
  % identity
                      67
.. NCBI Description
                     (AC004218) putative ribosomal protein L35 [Arabidopsis
                      thaliana]
                      236551
  Seq. No.
  Seq. ID
                      uC-gsflnu33B090c05b1
  Method
                      BLASTX
  NCBI GI
                      g729506
  BLAST score
                      530
  E value
                      3.0e-54
  Match length
                      110
  % identity
                      89
  NCBI Description
                     NARINGENIN, 2-OXOGLUTARATE 3-DIOXYGENASE
                      (FLAVONONE-3-HYDROXYLASE) (FHT) >gi_481216_pir__S38338
                      naringenin 3-dioxygenase - common stock
                      >gi_288107_emb_CAĀ51192_ (X72594) naringenin,2-oxoglutarate 3-dioxygenase [Matthiola incana]
  Seq. No.
                      236552
  Seq. ID
                     uC-gsflnu33B090d05b1
  Method
                     BLASTX
  NCBI GI
                     g2864625
  BLAST score
                     355
  E value
                      8.0e - 34
  Match length
                     102
  % identity
                      67
  NCBI Description
                    (AL021811) putative protein [Arabidopsis thaliana]
  Seq. No.
                     236553
  Seq. ID
                     uC-gsflnu33B090d06b1
  Method
                     BLASTX
  NCBI GI
                     g1632822
  BLAST score
                     245
  E value
                     3.0e-21
  Match length
                     75
  % identity
                     68
  NCBI Description
                     (Y08962) transmembrane protein [Oryza sativa] >gi 1667594
                      (U77297) transmembrane protein [Oryza sativa]
  Seq. No.
                     236554
  Seq. ID
                     uC-gsflnu33B090d10b1
  Method
                     BLASTX
  NCBI GI
                     g531389
  BLAST score
                     319
  E value
                     1.0e-29
  Match length
                     104
  % identity
                     60
  NCBI Description
                     (U12626) copia-like retrotransposon Hopscotch polyprotein
                     [Zea mays]
  Seq. No.
                     236555
  Seq. ID
                     uC-gsflnu33B090f03b1
  Method
                     BLASTX
```

```
Match length
                   122
% identity
                   93
NCBI Description (U80071) glycolate oxidase [Mesembryanthemum crystallinum]
Seq. No.
                   236556
Seq. ID
                   uC-gsflnu33B090g03b1
Method
                   BLASTX
NCBI GI
                   g1946364
BLAST score
                   225
E value
                   1.0e-18
Match length
                   104
% identity
                   47
NCBI Description (U93215) lipase isolog [Arabidopsis thaliana]
Seq. No.
                   236557
Seq. ID
                   uC-gsflnu33B090g06b1
Method
                   BLASTX
NCBI GI
                   g4027897
BLAST score
                   339
                   3.0e-32
E value
Match length
                   85
% identity
                   72
NCBI Description (AF049353) alpha-expansin precursor [Nicotiana tabacum]
Seq. No.
                   236558
Seq. ID
                  uC-gsflnu33B090g07b1
Method
                  BLASTX
NCBI GI
                   g3402718
BLAST score
                  163
                   2.0e-11
E value
Match length
                  48
% identity
                   56
NCBI Description (AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  236559
Seq. ID
                  uC-gsflnu33B090g11b1
Method
                  BLASTX
NCBI GI
                  g4454464
BLAST score
                  512
                  3.0e-52
E value
Match length
                  110
% identity
                  81
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236560
Seq. ID
                  uC-gsflnu33B090h03b1
Method
                  BLASTX
NCBI GI
                  g3335351
BLAST score
                  187
E value
                  3.0e-14
```

108

Match length

NCBI Description

% identity

come from this gene. [Arabidopsis thaliana]

(AC004512) Similar to ERECTA receptor protein kinase

gb D83257 from A. thaliana. ESTs gb\_T41629 and gb\_AA586072

```
Seq. ID
                   uC-gsflnu33B090h04b1
Method
                  BLASTX
NCBI GI
                  q4389417
BLAST score
                   509
E value
                   6.0e-52
Match length
                  105
% identity
                   87
NCBI Description
                 (AF055369) nitrate reductase [Glycine max]
                  236562
Seq. No.
Seq. ID
                  uC-gsflnu33B090h10b1
                  BLASTX
Method
NCBI GI
                  g4468990
BLAST score
                  138
E value
                  7.0e-09
Match length
                  53
% identity
                  58
NCBI Description (AL035605) putative protein [Arabidopsis thaliana]
                  236563
Seq. No.
Seq. ID
                  uC-gsflnu33B090h11b1
Method
                  BLASTX
NCBI GI
                  q2760837
BLAST score
                  256
                  4.0e-22
E value
Match length
                  129
% identity
                  40
NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  236564
Seq. ID
                  uC-gsflnu33B091b03b1
Method
                  BLASTX
NCBI GI
                  q2245132
BLAST score
                  279
E value
                  8.0e-25
Match length
                  77
% identity
                  70
NCBI Description (297344) syntaxin [Arabidopsis thaliana]
Seq. No.
                  236565
Seq. ID
                  uC-gsflnu33B091b11b1
Method
                  BLASTX
NCBI GI
                  q3582260
BLAST score
                  354
E value
                  9.0e - 34
Match length
                  82
% identity
                  84
NCBI Description
                  (M27221) lysyl-tRNA synthetase [Sinorhizobium meliloti]
```

Seq. ID uC-gsflnu33B091c07b1

Method BLASTX
NCBI GI g1345132
BLAST score 289
E value 2.0e-26
Match length 60
% identity 93



NCBI Description (U47029) ERECTA [Arabidopsis thaliana]

>gi\_1389566\_dbj\_BAA11869\_ (D83257) receptor protein kinase

[Arabidopsis thaliana] >gi\_3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 236567

Seq. ID uC-gsflnu33B091c12b1

Method BLASTX
NCBI GI g1706918
BLAST score 152
E value 4.0e-10
Match length 85

Match length 85 % identity 39

NCBI Description FLAVONOL SULFOTRANSFERASE-LIKE >gi\_498647 (U10277)

sulfotransferase-like flavonol [Flaveria bidentis]

Seq. No. 236568

Seq. ID uC-gsflnu33B091d05b1

Method BLASTX
NCBI GI g1532167
BLAST score 180
E value 4.0e-13
Match length 65
% identity 48

NCBI Description (U63815) localized according to blastn similarity to EST

sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis

thaliana]

Seq. No. 236569

Seq. ID uC-gsflnu33B091d06b1

Method BLASTX
NCBI GI g3810596
BLAST score 232
E value 2.0e-19
Match length 115
% identity 41

NCBI Description (AC005398) reverse-transcriptase-like protein [Arabidopsis

thaliana]

Seq. No. 236570

Seq. ID uC-gsflnu33B091g06b1

Method BLASTX
NCBI GI g2739000
BLAST score 433
E value 8.0e-43
Match length 107
% identity 68

NCBI Description (AF022459) CYP71D10p [Glycine max]

Seq. No. 236571

Seq. ID uC-gsflnu33B092a01b1

Method BLASTX
NCBI GI g4510399
BLAST score 261
E value 9.0e-23



Match length 73 % identity 62

NCBI Description (AC006587) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 236572

Seq. ID uC-gsflnu33B092a06b1

Method BLASTX
NCBI GI g602292
BLAST score 442
E value 6.0e-44
Match length 104
% identity 84

NCBI Description (U17987) RCH2 protein [Brassica napus]

Seq. No. 236573

Seq. ID uC-gsflnu33B092b01b1

Method BLASTX
NCBI GI g861366
BLAST score 359
E value 4.0e-34
Match length 125
% identity 57

NCBI Description (U28991) coded for by C. elegans cDNA cm21c7

[Caenorhabditis elegans]

Seq. No. 236574

Seq. ID uC-gsflnu33B092b10b1

Method BLASTX
NCBI GI g3024127
BLAST score 369
E value 1.0e-35
Match length 91
% identity 77

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2)

>qi 1655578 emb CAA95857 (Z71272) S-adenosyl-L-methionine

synthetase 2 [Catharanthus roseus]

Seq. No. 236575

Seq. ID uC-gsflnu33B092c08b1

Method BLASTX
NCBI GI g549750
BLAST score 148
E value 2.0e-09
Match length 116
% identity 34

NCBI Description HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION

>gi\_539221\_pir\_\_S38045 hypothetical protein YKL207w - yeast

(Saccharomyces Cerevisiae) >gi\_486369\_emb\_CAA82052\_(Z28207) ORF YKL207w [Saccharomyces cerevisiae]

Seq. No. 236576

Seq. ID uC-gsflnu33B092e07b1

Method BLASTX
NCBI GI g2245132
BLAST score 153



```
2.0e-10
E value
Match length
                  42
                  71
% identity
NCBI Description (Z97344) syntaxin [Arabidopsis thaliana]
Seq. No.
                  236577
                  uC-gsflnu33B092f11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2306917
BLAST score
                  239
E value
                  3.0e-36
Match length
                  85
                  93
% identity
NCBI Description (AF003728) plasma membrane intrinsic protein [Arabidopsis
                  thaliana]
                  236578
Seq. No.
Seq. ID
                  uC-gsflnu33B092g09b1
Method
                  BLASTX
NCBI GI
                  g3098571
BLAST score
                  236
                  9.0e-20
E value
Match length
                  134
                  37
% identity
NCBI Description (AF049028) BURP domain containing protein [Brassica napus]
                  236579
Seq. No.
Seq. ID
                  uC-gsflnu33B093b08b1
                  BLASTX
Method
NCBI GI
                  g3372233
BLAST score
                  134
E value
                  3.0e-12
Match length
                  70
                  60
% identity
NCBI Description (AF019248) RNA polymerase I, II and III 24.3 kDa subunit
                  [Arabidopsis thaliana]
Seq. No.
                  236580
Seq. ID
                  uC-gsflnu33B093b11b1
                  BLASTX
Method
                  g4467135
NCBI GI
BLAST score
                  395
E value
                  2.0e-38
Match length
                  130
% identity
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
                  236581
Seq. No.
Seq. ID
                  uC-gsflnu33B093c02b1
Method
                  BLASTX
NCBI GI
                  q2181190
BLAST score
                  152
E value
                  5.0e-10
Match length
                  99
% identity
                  37
```

NCBI Description (Y12531) serine/threonine kinase [Brassica oleracea]



uC-gsflnu33B093c03b1

Seq. No. Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g1076422
BLAST score
                  523
                  2.0e-53
E value
Match length
                  127
% identity
                  76
                  transcription factor OBF4 - Arabidopsis thaliana
NCBI Description
                  >gi 414613 emb CAA49524 (X69899) ocs-element binding
                  factor 4 [Arabidopsis thaliana]
                  236583
Seq. No.
Seq. ID
                  uC-qsflnu33B093c04b1
                  BLASTX
Method
NCBI GI
                  g2924514
BLAST score
                  472
E value
                  2.0e-47
Match length
                  124
                  70
% identity
NCBI Description (AL022023) protein kinase - like [Arabidopsis thaliana]
                  236584
Seq. No.
Seq. ID
                  uC-qsflnu33B093c08b1
Method
                  BLASTX
NCBI GI
                  q4314359
BLAST score
                  334
E value
                  2.0e-31
Match length
                  102
% identity
                  60
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  236585
                  uC-gsflnu33B093c10b1
Seq. ID
Method
                  BLASTX
                  g2829899
NCBI GI
BLAST score
                  147
                  3.0e-09
E value
                  65
Match length
% identity
                  45
                  (AC002311) similar to ripening-induced protein,
NCBI Description
                  gp_AJ001449_2465015 and major#latex protein,
                  gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                  236586
                  uC-gsflnu33B093c11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2144098
BLAST score
                  353
E value
                  2.0e-33
Match length
                  146
                  49
% identity
NCBI Description SC2 - rat >gi 256994 bbs 115268 (S45663) SC2=synaptic
                  glycoprotein [rats, brain, Peptide, 308 aa] [Rattus sp.]
Seq. No.
                  236587
Seq. ID
                  uC-gsflnu33B093d02b1
```



```
Method
                  BLASTX
NCBI GI
                  g4220472
BLAST score
                  394
                  3.0e-38
E value
                  122
Match length
                  58
% identity
                 (AC006069) similar to yeast cccl protein [Arabidopsis
NCBI Description
                  thaliana]
                  236588
Seq. No.
Seq. ID
                  uC-gsflnu33B093d04b1
                  BLASTX
Method
NCBI GI
                  g1632831
BLAST score
                  333
                  5.0e-31
E value
                  72
Match length
                  92
% identity
NCBI Description (Z49698) orf [Ricinus communis]
                  236589
Seq. No.
Seq. ID
                  uC-gsflnu33B093d10b1
                  BLASTX
Method
NCBI GI
                  g4185819
BLAST score
                  192
                  1.0e-14
E value
                  47
Match length
                  68
% identity
NCBI Description (AF116845) metallothionein-like type 1 protein [Ipomoea
                  batatas]
Seq. No.
                  236590
                  uC-gsflnu33B093e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3258570
BLAST score
                  297
                  7.0e-27
E value
                  143
Match length
% identity
                  46
NCBI Description (U89959) Unknown protein [Arabidopsis thaliana]
                  236591
Seq. No.
Seq. ID
                  uC-gsflnu33B093e08b1
Method
                  BLASTX
NCBI GI
                  q3850587
BLAST score
                  258
                  3.0e-22
E value
                  144
Match length
% identity
                  (AC005278) Strong similarity to gi 2244780 hypothetical
NCBI Description
                  protein from Arabidopsis thaliana chromosome 4 contig
                  gb_Z97335. [Arabidopsis thaliana]
```

Seq. ID uC-gsflnu33B093f12b1

Method BLASTX NCBI GI g1346172 BLAST score 284



2.0e-25 E value 57 Match length 91 % identity 78 KD GLUCOSE REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) NCBI Description (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOG) (BIP) >qi 170384 (L08830) glucose-regulated protein 78 [Lycopersicon esculentum] 236593 Seq. No. uC-gsflnu33B093g03b1 Seq. ID BLASTX Method g3549681 NCBI GI 391 BLAST score 6.0e - 38E value Match length 134 % identity 57 (AL031394) male sterility 2-like protein [Arabidopsis NCBI Description thaliana] 236594 Seq. No. uC-gsflnu33B093h09b1 Seq. ID BLASTX Method g1934730 NCBI GI 330 BLAST score 8.0e-31 E value 81 Match length 79 % identity (U95036) germin-like protein [Arabidopsis thaliana] NCBI Description 236595 Seq. No. uC-gsflnu33B094b01b1 Seq. ID BLASTX Method g3033400 NCBI GI 293 BLAST score 1.0e-26 E value 86 Match length 66 % identity (AC004238) putative Ser/Thr protein kinase [Arabidopsis NCBI Description thaliana] 236596 Seq. No. Seq. ID uC-gsflnu33B094b08b1 Method BLASTX q2499015 NCBI GI 173 BLAST score 2.0e-12 E value Match length 1Ò2 % identity NCBI Description TRIGGER FACTOR (TF) >gi 1001378 dbj BAA10868\_ (D64006) trigger factor [Synechocystis sp.]

Seq. No. 236597

Seq. ID uC-gsflnu33B094c07b1

MethodBLASTXNCBI GIg4220474BLAST score252E value9.0e-22



```
Match length
% identity
                   50
NCBI Description
                  (AC006069) putative myosin heavy chain [Arabidopsis
                  thaliana]
                  236598
Seq. No.
Seq. ID
                  uC-gsflnu33B094c11b1
Method
                  BLASTX
NCBI GI
                  q3819697
BLAST score
                  197
E value
                  2.0e-15
Match length
                  100
% identity
                  47
NCBI Description (AJ009608) BnMAP4K alpha1 [Brassica napus]
                  236599
Seq. No.
Seq. ID
                  uC-gsflnu33B094f05b1
Method
                  BLASTX
NCBI GI
                  g4545262
BLAST score
                  143
E value
                   2.0e-09
Match length
                  34
% identity
                  85
NCBI Description
                  (AF118230) metallothionein-like protein [Gossypium
                  hirsutum]
Seq. No.
                  236600
                  uC-gsflnu33B094g09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3236240
BLAST score
                  179
E value
                   2.0e-13
Match length
                  81
% identity
                   49
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
                   236601
Seq. No.
Seq. ID
                  uC-gsflnu33B094g10b1
Method
                  BLASTX
NCBI GI
                  g3702324
BLAST score
                  149
E value
                  1.0e-09
                  107
Match length
                   35
% identity
NCBI Description
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   236602
Seq. ID
                  uC-gsflnu33B094g12b1
                  BLASTX
Method
NCBI GI
                  g2290532
BLAST score
                   238
```

E value 3.0e-20 53 Match length % identity

(U94748) AN11 [Petunia x hybrida] . NCBI Description

Seq. No. 236603

34309



```
uC-qsflnu33B094h12b1
· Seq. ID
                   BLASTX
Method
                   g2583120
NCBI GI
                   332
BLAST score
                   3.0e - 31
 E value
                   100
Match length
                   69
 % identity
                   (AC002387) putative receptor-like protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   236604
 Seq. No.
                   uC-gsflnu33B095d10b1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q2493318
                   260
 BLAST score
                   1.0e-22
 E value
                   100
 Match length
 % identity
                   50
                   BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_
 NCBI Description
                   (Z25471) blue copper protein [Pisum sativum]
                   >gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]
 Seq. No.
                   236605
                   uC-gsflnu33B095f04b1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g3850111
                   275
 BLAST score
 E value
                   1.0e-24
                   74
 Match length
 % identity
                   58
 NCBI Description (AL033388) hypothetical integral membrane protein, putative
                   involvement in lipid metabolism [Schizosaccharomyces pombe]
                   236606
 Seq. No.
                   uC-gsflnu33B095g11b1
 Seq. ID
                   BLASTX
 Method
                   q4539545
 NCBI GI
                    605
 BLAST score
 E value
                    4.0e-63
                   121
 Match length
                    97
 % identity
 NCBI Description (Y16644) PRCI [Nicotiana tabacum]
 Seq. No.
                    236607
 Seq. ID
                    uC-gsflnu33B095h08b1
                   BLASTX
 Method
 NCBI GI
                    q3766299
                    163
 BLAST score
 E value
                    9.0e-12
                    34
 Match length
 % identity
 NCBI Description (AJ012080) sucrose synthase [Pisum sativum]
```

Seq. ID uC-gsflnu33B095h09b1

Method BLASTX NCBI GI g2662310



```
BLAST score
                   1.0e-11
E value
Match length
                  58
% identity
                   55
                  (AB009307) bpwl [Hordeum vulgare]
NCBI Description
                  236609
Seq. No.
                  uC-gsflnu33B097a12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352186
BLAST score
                   368
                   2.0e-35
E value
Match length
                   118
                   58
% identity
                  ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)
NCBI Description
                   (CYTOCHROME P450 74) >gi 404866 (U00428) allene oxide
                   synthase [Linum usitatissimum]
                   236610
Seq. No.
Seq. ID
                  uC-gsflnu33B097c08b1
                  BLASTX
Method
                   q1076746
NCBI GI
BLAST score
                   200
E value
                   8.0e-16
                   40
Match length
                   93
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza satīva]
Seq. No.
                   236611
                   uC-qsflnu33B098b10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3319882
BLAST score
                   303
E value
                   3.0e-28
Match length
                   65
% identity
                   91
                  (AJ004960) elongation factor 1-alpha (EF1-a) [Cicer
NCBI Description
                   arietinum]
                   236612
Seq. No.
                   uC-gsflnu33B100b06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g973313
BLAST score
                   346
E value
                   4.0e-55
                   117
Match length
                   93
% identity
                   (U30250) myo-inositol 1-phosphate synthase isozyme-2
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. ID uC-gsflnu33B100b09b1

Method BLASTX NCBI GI g421826 BLAST score 431



```
1.0e-42
E value
                  141
Match length
                   63
% identity
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                  >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis
                  thaliana]
                  236614
Seq. No.
                  uC-gsflnu33B100c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3522945
BLAST score
                  138
                   3.0e-12
E value
Match length
                  110
                   33
% identity
                  (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  236615
Seq. No.
                  uC-gsflnu33B100d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4335754
BLAST score
                   530
E value
                   3.0e-54
                   145
Match length
% identity
                   68
                  (AC006284) putative acid phophatase (contains
NCBI Description
                   metallo-phosphoesterase motif, prosite: QDOC50185)
                   [Arabidopsis thaliana]
                   236616
Seq. No.
Seq. ID
                   uC-gsflnu33B100e09b1
                   BLASTX
Method
NCBI GI
                   g3800952
BLAST score
                   206
E value
                   3.0e-16
Match length
                   109
% identity
                   47
                   (AF100657) No definition line found [Caenorhabditis
NCBI Description
                   elegans]
Seq. No.
                   236617
Seq. ID
                   uC-gsflnu33B100g01b1
Method
                   BLASTX
NCBI GI
                   g2842496
BLAST score
                   425
E value
                   5.0e-42
Match length
                   103
% identity
                   80
NCBI Description (AL021749) NAM / CUC2 -like protein [Arabidopsis thaliana]
```

Seq. ID uC-gsflnu33B101b04b1

Method BLASTX
NCBI GI g2642445BLAST score 368
E value 3.0e-35
Match length 136



```
% identity
NCBI Description
                  (AC002391) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                   236619
Seq. ID
                   uC-gsflnu33B101b07b1
                   {\tt BLASTX}
Method
                   g4512263
```

NCBI GI BLAST score 520 E value 4.0e-53 Match length 128 % identity 78

NCBI Description (AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]

Seq. No. 236620 Seq. ID uC-gsflnu33B101c03b1 Method BLASTX g1172995

NCBI GI BLAST score 268 E value 2.0e-23 Match length 107 % identity 52

NCBI Description 60S RIBOSOMAL PROTEIN L22 >gi 1083790 pir S52084 ribosomal

protein L22 - rat >gi\_710295\_emb\_CAA55204\_ribosomal protein L22 [Rattus norvegicus]

>gi 1093952 prf\_\_2105193A ribosomal protein L22 [Rattus

norvegicus]

Seq. No. 236621

Seq. ID uC-gsflnu33B101d03b1

BLASTX Method NCBI GI g544370 BLAST score 203 E value 7.0e-16 Match length 55 % identity 64

NCBI Description GAR1 PROTEIN >gi 422064 pir S33691 GAR1 protein - fission yeast (Schizosaccharomyces pombe) >gi 297009 emb CAA79628 (Z19576) snoRNP protein GAR1 [Schizosaccharomyces pombe] >gi\_1799516\_dbj\_BAA19143\_ (AB000537) snoRNP protein GAR 1

[Schizosaccharomyces pombe] >gi\_2104450 emb CAB08787

(Z95397) Garlp [Schizosaccharomyces pombe]

>gi\_2842463\_emb\_CAA16841.1\_ (AL021747) gar1 protein; small nucleolar rnp required for pre-mrna for pre-mrna processing

[Schizosaccharomyces pombe]

Seq. No. 236622

Seq. ID uC-gsflnu33B101d11b1

Method BLASTX NCBI GI g3096945 BLAST score 400 E value 5.0e-39 Match length 110 % identity 73

NCBI Description (AL023094) putative auxin-regulated protein [Arabidopsis

thaliana]



```
236623
Seq. No.
Seq. ID
                  uC-gsflnu33B101e02b1
Method
                  BLASTX
NCBI GI
                  g3128209
BLAST score
                  681
E value
                  8.0e-72
Match length
                  166
% identity
                  41
NCBI Description (AC004077) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236624
Seq. ID
                  uC-gsflnu33B101f03b1
Method
                  BLASTX
NCBI GI
                  q3023817
BLAST score
                  466
E value
                  1.0e-46
Match length
                  96
% identity
                  92
NCBI Description
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM
                  PRECURSOR (G6PD) >gi_1480344_emb_CAA67782_ (X99405)
                  glucose-6-phosphate dehydrogenase [Nicotiana tabacum]
Seq. No.
                  236625
Seq. ID
                  uC-gsflnu33B101f07b1
Method
                  BLASTX
NCBI GI
                  g2136348
BLAST score
                  142
E value
                  1.0e-08
Match length
                  95
% identity
                  36
NCBI Description
                  UDP-galactose transporter related isozyme 3 - human
                  >gi_1669564_dbj_BAA13527_ (D87991) UGTrel1 [Rattus rattus]
Seq. No.
                  236626
Seq. ID
                  uC-qsflnu33B101f08b1
Method
                  BLASTX
NCBI GI
                  q4454471
BLAST score
                  190
E value
                  2.0e-14
Match length
                  107
% identity
                  42
NCBI Description
                  (AC006234) putative G protein coupled receptor [Arabidopsis
                  thaliana]
Seq. No.
                  236627
Seq. ID
                  uC-gsflnu33B101h07b1
Method
                  BLASTX
NCBI GI
                  g464980
BLAST score
                  401
```

4.0e-39 E value Match length 76 % identity 93

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 166422 (L06967)

ubiquitin carrier protein [Medicago satīva]

Seq. No. 236628



```
uC-gsflnu33B107a07b1
Seq. ID
                  BLASTX
Method
                  g2695711
NCBI GI
                  211
BLAST score
                  6.0e-17
E value
                  57
Match length
                  63
% identity
                  (AJ001370) cytochome b5 [Olea europaea]
NCBI Description
                  236629
Seq. No.
                  uC-gsflnu33B107b10b1
Seq. ID
                  BLASTX
Method
                  g3426036
NCBI GI
                  242
BLAST score
                  2.0e-20
E value
                  144
Match length
                  43
% identity
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                  236630
Seq. No.
                  uC-gsflnu33B107b12b1
Seq. ID
Method
                  BLASTX
                  q1946372
NCBI GI
BLAST score
                 . 267
                  2.0e-23
E value
                  82
Match length
                  65
% identity
                  (U93215) yeast hypothetical protein YDB1_SCHPO isolog
NCBI Description
                   [Arabidopsis thaliana]
                  236631
Seq. No.
Seq. ID
                  uC-gsflnu33B107c08b1
                  BLASTX
Method
NCBI GI
                  g3785973
BLAST score
                  171
                  5.0e-12
E value
                  49
Match length
                  76
% identity
NCBI Description (AC005560) putative homeobox protein [Arabidopsis thaliana]
                   236632
Seq. No.
                  uC-gsflnu33B107c10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4580523
                  136
BLAST score
                  1.0e-08
E value
                  32
Match length
% identity
NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]
                   236633
Seq. No.
                   uC-gsflnu33B107g07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4388726
BLAST score
                   148
```

2.0e-09

40

E value Match length



```
% identity
NCBI Description
                  (AC006413) putative 12-oxophytodienoate-10,11-reductase
                  [Arabidopsis thaliana]
Seq. No.
                  236634
Seq. ID
                  uC-gsflnu33B107h02b1
Method
                  BLASTX
NCBI GI
                  g3935174
BLAST score
                  182
E value
                  2.0e-13
                  131
Match length
                  37
% identity
NCBI Description (AC004557) F17L21.17 [Arabidopsis thaliana]
Seq. No.
                  236635
                  uC-gsflnu33B1Q7h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4544462
BLAST score
                  555
E value
                  4.0e-57
                  140
Match length
                  75
% identity
NCBI Description (AC006580) putative NAM protein [Arabidopsis thaliana]
Seq. No.
                  236636
                  uC-gsflnu33B107h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406815
BLAST score
                  490
E value
                  2.0e-49
Match length
                  156
% identity
                  65
NCBI Description (AC006201) putative peptide methionine sulfoxide reductase
                  [Arabidopsis thaliana]
Seq. No.
                  236637
Seq. ID
                  uC-qsflnu33B107h11b1
                  BLASTX
Method
NCBI GI
                  g2959781
BLAST score
                  650
E value
                  3.0e-68
Match length
                  157
% identity
NCBI Description (AJ223508) Zwille protein [Arabidopsis thaliana]
                  236638
Seq. No.
Seq. ID
                  uC-gsflnu33B108a12b1
                  BLASTX
                  q4325369
```

Method BLASTX
NCBI GI g4325369
BLAST score 152
E value 3.0e-10
Match length 47

% identity 60

NCBI Description (AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No. 236639

Seq. ID uC-gsflnu33B108b08b1

```
BLASTX
Method
                  a2760321
NCBI GI
                  466
BLAST score
                  9.0e-47
E value
Match length
                  129
                  73
% identity
NCBI Description (AC002130) F1N21.6 [Arabidopsis thaliana]
                  236640
Seq. No.
                  uC-gsflnu33B108c01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2894308
BLAST score
                  181
                  2.0e-13
E value
                  42
Match length
                  18
% identity
                  (AJ223330) polyubiquitin [Nicotiana tabacum]
NCBI Description
                  236641
Seq. No.
                  uC-gsflnu33B108d01b1
Seq. ID
                  BLASTX
Method
                   g1363484
NCBI GI
                   341
BLAST score
                   5.0e-32
E value
                   103
Match length
                  <del>~</del>66
% identity
                  IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415)
NCBI Description
                   IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin
                   inducible protein, IAA13 [Arabidopsis thaliana]
                   236642
Seq. No.
                   uC-gsflnu33B108d10b1
Seq. ID
                   BLASTX
Method
                   q2342724
NCBI GI
                   244
BLAST score
                   7.0e-21
E value
Match length
                   59
% identity
                   80
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]
```

Seq. ID uC-gsflnu33B108e08b1

Method BLASTX
NCBI GI 93334244
BLAST score 380
E value 1.0e-36
Match length 88
% identity 80

NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)

(ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi\_2113825\_emb\_CAA73691\_ (Y13239) Glyoxalase I [Brassica

juncea]

Seq. No. 236644

Seq. ID uC-gsflnu33B108e12b1

Method BLASTX

Match length

% identity

76

53



```
NCBI GI
                     q2262118
  BLAST score
                    140
  E value
                    5.0e-09
                    35
  Match length
                    80
  % identity
  NCBI Description
                    (AC002343) cell division protein isolog [Arabidopsis
                    thaliana]
  Seq. No.
                    236645
  Seq. ID
                    uC-gsflnu33B108f04b1
  Method
                    BLASTX
  NCBI GI
                    q2505870
  BLAST score
                    156
  E value
                    3.0e-10
  Match length
                    48
  % identity
                    56
  NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                    236646
  Seq. ID
                    uC-gsflnu33B108g11b1
  Method
                    BLASTX
  NCBI GI
                    g2827715
  BLAST score
                    468
  E value
                    5.0e-47
  Match length
                    129
  % identity
                    69
                    (AL021684) receptor protein kinase - like protein
  NCBI Description
                     [Arabidopsis thaliana]
                    236647
  Seq. No.
  Seq. ID
                    uC-gsflnu33B108h04b1
  Method
                    BLASTX
  NCBI GI
                    g2244835
  BLAST score
                    283
  E value
                    3.0e-25
                    91
  Match length
                    62
  % identity
  NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana]
  Seq. No.
                    236648
  Seq. ID
                    uC-gsflnu33B109a02b1
  Method
                    BLASTX
  NCBI GI
                    g4006829
  BLAST score
                    459
                    9.0e-46
  E value
  Match length
                    168
  % identity
  NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]
  Seq. No.
                    236649
  Seq. ID
                    uC-gsflnu33B109b02b1
  Method
                    BLASTX
  NCBI GI
                    g3135274
. BLAST score
                    196
  E value
                    3.0e-15
```



```
NCBI Description
                  (AC003058) putative beta-1,3-endoglucanase [Arabidopsis
                  thaliana]
                  236650
Seq. No.
Seq. ID
                  uC-gsflnu33B109d01b1
Method
                  BLASTX
NCBI GI
                  g3738283
BLAST score
                  402
E value
                  3.0e-39
Match length
                  82
                  85
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236651
Seq. ID
                  uC-gsflnu33B109d04b1
Method
                  BLASTX
NCBI GI
                  g3461817
BLAST score
                  178
E value
                  6.0e-13
Match length
                  64
% identity
                  56
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236652
Seq. ID
                  uC-gsflnu33B109e02b1
Method
                  BLASTX
NCBI GI
                  g3785999
BLAST score
                  349
E value
                  6.0e-33
                  91
Match length
                  73
% identity
NCBI Description (AC005499) putative peptidyl-prolyl cis-trans isomerase
                  [Arabidopsis thaliana]
                  236653
Seq. No.
                  uC-gsflnu33B109f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006914
BLAST score
                  246
                  8.0e-21
E value
Match length
                  72
% identity
                  71
NCBI Description (Z99708) serine C-palmitoyltransferase like protein
                  [Arabidopsis thaliana]
                  236654
Seq. No.
Seq. ID
                  uC-gsflnu33B109f03b1
                  BLASTX
                  g1173043
```

Method NCBI GI BLAST score 308 4.0e-28 E value Match length 65 92 % identity

NCBI Description 60S RIBOSOMAL PROTEIN L38 >gi 479441 pir S33899 ribosomal

protein L38 - tomato (cv. Moneymaker)

>gi 313027 emb CAA49599 (X69979) ribosomal protein L38

[Lycopersicon esculentum]

34319

Seq. ID Method



```
236655
Seq. No.
                  uC-gsflnu33B109f09b1
Seq. ID
                  BLASTX
Method
                  g2213584
NCBI GI
BLAST score
                  443
                  6.0e-44
E value
Match length
                  143
% identity
                  58
NCBI Description (AC000348) T7N9.4 [Arabidopsis thaliana]
                  236656
Seq. No.
Seq. ID
                  uC-gsflnu33B109g04b1
Method
                  BLASTX
                  g2459429
NCBI GI
                  218
BLAST score
                  8.0e-18
E value
Match length
                  106
% identity
                  42
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236657
                  uC-qsflnu33B109h05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2088816
BLAST score
                  164
                  3.0e-11
E value
Match length
                  131
                  36
% identity
NCBI Description (AF003383) ZC250.3 gene product [Caenorhabditis elegans]
                  236658
Seq. No.
                  uC-gsflnu33B110a09b1
Seq. ID
                  BLASTX
Method
                  g2494264
NCBI GI
BLAST score
                  432
E value
                  1.0e-42
                  162
Match length
                  54
% identity
NCBI Description HYPOTHETICAL 66.0 KD GTP-BINDING PROTEIN SLR1105
                  >gi 1651837 dbj_BAA16764_ (D90900) elongation factor EF-G
                  [Synechocystis sp.]
                  236659
Seq. No.
                  uC-gsflnu33B110b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3790575
                  193
BLAST score
E value
                   9.0e-15
Match length
                  117
                   42
% identity
NCBI Description (AF078825) RING-H2 finger protein RHA3b [Arabidopsis
                  thaliana]
Seq. No.
                   236660
```

34320

uC-gsflnu33B110f11b1

BLASTX



```
g3738325
NCBI GI
BLAST score
                  570
                  8.0e-59
E value
Match length
                  158
                  73
% identity
                  (AC005170) putative CaMB-channel protein [Arabidopsis
NCBI Description
                  thaliana]
                  236661
Seq. No.
                  uC-gsflnu33B110g08b1
Seq. ID
                  BLASTX
Method
                  g3025299
NCBI GI
                  576
BLAST score
                  2.0e-59
E value
                  166
Match length
                   68
% identity
                  HYPOTHETICAL 62.3 KD PROTEIN T29M21.25 >gi 2088660
NCBI Description
                   (AF002109) ABC1 isolog [Arabidopsis thaliana]
                   236662
Seq. No.
                  uC-gsflnu33B111a09b1
Seq. ID
                  BLASTX
Method
                   g3024516
NCBI GI
                   724
BLAST score
                   8.0e-77
E value
                   143
Match length
                   99
% identity
                  RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong
NCBI Description
                   similarity to A. thaliana ara-2 (gb_ATHARA2). ESTs
                   gb_ATTS2483,gb_ATTS2484,gb_AA042159 come from this gene.
                   [Arabidopsis thaliana] >gi_2231303 (U74669) ras-related
                   small GTPase [Arabidopsis thaliana]
                   236663
Seq. No.
                   uC-gsflnu33B111b11b1
Seq. ID
                   BLASTX
Method
                   g2764574
NCBI GI
BLAST score
                   335
                   2.0e-31
E value
Match length
                   97
                   68
% identity
                  (AJ001009) pore protein of 24 kD (OEP24) [Pisum sativum]
NCBI Description
                   236664
Seq. No.
                   uC-gsflnu33B111c06b1
Seq. ID
                   BLASTX
Method
                   q2414584
NCBI GI
BLAST score
                   195
                   7.0e-15
E value
                   101
Match length
                   42
% identity
NCBI Description (Z99292) dna repair protein [Schizosaccharomyces pombe]
```

Seq. ID uC-gsflnu33B111c11b1

Method BLASTX NCBI GI g3242715

NCBI GI

E value

BLAST score

g3024491

4.0e-16

206



```
BLAST score
E value
                   3.0e-18
                   60
Match length
% identity
                   73
NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   236666
Seq. ID
                   uC-gsflnu33B111d04b1
Method
                   BLASTX
NCBI GI
                   g4432821
BLAST score
                   196
E value
                   6.0e-15
Match length
                   123
% identity
                   39
                   (AC006593) putative transmembrane protein [Arabidopsis
NCBI Description
                   thaliana]
                   236667
Seq. No.
Seq. ID
                   uC-gsflnu33B111d08b1
Method
                   BLASTX
NCBI GI
                   g113116
BLAST score
                   573
E value
                   4.0e-59
Match length
                   175
% identity
                   60
                   ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME)
NCBI Description
                   >gi_111396_pir__A35007 ATP citrate (pro-S)-lyase (EC 4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase
                    [Rattus norvegicus]
Seq. No.
                   236668
Seq. ID
                   uC-gsflnu33B111e08b1
                   BLASTX
Method
NCBI GI
                   g3236259
BLAST score
                   736
E value
                   3.0e-78
Match length
                   163
                   82
% identity
NCBI Description (AC004684) putative alcohol dehydrogenase [Arabidopsis
                   thaliana]
                   236669
Seq. No.
Seq. ID
                   uC-gsflnu33B111e12b1
                   BLASTX
Method
NCBI GI
                   g4049347
BLAST score
                   418
E value
                   6.0e-41
Match length
                   169
                   50
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
                   236670
Seq. No.
Seq. ID
                   uC-gsflnu33B111g03b1
                   BLASTX
Method
```

34322



```
112
 Match length
                    38
 % identity
                   PEROXISOMAL FARNESYLATED PROTEIN >gi_627824_pir_A54090 PxF
 NCBI Description
                    protein - Chinese hamster >gi 529146 (U05959) PxF
                    [Cricetulus griseus]
                    236671
 Seq. No.
                    uC-gsflnu33B111g04b1
 Seq. ID
 Method
                    BLASTX
                    q4558591
 NCBI GI
 BLAST score
                    585
 E value
                    1.0e-60
                    132
 Match length
% identity
                   (AC006555) putative beta-1,3-glucanase [Arabidopsis
 NCBI Description
                    thaliana]
                    236672
 Seq. No.
                    uC-gsflnu33B111g08b1
 Seq. ID
 Method
                    BLASTX
                    q4545262
 NCBI GI
                    212
 BLAST score
 E value
                    5.0e-17
Match length
                    41
                    98
 % identity
                    (AF118230) metallothionein-like protein [Gossypium
 NCBI Description
                    hirsutum
                    236673
 Seq. No.
                    uC-gsflnu33B111h07b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4098129
 BLAST score
                    389
                    1.0e-37
 E value
 Match length
                    73
 % identity
                    100
 NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                    236674
 Seq. No.
                    uC-gsflnu33B112b01b1
 Seq. ID
 Method
                    BLASTX
                    g4415921
 NCBI GI
                    466
 BLAST score
                    1.0e-46
 E value
                    139
 Match length
  % identity
                    61
                   (AC006282) putative glucosyl transferase [Arabidopsis
 NCBI Description
                    thaliana]
                    236675
  Seq. No.
                    uC-gsflnu33B112b06b1
  Seq. ID
  Method
                    BLASTX
 NCBI GI
                    g602076
                    197
  BLAST score
```

34323

2.0e-15

39 25

E value Match length

% identity

```
(X77456) pentameric polyubiquitin [Nicotiana tabacum]
NCBI Description
                  236676
Seq. No.
                  uC-gsflnu33B112b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3152572
BLAST score
                  215
                  3.0e-17
E value
Match length
                  91
                  49
% identity
                  (AC002986) Contains homology to DNAJ heatshock protein
NCBI Description
                  gb U32803 from Haemophilus influenzae. [Arabidopsis
                  thaliana]
Seq. No.
                  236677
                  uC-gsflnu33B112c11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1200256
                  577
BLAST score
E value
                  8.0e-60
                  113
Match length
% identity
NCBI Description (X90990) stpk1 protein kinase [Solanum tuberosum]
                  236678
Seq. No.
                  uC-qsflnu33B112d05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2244734
BLAST score
                   481
E value
                   2.0e-48
Match length
                   94
                   98
% identity
NCBI Description (D88414) actin [Gossypium hirsutum]
```

Seq. ID uC-gsflnu33B112d06b1

Method BLASTX
NCBI GI g1944575
BLAST score 554
E value 2.0e-59
Match length 129
% identity 84

NCBI Description (Z94058) pectinesterase [Lycopersicon esculentum]

Seq. No. 236680

Seq. ID uC-gsflnu33B112e02b1

Method BLASTX
NCBI GI 94006882
BLAST score 309
E value 3.0e-28
Match length 72
% identity 75

NCBI Description (Z99707) UDP-glucuronyltransferase-like protein

[Arabidopsis thaliana]

Seq. No. 236681

Seq. ID uC-gsflnu33B112e05b1



```
BLASTX
Method
                   g2088647
NCBI GI
                  249
BLAST score
E value
                   2.0e-26
                   98
Match length
                   67
% identity
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
                   236682
Seq. No.
                   uC-qsflnu33B112f02b1
Seq. ID
                   BLASTX
Method
                   q4006868
NCBI GI
BLAST score
                   353
                   2.0e-33
E value
                   150
Match length
                   56
% identity
NCBI Description (Z99707) putative protein [Arabidopsis thaliana]
                   236683
Seq. No.
                   uC-qsflnu33B112g05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2499773
                   267
BLAST score
E value
                   2.0e-23
                   112
Match length
                   46
% identity
                  46 KD FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL
NCBI Description
                   CIS-TRANS ISOMERASE) (PPIASE) >gi_1079010_pir__A55320
                   immunophilin FKBP46 - fall armyworm >gi_595845 (U15038)
                   immunophilin FKBP46 [Spodoptera frugiperda]
                   236684
Seq. No.
                   uC-qsflnu33B112h12b1
Seq. ID
                   BLASTX
Method
                   q4455258
NCBI GI
                   281
BLAST score
                   6.0e-25
E value
                   102
Match length
 % identity
                   48
                   (AL035523) acid phosphatase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   236685
Seq. No.
                   uC-gsflnu33B113a04b1
Seq. ID
                   BLASTX
Method
                   g3860333
NCBI GI
                   385
BLAST score
                   3.0e-37
E value
                   119
Match length
```

61 % identity

NCBI Description (AJ012693) basic blue copper protein [Cicer arietinum]

236686 Seq. No.

uC-qsflnu33B113c01b1 Seq. ID

BLASTX Method



236687

```
NCBI GI
                   q4539329
                   635
BLAST score
E value
                   2.0e-66
Match length
                   137
                   80
% identity
NCBI Description
```

(AL035679) ES43 like protein [Arabidopsis thaliana]

Seq. No. uC-gsflnu33B113c06b1 Seq. ID BLASTX Method g2864610 NCBI GI BLAST score 348 8.0e-33 E value 103 Match length

% identity 64 (AL021811) putative protein [Arabidopsis thaliana] NCBI Description >qi 4049336 emb CAA22561 (AL034567) putative protein

[Arabidopsis thaliana]

236688 Seq. No.

uC-gsflnu33B113c12b1 Seq. ID

BLASTX Method NCBI GI g461812 475 BLAST score 1.0e-47 E value 156 Match length 56 -% identity

CYTOCHROME P450 72 (CYPLXXII) (PROBABLE NCBI Description

GERANIOL-10-HYDROXYLASE) (GE10H) >gi\_167484 (L10081)

Cytochrome P-450 protein [Catharanthus roseus]

>gi 445604 prf 1909351A cytochrome P450 [Catharanthus

roseus]

236689 Seq. No.

uC-gsflnu33B113d07b1 Seq. ID

BLASTX Method NCBI GI q4056552 BLAST score 444 E value 4.0e-44 120 Match length 62 % identity

NCBI Description (AL034583) putative nucleotide binding protein

[Schizosaccharomyces pombe]

236690 Seq. No.

uC-gsflnu33B113d10b1 Seq. ID

Method BLASTX NCBI GI g1619300 BLAST score 717 4.0e-76 E value Match length 150 92 % identity

(X95269) LRR protein [Lycopersicon esculentum] NCBI Description

Seq. No. 236691

uC-gsflnu33B113e03b1 Seq. ID

Method BLASTX

Match length

% identity

62

68



```
q4455234
NCBI GI
BLAST score
                   344
E value
                   2.0e-32
                  99
Match length
                   69
% identity
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  236692
Seq. ID
                  uC-gsflnu33B113e08b1
Method
                  BLASTX
NCBI GI
                  g4103952
BLAST score
                  624
E value
                   3.0e-65
Match length
                  153
% identity
                   73
                  (AF029980) A37 [Arabidopsis thaliana] >gi 4103954
NCBI Description
                   (AF029981) A37 [Arabidopsis thaliana]
Seq. No.
                   236693
                  uC-gsflnu33B113e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4239845
BLAST score
                  205
E value
                   4.0e-16
Match length
                  108
% identity
                   43
NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]
Seq. No.
                   236694
Seq. ID
                  uC-gsflnu33B113h11b1
Method
                  BLASTX
NCBI GI
                  g3860323
BLAST score
                   372
E value
                  1.0e-35
Match length
                  78
% identity
                   87
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                   236695
Seq. ID
                  uC-gsflnu33B113h12b1
Method
                  BLASTX
NCBI GI
                  g4567309
BLAST score
                  334
E value
                   4.0e-31
Match length
                  125
% identity
NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   236696
                  uC-gsflnu33B114a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4580391
BLAST score
                  236
E value
                   9.0e-20
```

34327

NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

E value

Match length

NCBI Description

% identity

2.0e-16

trifidal

95



```
Seq. No.
                  236697
Seq. ID
                  uC-gsflnu33B114a09b1
Method
                  BLASTX
NCBI GI
                  g2224933
BLAST score
                  255
E value
                  6.0e-22
Match length
                  73
% identity
                  68
NCBI Description
                  (AF004216) ethylene-insensitive3 [Arabidopsis thaliana]
                  >gi 2224935 (AF004217) ethylene-insensitive3 [Arabidopsis
                  thaliana]
                  236698
Seq. No.
Seq. ID
                  uC-gsflnu33B114b03b1
Method
                  BLASTX
NCBI GI
                  g4220485
BLAST score
                  338
                  7.0e-32
E value
Match length
                  115
% identity
                  56
NCBI Description
                  (AC006069) putative beta-1,3-glucanase [Arabidopsis
                  thaliana]
Seq. No.
                  236699
Seq. ID
                  uC-gsflnu33B114b09b1
Method
                  BLASTX
NCBI GI
                  g2760320
BLAST score
                  314
E value
                  6.0e-29
Match length
                  99
                  65
% identity
NCBI Description (AC002130) F1N21.4 [Arabidopsis thaliana]
Seq. No.
                  236700
Seq. ID
                  uC-gsflnu33B114b12b1
Method
                  BLASTX
NCBI GI
                  g282964
BLAST score
                  387
E value
                  2.0e-37
Match length
                  140
% identity
                  65
NCBI Description
                  transforming protein (myb) homolog (clone myb.Ph3) - garden
                  petunia >gi_20563_emb_CAA78386 (Z13996) protein 1 [Petunia
                  x hybrida]
                  236701
Seq. No.
Seq. ID
                  uC-gsflnu33B114c04b1
Method
                  BLASTX
NCBI GI
                  q3598857
BLAST score
                  205
```

34328

(AF072447) short-chain alcohol dehydrogenase [Ipomoea

Seq. ID Method

NCBI GI



```
236702
Seq. No.
                  uC-qsflnu33B114e03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2660670
BLAST score
                   265
                   3.0e-23
E value
                   92
Match length
                   54
% identity
                   (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
NCBI Description
                   thaliana]
                   236703
Seq. No.
Seq. ID
                   uC-qsflnu33B114e04b1
                   BLASTX
Method
NCBI GI
                   q4455198
                   246
BLAST score
                   4.0e-21
E value
                   58
Match length
                   84
% identity
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   236704
Seq. No.
                   uC-qsflnu33B115b03b1
Seq. ID
Method
                   BLASTX
                   q4455342
NCBI GI
BLAST score
                   345
                   1.0e-32
E value
Match length
                   110
                   62
% identity
                   (AL035522) O-methyltransferase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   236705
Seq. No.
Seq. ID
                   uC-gsflnu33B115b04b1
Method
                   BLASTX
NCBI GI
                   g4455217
BLAST score
                   385
E value
                   3.0e - 37
                   77
Match length
% identity
                   (AL035440) Avr9 elicitor response like protein [Arabidopsis
NCBI Description
                   thaliana]
                   236706
Seq. No.
                   uC-gsflnu33B115c11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g285286
                   352
BLAST score
                   2.0e-33
E value
                   131
Match length
                   50
% identity
NCBI Description flavonol 4'-sulfotransferase - Flaveria chloraefolia
                   236707
Seq. No.
```

uC-gsflnu33B115d05b1

BLASTX

g3775999



```
BLAST score
E value
                   1.0e-20
Match length
                   110
% identity
                   52
NCBI Description
                  (AJ010463) RNA helicase [Arabidopsis thaliana]
                   236708
Seq. No.
                   uC-gsflnu33B115e09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4219092
BLAST score
                   277
E value
                   2.0e-24
                   75
Match length
% identity
                   72
NCBI Description
                  (AF117707) putative copper/zinc superoxide dismutase copper
                   chaperone precursor [Lycopersicon esculentum]
                   236709
Seq. No.
Seq. ID
                   uC-gsflnu33B115e11b1
Method
                   BLASTX
                   g1076291
NCBI GI
BLAST score
                   378
E value
                   1.0e-36
Match length
                   95
                   75
% identity
NCBI Description
                   amino acid transporter AAT1 - Arabidopsis thaliana
                   >gi_2911069_emb_CAA17531_ (AL021960) amino acid transport
protein AAT1 [Arabidopsis thaliana]
                   236710
Seq. No.
Seq. ID
                   uC-gsflnu33B115f02b1
Method
                   BLASTX
NCBI GI
                   q2832629
BLAST score
                   182
E value
                   2.0e-13
Match length
                   87
% identity
                   (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   236711
                   uC-gsflnu33B115f08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3241945
                   269
BLAST score
E value
                   9.0e-24
Match length
                   76
% identity
NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]
Seq. No.
                   236712
Seq. ID
                   uC-gsflnu33B115g02b1
```

Method BLASTX
NCBI GI g3335378
BLAST score 303
E value 1.0e-27
Match length 72



```
% identity
NCBI Description
                   (AC003028) Myb-related transcription activator [Arabidopsis
                   thaliana]
                   236713
Seq. No.
Seq. ID
                  uC-gsflnu33B115g04b1
                  BLASTX
Method
NCBI GI
                   g2570338
BLAST score
                   213
E value
                   6.0e-17
Match length
                   69
% identity
NCBI Description (U90927) glyoxalase II isozyme [Arabidopsis thaliana]
Seq. No.
                   236714
Seq. ID
                  uC-gsflnu33B115g05b1
Method
                  BLASTX
NCBI GI
                  g2245131
BLAST score
                   197
E value
                   3.0e-15
Match length
                  58
% identity
                   74
NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   236715
Seq. ID
                  uC-gsflnu33B115g07b1
Method
                  BLASTX
NCBI GI
                  g1495806
BLAST score
                   255
E value
                   6.0e-22
Match length
                  117
% identity
                   44
NCBI Description (X95514) lipoxygenase [Solanum tuberosum]
Seq. No.
                   236716
Seq. ID
                  uC-gsflnu33B115h07b1
                  BLASTX
Method
NCBI GI
                   q4567248
BLAST score
                   199
E value
                   2.0e-16
Match length
                   95
% identity
NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]
Seq. No.
                   236717
                  uC-qsflnu33B126a12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2708745
BLAST score
                   438
E value
                   1.0e-43
Match length
                   96
% identity
```

NCBI Description (AC003952) putative calcium-dependent ser/thr protein

kinase [Arabidopsis thaliana]

Seq. No. 236718

Seq. ID uC-gsflnu33B126b01b1



```
Method
                  BLASTX
NCBI GI
                  q4539314
BLAST score
                  194
E value
                  2.0e-15
Match length
                  59
                  64
% identity
NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]
Seq. No.
                  236719
Seq. ID
                  uC-gsflnu33B126b08b1
Method
                  BLASTX
NCBI GI
                  q629602
BLAST score
                  243
E value
                  8.0e-31
Match length
                  90
                  76
% identity
                  probable imbibition protein - wild cabbage
NCBI Description
                  >gi 488787 emb CAA55893 (X79330) putative imbibition
                  protein [Brassica oleracea]
                  236720
Seq. No.
Seq. ID
                  uC-gsflnu33B126f12b1
Method
                  BLASTX
NCBI GI
                  q2673914
BLAST score
                  314
E value
                  8.0e-29
Match length
                  154
% identity
                  49
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  236721
                  uC-gsflnu33B126g11b1
Seq. ID
Method
                  BLASTX
                  g1778376
NCBI GI
BLAST score
                  604
E value
                  7.0e-63
Match length
                  148
                  78
% identity
NCBI Description (U81288) PsRT17-1 [Pisum sativum]
Seq. No.
                  236722
Seq. ID
                  uC-gsflnu33B126h04b1
                  BLASTX
Method
NCBI GI
                  g3831467
BLAST score
                  161
                  3.0e-11
E value
                  78
Match length
% identity
NCBI Description (AC005700) putative beta-amylase [Arabidopsis thaliana]
```

uC-gsflnu33B126h10b1 Seq. ID

Method BLASTX NCBI GI g1769907 BLAST score 142 E value 1.0e-08 Match length 32



```
% identity
                   (X92975) xyloglucan endo-transglycosylase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   236724
Seq. ID
                   uC-gsflnu33B127b02b1
                  BLASTX
Method
NCBI GI
                   g2501449
BLAST score
                   216
E value
                   4.0e-20
Match length
                   61
% identity
                   90
NCBI Description UBIQUITIN-LIKE PROTEIN SMT3 >qi 1668773 emb CAA67922
                   (X99608) ubiquitin-like protein [Oryza sativa]
                   236725
Seq. No.
                   uC-gsflnu33B127b06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1402916
BLAST score
                   192
                   1.0e-14
E value
Match length
                   66
% identity
                   64
NCBI Description
                  (X98319) peroxidase [Arabidopsis thaliana]
                   >gi 1429217 emb CAA67311 (X98775) peroxidase ATP12a
                   [Arabidopsis thaliana]
                   236726
Seq. No.
Seq. ID
                   uC-gsflnu33B127b08b1
Method
                   BLASTX
                   g1771780
NCBI GI
BLAST score
                   315
E value
                   6.0e-29
                   57
Match length
% identity
                   98
NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]
Seq. No.
                   236727
Seq. ID
                   uC-gsflnu33B127c04b1
Method
                   BLASTX
NCBI GI
                   g2160322
BLAST score
                   201
E value
                   8.0e-16
Match length
                   58
% identity
                   66
                  (D16139) cytokinin binding protein CBP57 [Nicotiana
NCBI Description
                   sylvestris]
Seq. No.
                   236728
Seq. ID
                   uC-qsflnu33B127c07b1
Method
                   BLASTX
NCBI GI
                   g548852
BLAST score
                   171
```

E value 2.0e-12 Match length 40 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal



protein S21 - rice >gi\_303839\_dbj\_BAA02158\_ (D12633) 40S subunit ribosomal protein [Oryza sativa]

Seq. No. 236729

Seq. ID uC-gsflnu33B127c10b1

Method BLASTX
NCBI GI g3122572
BLAST score 739
E value 1.0e-78
Match length 143
% identity 97

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR

(COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi\_1084434\_pir\_\_S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato

>gi\_758340\_emb\_CAA59818\_ (X85808) 76 kDa mitochondrial

complex I subunit [Solanum tuberosum]

Seq. No. 236730

Seq. ID uC-gsflnu33B127g02b1

Method BLASTX
NCBI GI g2213584
BLAST score 338
E value 8.0e-32
Match length 120
% identity 58

NCBI Description (AC000348) T7N9.4 [Arabidopsis thaliana]

Seq. No. 236731

Seq. ID uC-gsflnu33B127g11b1

Method BLASTX
NCBI GI g4539010
BLAST score 143
E value 7.0e-09
Match length 131

Match length 131 % identity 39

NCBI Description (AL049481) putative DNA-directed RNA polymerase

[Arabidopsis thaliana]

Seq. No. 236732

Seq. ID uC-gsflnu33B128b07b1

Method BLASTX
NCBI GI g2342676
BLAST score 568
E value 1.0e-58
Match length 129
% identity 81

NCBI Description (AC000106) Strong similarity to Oryza NADPH oxidase

(gb X93301). [Arabidopsis thaliana]

Seq. No. 236733

Seq. ID uC-gsflnu33B128c04b1

Method BLASTX
NCBI GI g3395431
BLAST score 378
E value 2.0e-36
Match length 85



% identity (AC004683) unknown protein [Arabidopsis thaliana] NCBI Description 236734 Seq. No. uC-qsflnu33B128c06b1 Seq. ID BLASTX Method NCBI GI g3033375 305 BLAST score E value 7.0e-28 Match length 128 48 % identity

(AC004238) putative berberine bridge enzyme [Arabidopsis NCBI Description thaliana]

236735 Seq. No. Seq. ID

uC-gsflnu33B128d02b1

Method BLASTX g3834322 NCBI GI BLAST score 268 1.0e-23 E value Match length 87 61 % identity

NCBI Description (AC005679) EST gb\_R30300 comes from this gene. [Arabidopsis

thaliana]

236736 Seq. No.

Seq. ID uC-gsflnu33B128d11b1

Method BLASTX g2832304 NCBI GI BLAST score 347 E value 6.0e-33 Match length 115 % identity

NCBI Description (AF044489) receptor-like protein kinase [Oryza sativa]

Seq. No. 236737

Seq. ID uC-gsflnu33B128e11b1

Method BLASTX NCBI GI q2129921 BLAST score 178 E value 4.0e-13 Match length 35 94 % identity

NCBI Description hypothetical protein 1 - Madagascar periwinkle >gi\_758694

(U12573) putative [Catharanthus roseus]

Seq. No. 236738

Seq. ID uC-qsflnu33B128f02b1

Method BLASTX NCBI GI q4098246 BLAST score 356 E value 6.0e - 34Match length 116 % identity 63

NCBI Description (U76410) homeobox 2 protein [Lycopersicon esculentum]

Seq. No. 236739



```
uC-qsflnu33B128f10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3236241
                  371
BLAST score
                  1.0e-35
E value
                  100
Match length
                  66
% identity
                  (AC004684) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  236740
Seq. No.
                  uC-gsflnu33B128g10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1168470
                  239
BLAST score
                  4.0e-20
E value
                  109
Match length
% identity
                  54
                  PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase,
NCBI Description
                  tyrosine/serine/threonine-specific (EC 2.7.1.-) -
                  Arabidopsis thaliana >gi 217829_dbj_BAA02092_ (D12522)
                  protein tyrosine-serine-threonine kinase [Arabidopsis
                  thaliana]
Seq. No.
                  236741
                  uC-gsflnu33B129d05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4115383
BLAST score
                  284
E value
                  2.0e-25
                  119
Match length
% identity
                  18
NCBI Description (AC005967) receptor-like protein kinase [Arabidopsis
                  thaliana]
                  236742
Seq. No.
                  uC-gsflnu33B129e01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2062172
                  379
BLAST score
E value
                  9.0e-37
                  82
Match length
% identity
NCBI Description (AC001645) unknown protein [Arabidopsis thaliana]
                  236743
Seq. No.
                  uC-gsflnu33B129e04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2935298
BLAST score
                   472
E value
                   2.0e-47
                   97
Match length
```

% identity NCBI Description (AF038045) 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1 [Gossypium hirsutum]

97

236744 Seq. No.



```
uC-gsflnu33B130a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3746060
                  235
BLAST score
                   1.0e-19
E value
                  59
Match length
% identity
                   68
NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]
Seq. No.
                   236745
Seq. ID
                  uC-gsflnu33B130a07b1
                  BLASTX
Method
NCBI GI
                  q2920706
BLAST score
                   231
E value
                   4.0e-19
                  97
Match length
                   46
% identity
NCBI Description (Y13568) beta-xylosidase [Emericella nidulans]
                   236746
Seq. No.
Seq. ID
                  uC-gsflnu33B130b04b1
Method
                  BLASTX
NCBI GI
                   g231660
BLAST score
                   341
E value
                   4.0e-32
Match length
                  131
% identity
                   62
NCBI Description HYPOTHETICAL 226 KD PROTEIN (ORF 1901)
Seq. No.
                   236747
Seq. ID
                  uC-gsflnu33B130d08b1
                  BLASTX
Method
NCBI GI
                   g125393
BLAST score
                   176
                   7.0e-13
E value
                   101
Match length
                   39
% identity
NCBI Description HOMOSERINE KINASE (HK) >gi 79795 pir S03743 homoserine
                   kinase (EC 2.7.1.39) - Calothrix sp >gi 43396 emb CAA68576
                   (Y00522) homoserine kinase (AA 1-307) [Calothrix PCC7601]
                   236748
Seq. No.
Seq. ID
                   uC-gsflnu33B130f05b1
Method
                  BLASTX
NCBI GI
                   q1705930
BLAST score
                   312
E value
                   1.0e-28
Match length
                   93
% identity
                   68
NCBI Description ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1
                   (ENDOPEPTIDASE CLP 1) >gi 1001349 dbj BAA10836 (D64006)
                   ATP-dependent protease ClpP [Synechocystis sp.]
Seq. No.
                   236749
Seq. ID
                   uC-qsflnu33B130h09b1
```

Method BLASTX NCBI GI q4234955



```
BLAST score
                   217
                   2.0e-17
E value
Match length
                   109
                   25
% identity
NCBI Description (AF098971) NBS-LRR-like protein cD8 [Phaseolus vulgaris]
Seq. No.
                   236750
Seq. ID
                   uC-gsflnu33B131a01b1
Method
                   BLASTX
NCBI GI
                   g3273243
BLAST score
                   537
E value
                   3.0e-55
Match length
                   120
% identity
                   29
                   (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                   >gi 3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza
                   sativa]
Seq. No.
                   236751
                   uC-gsflnu33B131a04b1
Seq. ID
Method
                   BLASTX
*NCBI GI
                   q1518113
BLAST score
                   155
E value
                   7.0e-11
Match length
                   52
% identity
                   54
NCBI Description (U66193) SLL2 [Brassica napus]
                   236752
Seq. No.
Seq. ID
                   uC-gsflnu33B131c01b1
Method
                   BLASTX
NCBI GI
                   g2462760
BLAST score
                   287
E value
                   8.0e-26
Match length
                   119
                   51
% identity
NCBI Description (AC002292) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   236753
Seq. ID
                   uC-gsflnu33B131e01b1
Method
                   BLASTX
NCBI GI
                   g4539351
BLAST score
                   255
E value
                   4.0e-22
Match length
                   116
% identity
                   44
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
                   236754
Seq. No.
                   uC-gsflnu33B131e12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2865623
BLAST score
                   282
```

E value 2.0e-25 Match length 67

79 % identity

NCBI Description (AF045286)



GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No. 236755

Seq. ID uC-gsflnu33B131f03b1

Method BLASTX
NCBI GI g3005931
BLAST score 398
E value 9.0e-39
Match length 129
% identity 42

NCBI Description (AJ005016) ABC transporter [Homo sapiens]

Seq. No. 236756

Seq. ID uC-gsflnu33B131f10b1

Method BLASTX
NCBI GI g3046995
BLAST score 178
E value 3.0e-13
Match length 86
% identity 44

NCBI Description (AF056717) ash212 [Homo sapiens]

Seq. No. 236757

Seq. ID uC-gsflnu33B131h02b1

Method BLASTX
NCBI GI g1621463
BLAST score 250
E value 9.0e-22
Match length 49
% identity 88

NCBI Description (U73104) laccase [Liriodendron tulipifera]

Seq. No. 236758

Seq. ID uC-gsflnu33B131h10b1

Method BLASTX
NCBI GI g2462748
BLAST score 137
E value 9.0e-09
Match length 27
% identity 100

NCBI Description (AC002292) putative Clathrin Coat Assembly protein

[Arabidopsis thaliana]

Seq. No. 236759

Seq. ID uC-gsflnu33B132e12b1

Method BLASTX
NCBI GI g139799
BLAST score 266
E value 2.0e-23
Match length 102
% identity 53

NCBI Description XANTHINE DEHYDROGENASE (XD) (ROSY LOCUS PROTEIN)

>gi\_8831\_emb\_CAA68409\_ (Y00308) xanthine dehydrogenase

[Drosophila melanogaster]

Seq. No. 236760

NCBI GI

BLAST score

g129590

567



```
uC-gsflnu33B132g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2673912
BLAST score
                  167
                  9.0e-12
E value
Match length
                  46
% identity
                  74
NCBI Description (AC002561) unknown protein [Arabidopsis thaliana]
                  236761
Seq. No.
                  uC-gsflnu33B132h10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4454051
                  572
BLAST score
                  4.0e-59
E value
Match length
                  139
                  76
% identity
                 (AL035394) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  236762
Seq. ID
                  uC-gsflnu33B132h12b1
Method
                  BLASTX
NCBI GI
                  q4544427
BLAST score
                  286
E value
                  2.0e-25
                  76
Match length
                  82
% identity
NCBI Description (AC006955) putative ferredoxin-thioredoxin reductase
                  [Arabidopsis thaliana]
Seq. No.
                  236763
Seq. ID
                  uC-gsflnu33B133b03b1
Method
                  BLASTX
NCBI GI
                  g2827715
BLAST score
                  280
E value
                  2.0e-25
Match length
                  71
                  77
% identity
NCBI Description (AL021684) receptor protein kinase - like protein
                  [Arabidopsis thaliana]
Seq. No.
                  236764
Seq. ID
                  uC-gsflnu33B133b07b1
Method
                  BLASTX
NCBI GI
                  q1498338
BLAST score
                  366
                  3.0e-35
E value
Match length
                  79
                  95
% identity
NCBI Description (U60502) actin [Glycine max]
Seq. No.
                  236765
Seq. ID
                  uC-gsflnu33B133f12b1
Method
                  BLASTX
```



9.0e-59 E value Match length 116 % identity 94 PHENYLALANINE AMMONIA-LYASE >gi 99990 pir\_S17444 NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) 1 - alfalfa >gi\_19650\_emb\_CAA41169\_ (X58180) phenylalanine ammonia-lyase [Medicago sativa] Seq. No. 236766 Seq. ID uC-gsflnu33B133h09b1 Method BLASTX NCBI GI q422029 BLAST score 292 E value 2.0e-26 Match length 66 77 % identity transcription factor OBF3.2, ocs element-binding - maize NCBI Description >gi\_297018\_emb\_CAA48904\_ (X69152) ocs-element binding factor 3.2 [Zea mays] 236767 Seq. No. Seq. ID uC-gsflnu33B134b08b1 Method BLASTX NCBI GI g3242789 BLAST score 515 E value 2.0e-52 Match length 136 76 % identity (AF055357) respiratory burst oxidase protein D [Arabidopsis NCBI Description thaliana] 236768 Seq. No. uC-gsflnu33B134b12b1 Seq. ID Method BLASTX NCBI GI g2244835 261 BLAST score 7.0e-23 E value 80 Match length % identity 64 NCBI Description (Z97337) protein kinase homolog [Arabidopsis thaliana] 236769 Seq. No. uC-gsflnu33B134c10b1 Seq. ID BLASTX Method NCBI GI g4388727 BLAST score 226 9.0e-19E value 76 Match length % identity 61 NCBI Description (AC006413) hypothetical protein [Arabidopsis thaliana] 236770 Seq. No.

Seq. ID uC-gsflnu33B135a10b1

BLASTX Method NCBI GI q1174592 BLAST score 343 E value 8.0e-53



```
Match length
                   99
% identity
NCBI Description
Seq. No.
```

TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 alpha-tubulin - garden pea >qi 525332 (U12589) alpha-tubulin [Pisum

sativum]

236771

uC-gsflnu33B135c08b1 Seq. ID

Method BLASTX NCBI GI q4220531 BLAST score 152 5.0e-10 E value Match length 96 % identity 36

NCBI Description (AL035356) hypothetical protein [Arabidopsis thaliana]

Seq. No. Seq. ID

236772 uC-gsflnu33B135h01b1

Method BLASTX NCBI GI q1710664 BLAST score 177 4.0e-13 E value Match length 49 % identity 59

DNA-DIRECTED RNA POLYMERASES I, II, AND III 7.0 KD NCBI Description

> POLYPEPTIDE (ABC10-ALPHA) (RPB7.0) >gi 1082770 pir RNA polymerase II - human >gi\_717187\_emb\_CAA87656\_ (Z47727)

RNA polymerase II [Homo sapiens]

Seq. No.

Seq. ID uC-gsflnu33B135h07b1

Method BLASTX NCBI GI g2506788 BLAST score 338 E value 7.0e-32Match length 98

% identity 61

GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (RAB NCBI Description

> GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) >gi\_1332508\_emb\_CAA66638\_ (X98001) geranylgeranyl transferase II [Homo sapiens]

Seq. No. 236774

Seq. ID uC-gsflnu33B136a01b1

Method BLASTX NCBI GI g1076317 BLAST score 497 E value 2.0e-50 Match length 116 77 % identity

NCBI Description dihydrodipicolinate synthase (EC 4.2.1.52) precursor -

Arabidopsis thaliana

Seq. No. 236775

uC-gsflnu33B136b09b1 Seq. ID

Method BLASTX

% identity



```
q2288988
NCBI GI
BLAST score
                   231
E value
                   3.0e-19
Match length
                  113
% identity
                   41
                  (AC002335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  236776
Seq. ID
                  uC-gsflnu33B136c12b1
Method
                  BLASTX
NCBI GI
                  q4490303
BLAST score
                  410
E value
                   4.0e-40
Match length
                  99
                   77
% identity
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                  236777
Seq. ID
                  uC-gsflnu33B136d07b1
Method
                  BLASTX
NCBI GI
                  g3763933
BLAST score
                  192
E value
                   4.0e-15
Match length
                  67
% identity
                   76
NCBI Description (AC004450) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236778
                  uC-gsflnu33B136e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135392
BLAST score
                  153
E value
                   3.0e-10
Match length
                  46
% identity
                   63
                  TUBULIN ALPHA-1 CHAIN >gi 101808 pir S13336 tubulin
NCBI Description
                  alpha-1 chain - Emericella nidulans
Seq. No.
                   236779
Seq. ID
                  uC-gsflnu33B136e04b1
Method
                  BLASTX
NCBI GI
                  g2982268
BLAST score
                  280
E value
                   4.0e-25
Match length
                  57
                   93
% identity
                  (AF051217) probable 40S ribosomal protein S15 [Picea
NCBI Description
                  mariana]
                   236780
Seq. No.
Seq. ID
                  uC-gsflnu33B136g01b1
Method
                  BLASTX
NCBI GI
                  q3980377
BLAST score
                  416
E value
                  7.0e-41
Match length
                  140
```



```
NCBI Description (AC004561) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236781
                  uC-gsflnu33B136g07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3522952
BLAST score
                  394
                   3.0e-38
E value
Match length
                  122
                   62
% identity
                  (AC004411) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                   236782
Seq. No.
Seq. ID
                  uC-gsflnu33B137c07b1
Method
                  BLASTX
NCBI GI
                   g2739168
BLAST score
                   267
E value
                   1.0e-23
Match length
                  87
                   55
% identity
NCBI Description
                  (AF032386) aldose-1-epimerase-like protein [Nicotiana
                  tabacum]
Seq. No.
                   236783
Seq. ID
                   uC-qsflnu33B137c09b1
Method
                  BLASTX
NCBI GI
                   q3057150
BLAST score
                   158
E value
                   5.0e-11
                   35
Match length
% identity
                   43
NCBI Description (AF059037) chaperonin 10 [Arabidopsis thaliana]
Seq. No.
                   236784
                   uC-gsflnu33B137d04b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3237190
BLAST score
                   177
                   5.0e-13
E value
                   70
Match length
% identity
NCBI Description (AB014760) cystein proteinase inhibitor [Cucumis sativus]
Seq. No.
                   236785
                  uC-gsflnu33B137e02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1142621
                   206
BLAST score
E value
                   2.0e-16
Match length
                   51
                   80
% identity
                  (U18349) phaseolin G-box binding protein PG2 [Phaseolus
NCBI Description
                   vulgaris]
```

34344

236786

uC-gsflnu33B137e03b1

Seq. No. Seq. ID



Method BLASTX NCBI GI q1174595 BLAST score 416 E value 6.0e-41Match length 105 % identity 56 TUBULIN BETA-1 CHAIN >gi 1076658 pir S50747 beta-tubulin -NCBI Description potato >gi 609268 emb CAA83847 (Z33382) beta-tubulin [Solanum tuberosum]

Seq. No. 236787

Seq. ID uC-qsflnu33B137f01b1

Method BLASTX NCBI GI q3915737 BLAST score 255 4.0e-22 E value Match length 57 89 % identity

IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (KAP NCBI Description

ALPHA) >gi\_3228370 (AF017252) importin alpha [Lycopersicon

esculentum]

Seq. No. 236788

Seq. ID uC-gsflnu33B137g12b1

Method BLASTX NCBI GI q3451074 BLAST score 592 E value 2.0e-61 Match length 135 76 % identity

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 236789

Seq. ID uC-gsflnu33B137h11b1

Method BLASTX NCBI GI g2252841 BLAST score 176 E value 2.0e-16 Match length 81

57 % identity

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

236790 Seq. No.

Seq. ID uC-gsflnu33B138a09b1

Method BLASTX NCBI GI g1495366 BLAST score 234 E value 1.0e-19 134 Match length 41 % identity

NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

236791 Seq. No.

Seq. ID uC-gsflnu33B138b07b1

Method BLASTX NCBI GI g4455364 BLAST score 174



```
1.0e-12
E value
Match length
                  42
                  79
% identity
                  (AL035524) senescence-associated protein-like [Arabidopsis
NCBI Description
                  thaliana]
                  236792
Seq. No.
                  uC-gsflnu33B138b10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2827528
                  473
BLAST score
                  2.0e-47
E value
Match length
                  132
                  69
% identity
                  (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
                  236793
Seq. No.
                  uC-gsflnu33B138c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1871192
BLAST score
                  612
                  8.0e-64
E value
                  127
Match length
                  81
% identity
                  (U90439) Cys3His zinc finger protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                   236794
Seq. No.
                  uC-qsflnu33B138c12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1279600
BLAST score
                   433
                   5.0e-43
E value
                   104
Match length
                   77
% identity
NCBI Description (Z71753) pectin methylesterase [Nicotiana plumbaginifolia]
                   236795
Seq. No.
                   uC-qsflnu33B138d11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4510368
BLAST score
                   331
E value
                   2.0e-31
Match length
                   138
% identity
                   (AC007017) putative transcription factor E2F5 [Arabidopsis
NCBI Description
                   thaliana]
                   236796
Seq. No.
                   uC-gsflnu33B138f12b1
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3860256
BLAST score 177
E value 7.0e-13
Match length 70
% identity 54

NCBI Description (AC005824) putative tRNA isopentenylpyrophosphate

NCBI Description



## transferase [Arabidopsis thaliana]

```
236797
Seq. No.
Seq. ID
                  uC-gsflnu33B138g11b1
Method
                  BLASTX
NCBI GI
                  g3747026
BLAST score
                  216
                  2.0e-17
E value
                  79
Match length
                  44
% identity
                 (AF093244) import protein Tim9p [Saccharomyces cerevisiae]
NCBI Description
Seq. No.
                  236798
Seq. ID
                  uC-gsflnu33B138h08b1
Method
                  BLASTX
NCBI GI
                  g3395441
BLAST score
                  249
E value
                  2.0e-21
Match length
                  69
% identity
                  67
                 (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                  236799
Seq. No.
Seq. ID
                  uC-gsflnu33B138h11b1
Method
                  BLASTX
NCBI GI
                  q584998
BLAST score
                  312
                  1.0e-28
E value
                  107
Match length
                  54
% identity
NCBI Description FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTOCHROME P450
                  LXXVA2) (P-450EG1) >gi 629713 pir S43342 flavonoid
                  hydroxylase cytochrome P450 - eggplant
                  >gi 395261 emb CAA50155 (X70824) flavonoid hydroxylase
                  (P450) [Solanum melongena]
Seq. No.
                  236800
Seq. ID
                  uC-qsflnu33B139a09b1
Method
                  BLASTX
                  g3157949
NCBI GI
BLAST score
                  462
E value
                  2.0e-46
Match length
                  104
% identity
                  (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase
NCBI Description
                  precursor qb Z28697 from Nicotiana tabacum. ESTs qb Z18185
                  and gb AA605362 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  236801
Seq. ID
                  uC-gsflnu33B139b02b1
Method
                  BLASTX
NCBI GI
                  q3790587
BLAST score
                  329
E value
                  1.0e-30
Match length
                  85
% identity
                  79
```

(AF079182) RING-H2 finger protein RHF2a [Arabidopsis



## thaliana]

```
236802
Seq. No.
                   uC-gsflnu33B140a09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g464981
BLAST score
                   683
E value
                   4.0e-72
Match length
                   142
                   87
% identity
NCBI Description
```

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi\_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

 Seq. No.
 236803

 Seq. ID
 uC-gsflnu33B140b01b1

 Method
 BLASTX

 NCBI GI
 g2443886

 BLAST score
 383

 E value
 4.0e-37

Match length 91 % identity 81

NCBI Description (AC002294) Unknown protein [Arabidopsis thaliana]

Seq. No. 236804

Seq. ID uC-gsflnu33B140b06b1

Method BLASTX
NCBI GI g3510254
BLAST score 494
E value 5.0e-50
Match length 108
% identity 88

NCBI Description (AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No. 236805

Seq. ID uC-gsflnu33B140c01b1

Method BLASTX
NCBI GI g1771780
BLAST score 430
E value 2.0e-42
Match length 106
% identity 78

NCBI Description (Y10024) ubiquitin extension protein [Solanum tuberosum]

Seq. No. 236806

Seq. ID uC-gsflnu33B140d06b1

Method BLASTX
NCBI GI g3236241
BLAST score 365
E value 7.0e-35
Match length 103
% identity 71

NCBI Description (AC004684) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 236807

Seq. ID uC-gsflnu33B140d10b1



```
BLASTX
 Method
 NCBI GI
                    g4545262
 BLAST score
                    147
                    2.0e-09
 E value
 Match length
                    54
                    52
 % identity
                    (AF118230) metallothionein-like protein [Gossypium
 NCBI Description
                    hirsutum]
                    236808
 Seq. No.
                    uC-gsflnu33B140e12b1
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g4336434
 BLAST score
                    380
                    6.0e-37
 E value
 Match length
                    94
                    77
  % identity
                    (AF092431) nodule-enhanced protein phosphatase type 2C
 NCBI Description
                    [Lotus japonicus]
                    236809
 Seq. No.
                    uC-gsflnu33B140g08b1
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    q548770
                    295
 BLAST score
                    4.0e-27
 E value
                    60
 Match length
                    90
  % identity
                    60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal
 NCBI Description
                    protein L3 - rice >gi_303853_dbj_BAA02155 (D12630)
                    ribosomal protein L3 [Oryza sativa]
                    236810
 Seq. No.
                    uC-gsflnu33B141b10b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q4105772
BLAST score
                    202
                    9.0e-16
 E value
 Match length
                    42
                    49
  % identity
  NCBI Description (AF049917) PGP9B [Petunia x hybrida]
                    236811
  Seq. No.
                    uC-gsflnu33B141c11b1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q3776084
                    180
  BLAST score
                    4.0e-13
  E value
  Match length
                    77
  % identity
  NCBI Description (Y18251) NtN2 [Medicago truncatula]
                    236812
  Seq. No.
  Seq. ID
                    uC-qsflnu33B141c12b1
```

Method BLASTX NCBI GI q3894168 BLAST score 235



```
1.0e-19
E value
                   133
Match length
                   36
% identity
                   (AC005312) similar to phloem-specific lectin [Arabidopsis
NCBI Description
                   thaliana]
                   236813
Seq. No.
                   uC-gsflnu33B141d09b1
Seq. ID
Method
                   BLASTX
                   q1709692
NCBI GI
BLAST score
                   461
E value
                   3.0e - 46
Match length
                   101
                   84
% identity
                  PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O)
NCBI Description
                   REDUCTASE) (FRUIT-RIPENING PROTEIN E4)
                   >gi 100204 pir JQ0988 DNA-binding E4 protein - Tomato
                   236814
Seq. No.
                   uC-gsflnu33B141d12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2921323
BLAST score
                   383
                   7.0e - 37
E value
Match length
                   139
                   56
% identity
                  (AF034112) beta-1,3-glucanase 7 [Glycine max]
NCBI Description
                   236815
Seq. No.
                   uC-gsflnu33B141h04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3169719
BLAST score
                   255
                   2.0e-22
E value
Match length
                   80
% identity
                   66
                  (AF007109) similar to yeast dcp1 [Arabidopsis thaliana]
NCBI Description
                   236816
Seq. No.
                   uC-qsflnu33B142b04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2632105
BLAST score
                   144
E value
                   5.0e-09
                   55
Match length
% identity
                   58
                   (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                   >gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA
                   synthetase [Arabidopsis thaliana]
```

236817 Seq. No.

uC-gsflnu33B142g02b1 Seq. ID

BLASTX Method NCBI GI g2702279 BLAST score 283 E value 7.0e-2669 Match length



% identity (AC003033) putative phosphate transporter [Arabidopsis NCBI Description thaliana] >gi\_2780345\_dbj\_BAA24280\_ (AB000093) inorganic phosphate transporter [Arabidopsis thaliana] >gi\_2914691 (AC003974) putative phosphate transporter [Arabidopsis thaliana] 236818 Seq. No. uC-qsflnu33B142g04b1 Seq. IĐ Method BLASTX g4263519 NCBI GI BLAST score 435 3.0e-43E value 89 Match length 93 % identity (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis NCBI Description thaliana] 236819 Seq. No. uC-gsflnu33B143a06b1 Seq. ID Method BLASTX NCBI GI q584892 BLAST score 354 E value 1.0e-33 123 Match length 56 % identity SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C) NCBI Description >gi\_629805\_pir\_\_S43516 serine carboxypeptidase I - rice >gi 409580 dbj BAA04510 (D17586) serine carboxypeptidase I [Oryza sativa] 236820 Seq. No. Seq. ID uC-qsflnu33B143a07b1 Method BLASTX NCBI GI q3287693 BLAST score 617 E value 2.0e-64 Match length 150 % identity 73 (AC003979) Similar to LIM17 gene product gb 1653769 from NCBI Description the genome of Synechocystis sp. gb\_D90916. [Arabidopsis thaliana] 236821 Seq. No. uC-gsflnu33B143b09b1 Seq. ID Method BLASTX NCBI GI q4567228 268 BLAST score 1.0e-23 E value 74 Match length % identity (AC007119) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 236822

Seq. ID uC-gsflnu33B143d03b1

Method BLASTX NCBI GI g1653395



```
BLAST score
                   362
                   2.0e - 34
E value
Match length
                   141
                   50
% identity
                  (D90913) PET112 [Synechocystis sp.]
NCBI Description
Seq. No.
                   236823
                   uC-gsflnu33B143e09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1706263
BLAST score
                   322
E value
                   7.0e-30
Match length
                   129
                   48
% identity
                   CYSTEINE PROTEINASE 5 PRECURSOR >gi 1222694 (L36205) CP5
NCBI Description
                   [Dictyostelium discoideum]
                   236824
Seq. No.
                   uC-gsflnu33B143f02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1076809
BLAST score
                   459
                   5.0e-46
E value
                   125
Match length
                   78
% identity
                   H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi 758355 emb_CAA59800_ (X85805) H(+)-transporting ATPase
                   [Zea mays]
                   236825
Seq. No.
                   uC-gsflnu33B143f06b1
Seq. ID
                   BLASTX
Method
                   q4426964
NCBI GI
BLAST score
                   331
                   6.0e-31
E value
Match length
                   80
 % identity
                   71
                   (AF126255) purple acid phosphatase precursor [Anchusa
NCBI Description
                   officinalis]
 Seq. No.
                   236826
                   uC-gsflnu33B143g12b1
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g4249384
BLAST score
                   241
E value
                   3.0e-20
                   99
Match length
 % identity
                   44
                   (AC005966) Similar to gi 4056506 F3G5.25 nodulin-like
NCBI Description
                   protein from Arabidopsis thaliana BAC gb AC005896.
                   [Arabidopsis thaliana]
                   236827
 Seq. No.
```

Seq. ID uC-gsflnu33B143h10b1

Method BLASTX
NCBI GI g1172977
BLAST score 562



```
E value
                   6.0e-58
Match length
                   135
% identity
                   81
NCBI Description
                   60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
                   ribosomal protein L18 [Arabidopsis thaliana]
                   236828
Seq. No.
                   uC-gsflnu33B144a01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2352084
BLAST score
                   144
E value
                   6.0e-09
Match length
                   77
                   49
% identity
NCBI Description
                  (U96613) serine/threonine kinase [Arabidopsis thaliana]
                   236829
Seq. No.
Seq. ID
                   uC-gsflnu33B144b03b1
Method
                   BLASTX
NCBI GI
                   g1172004
BLAST score
                   586
E value
                   8.0e-61
Match length
                   134
                   84
% identity
NCBI Description
                   PHENYLALANINE AMMONIA-LYASE >gi_1345583_emb_CAA53581
                   (X75967) phenylalanine ammonium lyase [Vitis vinifera]
Seq. No.
                   236830
Seq. ID
                   uC-gsflnu33B144c06b1
Method
                   BLASTX
NCBI GI
                   g2760362
BLAST score
                   239
E value
                   2.0e-26
Match length
                   75
                   85
 % identity
NCBI Description
                   (AF016511) 15.9 kDa subunit of RNA polymerase II
                   [Arabidopsis thaliana]
Seq. No.
                   236831
Seq. ID
                   uC-qsflnu33B144c08b1
Method
                   BLASTX
NCBI GI
                   g4455351
BLAST score
                   150
E value
                   8.0e-10
Match length
                   44
 % identity
                   57
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                   236832
Seq. ID
                   uC-gsflnu33B144d01b1
Method
                   BLASTX
NCBI GI
                   g2995366
```

NCBI GI g2995366
BLAST score 172
E value 2.0e-12
Match length 107
% identity 36

NCBI Description (AL022245) hypothetical protein [Schizosaccharomyces pombe]



```
Seq. No.
                   236833
Seq. ID
                   uC-qsflnu33B144d09b1
Method
                   BLASTX
NCBI GI
                   g3776557
BLAST score
                   150
E value
                   1.0e-09
Match length
                   55
% identity
                   53
NCBI Description
```

(AC005388) Contains similarity to gi 2924495 hypothetical protein Rv1920 from Mycobacterium tuberculosis genome

gb\_AL022020. [Arabidopsis thaliana]

Seq. No. Seq. ID uC-qsflnu33B144e02b1 Method BLASTX NCBI GI g974294 BLAST score 203 E value 5.0e-16 Match length 81

52 % identity

NCBI Description (U31309) LP6 [Pinus taeda]

236834

Seq. No. 236835

Seq. ID uC-gsflnu33B144e05b1

Method BLASTX NCBI GI q3914997 BLAST score 443 E value 5.0e-44Match length 130 67 % identity

ARGININE DECARBOXYLASE (ARGDC) (ADC) NCBI Description

>gi\_2129876\_pir\_\_S59553 arginine decarboxylase (EC 4.1.1.19) - garden pea >gi\_609220\_emb\_CAA85773\_ (Z37540)

arginine decarboxylase [Pisum satīvum]

236836 Seq. No.

Seq. ID uC-gsflnu33B144e06b1

Method BLASTX NCBI GI g3193324 BLAST score 334 3.0e-31 E value Match length 126 42 % identity

NCBI Description (AF069299) contains similarity to WD domains, G-beta

repeats (Pfam: G-beta.hmm, score: 22.80 and 35.84)

[Arabidopsis thaliana]

Seq. No. 236837

Seq. ID uC-gsflnu33B144g07b1

Method BLASTX NCBI GI g4558673 BLAST score 153 3.0e-10 E value Match length 108 % identity 33

NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]



```
236838
Seq. No.
Seq. ID
                   uC-gsflnu33B144g09b1
                   BLASTX
Method
                   g2970051
NCBI GI
BLAST score
                   341
                   3.0e-32
E value
Match length
                   69
% identity
                   93
NCBI Description (AB012110) ARG10 [Vigna radiata]
Seq. No.
                   236839
Seq. ID
                   uC-qsflnu33B144q12b1
Method
                   BLASTX
NCBI GI
                   q1706917
BLAST score
                   149
E value
                   1.0e-09
Match length
                   76
% identity
                   37
NCBI Description FLAVONOL SULFOTRANSFERASE-LIKE >gi 2129586 pir S69188
                   flavonol sulfotransferase - Arabidopsis thaliana >gi_833767_emb_CAA86850.1_ (Z46823) Flavonol
                   sulfotransferase [Arabidopsis thaliana]
Seq. No.
                   236840
                   uC-qsflnu33B144h08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3123264
BLAST score
                   469
E value
                   4.0e-47
                   121
Match length
                   75
% identity
                  60S RIBOSOMAL PROTEIN L27 >gi 2244857 emb CAB10279
NCBI Description
                   (Z97337) hypothetical protein [Arabidopsis thaliana]
                   236841
Seq. No.
Seq. ID
                   uC-gsflnu33B145b01b1
                   BLASTX
Method
NCBI GI
                   g3182921
BLAST score
                   334
E value
                   3.0e-31
                   69
Match length
                   90
% identity
NCBI Description
                  ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING)
                   (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_1432054
                   (U55873) asparagine synthetase [Oryza sativa]
                   >gi 1902992 dbj BAA18951 (D83378) asparagine synthetase
                   [Oryza sativa]
                   236842
Seq. No.
Seq. ID
                   uC-gsflnu33B145c04b1
Method
                   BLASTX
NCBI GI
                   g2129622
BLAST score
                   149
```

34355

4.0e-10

47

62

E value

Match length % identity

```
immunophilin FKBP15-1 - Arabidopsis thaliana >gi 1272406
NCBI Description
                  (U52046) immunophilin [Arabidopsis thaliana]
                  236843
Seq. No.
                  uC-gsflnu33B145c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3643603
BLAST score
                  460
E value
                  4.0e-46
Match length
                  126
                  73
% identity
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  236844
                  uC-gsflnu33B145d02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2723477
BLAST score
                  617
E value
                  2.0e-64
Match length
                  149
% identity
                  80
NCBI Description (D89824) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                  236845
Seq. ID
                  uC-gsflnu33B145e04b1
                  BLASTX
Method
NCBI GI
                  q4455202
BLAST score
                  458
                  1.0e-45
E value
Match length
                  146
                  60
% identity
                  (AL035440) putative APG protein [Arabidopsis thaliana]
NCBI Description
                  236846
Seq. No.
                  uC-gsflnu33B145e06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172597
BLAST score
                  226
E value
                  1.0e-18
Match length
                  47
                  91
% identity
                  WOUND-INDUCED BASIC PROTEIN >gi 81888 pir JS0731
NCBI Description
                  wound-inducible basic protein - kidney bean >gi 169365
                   (L00625) basic protein [Phaseolus vulgaris]
                  >gi_217989_dbj_BAA02299_ (D12914) 5.8 kb basic protein
                   [Phaseolus vulgaris]
                  236847
Seq. No.
```

Seq. ID uC-gsflnu33B145e10b1

Method BLASTX
NCBI GI g2662415
BLAST score 173
E value 2.0e-12
Match length 56
% identity 54

NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca]



```
236848
Seq. No.
Seq. ID
                  uC-gsflnu33B145f01b1
                  BLASTX
Method
NCBI GI
                  g3980384
BLAST score
                  351
                  3.0e-33
E value
Match length
                  109
% identity
                  61
                  (AC004561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  236849
Seq. No.
Seq. ID
                  uC-gsflnu33B145f06b1
                  BLASTX
Method
NCBI GI
                  q21309
BLAST score
                  341
                  4.0e-32
E value
Match length
                  81
                  42
% identity
                 (X57955) 28kD RNA binding protein [Spinacia oleracea]
NCBI Description
                  236850
Seq. No.
Seq. ID
                  uC-qsflnu33B145g05b1
                  BLASTX
Method
NCBI GI
                  g3152560
                  176
BLAST score
E value
                  8.0e-13
                  65
Match length
                  51
% identity
                  (AC002986) Strong similarity to ser/thr protein kinases,
NCBI Description
                  especially gb X97980 from solanum berthaultii, gb_X90990
                  from solanum tuberosum and gb D10909 from A. thaliana.
                   [Arabidopsis thaliana]
                  236851
Seq. No.
Seq. ID
                  uC-gsflnu33B145g06b1
                  BLASTX
Method
NCBI GI
                  q21309
BLAST score
                  346
E value
                  1.0e-32
                  79
Match length
                  43
% identity
NCBI Description (X57955) 28kD RNA binding protein [Spinacia oleracea]
                  236852
Seq. No.
Seq. ID
                  uC-gsflnu33B145h10b1
Method
                  BLASTX
NCBI GI
                  g1223579
BLAST score
                  215
E value
                  2.0e-17
Match length
                  108
```

% identity 52

NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]

236853 Seq. No.

uC-gsflnu33B146a01b1 Seq. ID

BLASTX Method NCBI GI g4559327



BLAST score 316 3.0e-29 E value 108 Match length % identity 58

(AC007087) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 236854

Seq. ID uC-gsflnu33B146a10b1

Method BLASTX NCBI GI g3482967 BLAST score 272 E value 1.0e-24Match length 65 % identity 74

(AL031369) Protein phosphatase 2C-like protein [Arabidopsis NCBI Description

thaliana] >gi\_4559345\_gb\_AAD23006.1\_AC006585\_1 (AC006585)

protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 236855

uC-gsflnu33B146c06b1 Seq. ID

Method BLASTX NCBI GI g81857 BLAST score 221 E value 4.0e-18 Match length 45 % identity 87

IqE-dependent histamine-releasing factor homolog - alfalfa NCBI Description

(fragment) >gi\_19658\_emb\_CAA45349\_ (X63872) translationally

controlled tumor protein [Medicago sativa]

236856 Seq. No.

uC-gsflnu33B146e02b1 Seq. ID

BLASTX Method q2129927 NCBI GI BLAST score 306 E value 3.0e-28Match length 62 92 % identity

zeta-carotene desaturase precursor - pepper NCBI Description

>gi 1176437 bbs 171885 zeta-carotene desaturase,

CapZDS=phytoene desaturase homolog [Capsicum annuum, early

ripening fruit, Peptide, 588 aa]

236857 Seq. No.

Seq. ID uC-gsflnu33B146e10b1

BLASTX Method NCBI GI g3915866 BLAST score 555 E value 3.0e-57

Match length 120 82 % identity

GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) NCBI Description

>gi 2995455 emb CAA62901 (X91787) tRNA-glutamine

synthetase [Lupinus luteus]

Seq. No. 236858

Seq. ID uC-gsflnu33B146f06b1



Method BLASTX
NCBI GI g2288999
BLAST score 153
E value 5.0e-10
Match length 127
% identity 46

NCBI Description (AC002335) electron transfer flavoprotein ubiquinone

oxidoreductase isolog [Arabidopsis thaliana]

Seq. No. 236859

Seq. ID uC-gsflnu33B146f12b1

Method BLASTX
NCBI GI g3641647
BLAST score 447
E value 1.0e-44
Match length 101
% identity 78

NCBI Description (AB006804) ACC synthase [Cucumis sativus]

Seq. No. 236860

Seq. ID uC-gsflnu33B146g01b1

Method BLASTX
NCBI GI g4240253
BLAST score 141
E value 6.0e-09
Match length 75
% identity 41

NCBI Description (AB020689) KIAA0882 protein [Homo sapiens]

Seq. No. 236861

Seq. ID uC-gsflnu33B146g04b1

Method BLASTX
NCBI GI 94115913
BLAST score 508
E value 1.0e-51
Match length 152
% identity 61

NCBI Description (AF118222) contains similarity to Iron/Ascorbate family of

oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana] >gi 4539409 emb CAB40042.1

(AL049524) putative flavanone 3-beta-hydroxylase

[Arabidopsis thaliana]

Seq. No. 236862

Seq. ID uC-gsronu33B001a07b1

Method BLASTX
NCBI GI g4106696
BLAST score 262
E value 9.0e-23
Match length 68

NCBI Description (AB021872) ribosome-sedimenting protein [Pisum sativum]

Seq. No. 236863

% identity

Seq. ID uC-gsronu33B001a09b1

Method BLASTX NCBI GI g1850546



```
241
BLAST score
                   3.0e-20
E value
Match length
                   61
                   74
% identity
                   (U88045) syntaxin related protein AtVam3p [Arabidopsis
NCBI Description
                   thaliana]
                   236864
Seq. No.
                   uC-gsronu33B001c02b1
Seq. ID
                   BLASTX
Method
                   g4220469
NCBI GI
BLAST score
                   145
                   5.0e-09
E value
Match length
                   51
                   63
% identity
                   (AC006069) putative receptor protein kinase, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
                   236865
Seq. No.
                   uC-gsronu33B001c04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g136057
                   510
BLAST score
                   7.0e-52
E value
                   130
Match length
                   75
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                   >gi_99499_pir__A32187 (S)-tetrahydroberberine oxidase -
                   Coptis japonica >gi 556171 (J04121) triosephosphate
                   isomerase [Coptis japonica]
Seq. No.
                   236866
                   uC-gsronu33B001c10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1907076
BLAST score
                   378
E value
                   2.0e-36
Match length
                   118
% identity
                   60
                   (Y07867) pirin [Homo sapiens] >gi 1907078_emb_CAA69195_
NCBI Description
                   (Y07868) pirin [Homo sapiens]
                   >gi_4505823_ref_NP_003653.1_pPIR_ pirin
                   236867
Seq. No.
                   uC-gsronu33B001f03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2979549
```

BLAST score 376 E value 4.0e-36 Match length 128 52 % identity

NCBI Description (AC003680) putative 7-ethoxycoumarin O-deethylase

[Arabidopsis thaliana]

Seq. No. 236868

uC-gsronu33B001g03b1 Seq. ID

Method BLASTX



```
q538607
NCBI GI
BLAST score
                   141
E value
                   1.0e-11
Match length
                   44
% identity
                   89
NCBI Description
                   superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4A - maize
                   >gi 1885354 (U34727) superoxide dismutase 4A [Zea mays]
Seq. No.
                   236869
Seq. ID
                   uC-gsronu33B001g07b1
Method
                   BLASTX
NCBI GI
                   q3643611
BLAST score
                   577
E value
                   1.0e-59
Match length
                   149
% identity
                   70
NCBI Description
                   (AC005395) putative casein kinase [Arabidopsis thaliana]
Seq. No.
                   236870
                   uC-gsronu33B001g12b1
Seq. ID
Method
                   BLASTX
·NCBI GI
                   q112863
BLAST score
                   466
E value
                   7.0e-47
Match length
                   117 -
% identity
                   72
NCBI Description
                   STYLE DEVELOPMENT-SPECIFIC PROTEIN 9612 PRECURSOR
                   >gi_100227_pir__S12209 hypothetical protein - tomato
>gi_19162_emb_CAA38979_ (X55193) 9612 [Lycopersicon
                   esculentum]
                   236871
Seq. No.
Seq. ID
                   uC-gsronu33B001h08b1
Method
                   BLASTX
NCBI GI
                   q1362015
BLAST score
                   201
E value
                   2.0e-15
Match length
                   74
% identity
                   58
NCBI Description
                   zinc finger protein 1 - Arabidopsis thaliana
                   >gi_2129779_pir__S71240 zinc finger protein 1 - Arabidopsis
                   thaliana >gi 790673 (L39644) zinc finger protein
                   [Arabidopsis thaliana] >gi_1297186 (U53501) zinc finger
                   protein 1 [Arabidopsis thaliana]
                   236872
Seq. No.
                   uC-gsronu33B002c01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3402687
BLAST score
                   417
E value
                   6.0e-41
Match length
                   123
% identity
NCBI Description
                   (AC004697) unknown protein [Arabidopsis thaliana]
```

236873

uC-gsronu33B002c10b1

Seq. No. Seq. ID

% identity



```
Method
                   BLASTX
NCBI GI
                   q1706956
                   368
BLAST score
E value
                   4.0e-35
Match length
                   72
                   97
% identity
NCBI Description
                  (U58283) cellulose synthase [Gossypium hirsutum]
Seq. No.
                   236874
Seq. ID
                   uC-gsronu33B002d07b1
Method
                   BLASTX
NCBI GI
                   g4510356
BLAST score
                   326
E value
                   2.0e-30
Match length
                   117
% identity
                   53
NCBI Description
                   (AC006921) putative kinesin-related protein TKRP125
                   [Arabidopsis thaliana]
Seq. No.
                   236875
Seq. ID
                   uC-gsronu33B002d10b1
Method
                   BLASTX
NCBI GI
                   g2920706
BLAST score
                   226
E value
                   1.0e-18
Match length
                   139
% identity
                   41
NCBI Description
                  (Y13568) beta-xylosidase [Emericella nidulans]
                   236876
Seq. No.
Seq. ID
                   uC-gsronu33B002e10b1
Method
                   BLASTX
NCBI GI
                   g3688173
BLAST score
                   637
E value
                   9.0e-67
Match length
                   146
% identity
                   78
NCBI Description
                  (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                   236877
Seq. ID
                   uC-qsronu33B002q01b1
Method
                   BLASTX
NCBI GI
                   g3668079
BLAST score
                   232
E value
                   5.0e-30
Match length
                   114
% identity
                   67
NCBI Description
                   (AC004667) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   236878
Seq. ID
                   uC-gsronu33B002g11b1
Method
                   BLASTX
NCBI GI
                   g3834350
BLAST score
                   149
E value
                   2.0e-09
Match length
                   72
```

Seq. No.





```
NCBI Description
                  (AB010991) 3b-hydroxylase [Lycopersicon esculentum]
                  236879
Seq. No.
Seq. ID
                  uC-gsronu33B002h05b1
Method
                  BLASTX
NCBI GI
                  g2244855
BLAST score
                  198
E value
                  2.0e-15
Match length
                  97
% identity
                  45
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  236880
Seq. ID
                  uC-gsronu33B004a01b1
Method
                  BLASTX
NCBI GI
                  g2262111
BLAST score
                  234
E value
                  5.0e-24
Match length
                  81
% identity
                  65
                  (AC002343) ribitol dehydrogenase isolog [Arabidopsis
NCBI Description
                  thaliana]
                  236881
Seq. No.
Seq. ID
                  uC-gsronu33B004a06b1
Method
                  BLASTX
NCBI GI
                  g3377850
BLAST score
                  147
E value
                  8.0e-10
Match length
                  39
                  77
% identity
NCBI Description
                  (AF076274) contains simlarity to Canis familiaris signal
                  peptidase complex 25 kDa subunit (GB:U12687) [Arabidopsis
                  thaliana]
                  236882
Seq. No.
Seq. ID
                  uC-gsronu33B004a08b1
Method
                  BLASTX
NCBI GI
                  g4522005
BLAST score
                  167
                  1.0e-11
E value
Match length
                  86
% identity
                  41
NCBI Description
                  (AC007069) putative reverse transcriptase [Arabidopsis
                  thaliana]
Seq. No.
                  236883
                  uC-gsronu33B004b02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3242710
BLAST score
                  282
E value
                  2.0e-25
Match length
                  102
% identity
                  62
NCBI Description
                  (AC003040) hypothetical protein [Arabidopsis thaliana]
```



```
uC-gsronu33B004b04b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1922251
BLAST score
                    372
E value
                    1.0e-35
                    79
Match length
% identity
                    92
NCBI Description
                    (Y12072) farnesyl pyrophosphate synthase [Gossypium
Seq. No.
                    236885
Seq. ID
                    uC-gsronu33B004d05b1
Method
                    BLASTX
NCBI GI
                    q120669
BLAST score
                    321
E value
                    6.0e - 30
Match length
                    63
% identity
                    95
NCBI Description
                    GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                    >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                    >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                    3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                    236886
Seq. ID
                    uC-gsronu33B004e10b1
Method
                    BLASTX
NCBI GI
                    q4006888
BLAST score
                    355
E value
                    8.0e-34
Match length
                    104
% identity
                    62
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                    236887
Seq. ID
                    uC-gsronu33B005a06b1
Method
                    BLASTX
NCBI GI
                    g119150
BLAST score
                    453
E value
                    3.0e-45
                    92
Match length
                    95
% identity
NCBI Description
                    ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                    >gi_82081_pir__S10507 translation elongation factor eEF-1
alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF
                    1-alpha (AA 1-448) [Lycopersicon esculentum]
                    >gi_295810_emb_CAA37212_ (X53043) elongation factor 1-alpha
                    [Lycopersicon esculentum]
                    236888
Seq. No.
Seq. ID
                    uC-gsronu33B005c05b1
Method
                    BLASTX
```

NCBI GI g4522004 BLAST score 342 E value 3.0e - 32Match length 123 % identity 66



(AC007069) putative histidine kinase, sensory transduction NCBI Description [Arabidopsis thaliana] 236889 Seq. No. Seq. ID uC-gsronu33B005d09b1 Method BLASTX NCBI GI g1174870 BLAST score 214 E value 4.0e-17

69 % identity UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN NCBI Description >gi 633685 emb CAA55861 (X79274) ubiquinol--cytochrome c

reductase [Solanum tuberosum]

236890 Seq. No.

Match length

Seq. ID uC-gsronu33B005d11b1

59

 ${\tt BLASTX}$ Method NCBI GI q2664210 209 BLAST score 1.0e-16 E value Match length 51

% identity (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis NCBI Description

thaliana]

Seq. No. 236891

Seq. ID uC-gsronu33B007b02b1

73

BLASTX Method NCBI GI g3327269 BLAST score 284 1.0e-25 E value Match length 108 % identity 55

NCBI Description (AB015999) PKn1 [Ipomoea nil]

Seq. No. 236892

Seq. ID uC-gsronu33B007d05b1

Method BLASTX NCBI GI g1173209 BLAST score 142 1.0e-08 E value 58 Match length % identity 60

NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal

protein S16 protein - upland cotton

>gi\_439654\_emb\_CAA53567\_ (X75954) RS16 protein, 40S subunit

[Gossypium hirsutum]

Seq. No. 236893

Seq. ID uC-gsronu33B007e02b1

Method BLASTX NCBI GI q4467147 BLAST score 412 E value 2.0e-40 Match length 91 % identity 89



```
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
Seq. No.
                  236894
                  uC-gsronu33B007f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3924597
BLAST score
                  140
E value
                  1.0e-08
Match length
                  59
% identity
                  44
NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  236895
                  uC-gsronu33B007f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4185819
BLAST score
                  192
                  7.0e-15
E value
Match length
                  47
% identity
                  68
                  (AF116845) metallothionein-like type 1 protein [Ipomoea
NCBI Description
                  batatas]
                  236896
Seq. No.
Seq. ID
                  uC-gsronu33B007g03b1
Method
                  BLASTX
NCBI GI
                  g122106
BLAST score
                  410
E value
                   4.0e-40
Match length
                  82
% identity
                  100
                  HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize
NCBI Description
                  >gi 81642 pir S06904 histone H4 - Arabidopsis thaliana
                  >gi 2119028 pir S60475 histone H4 - garden pea
                  >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum
                  aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis
                   thaliana] >gi 166742 (M17133) histone H4 [Arabidopsis
                  thaliana] >gi 168499 (M36659) histone H4 (H4C13) [Zea mays]
                  >gi_168501 (M\overline{1}3370) histone H4 [Zea mays] >gi_168503
                   (M13377) histone H4 [Zea mays] >gi 498898 (U10042) histone
                  H4 homolog [Pisum sativum] >gi_1806285_emb CAB01914
                   (Z79638) histone H4 homologue [Sesbania rostrata]
                  >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                  >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4
                   [Arabidopsis thaliana] >gi 225838 prf 1314298A histone H4
                   [Arabidopsis thaliana]
                  236897
Seq. No.
Seq. ID
                  uC-gsronu33B007h03b1
Method
                  BLASTX
NCBI GI
                  g113621
BLAST score
                  395
                  1.0e-38
E value
                  91
Match length
% identity
                  86
```

>gi 68196 pir ADZM fructose-bisphosphate aldolase (EC

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME



4.1.2.13), cytosolic - maize >gi\_168420 (M16220) aldolase [Zea mays] >gi\_295850\_emb\_CAA31366\_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi 225624 prf 1307278A cytoplasmic aldolase [Zea mays]

236898 Seq. No.

uC-gsronu33B008a09b1 Seq. ID

Method BLASTX NCBI GI g3023194 BLAST score 708 5.0e-75E value Match length 163 % identity 94

14-3-3-LIKE PROTEIN A (SGF14A) >gi 1575725 (U70533) SGF14A NCBI Description

[Glycine max]

236899

Seq. No. Seq. ID uC-gsronu33B008b02b1

Method BLASTX NCBI GI g3643088 BLAST score 167 3.0e-12E value Match length 52 % identity 62

(AF075581) protein phosphatase-2C; PP2C [Mesembryanthemum NCBI Description

crystallinum]

236900 Seq. No.

Seq. ID uC-gsronu33B008b06b1

Method BLASTX g2342690 NCBI GI 293 BLAST score E value 2.0e-26 85 Match length

% identity 71

NCBI Description (AC000106) Similar to Homo copine I (gb U83246).

[Arabidopsis thaliana]

Seq. No. 236901

uC-gsronu33B008b10b1 Seq. ID

BLASTX Method NCBI GI g629602 BLAST score 321 E value 9.0e-42 Match length 180 49 % identity

NCBI Description probable imbibition protein - wild cabbage

>qi.488787 emb CAA55893 (X79330) putative imbibition

protein [Brassica oleracea]

236902 Seq. No.

uC-gsronu33B008c06b1 Seq. ID

BLASTX Method NCBI GI q3176660 BLAST score 613 E value 7.0e-64 Match length 159



% identity NCBI Description (AC004393) Similar to ERECTA receptor protein kinase gb U47029 from A. thaliana. [Arabidopsis thaliana] 236903 Seq. No. Seq. ID uC-gsronu33B008e02b1 Method BLASTX NCBI GI g3603473 BLAST score 206 E value 4.0e-16 Match length 76 % identity 57 NCBI Description (AF090698) elicitor-responsive gene-3 [Oryza sativa] Seq. No. 236904 Seq. ID uC-gsronu33B008e04b1 Method BLASTX NCBI GI g4038352 BLAST score 239 E value 3.0e-20 Match length 101 % identity 47 (AF098951) breast cancer resistance protein [Homo sapiens] NCBI Description Seq. No. 236905 Seq. ID uC-gsronu33B008f03b1 Method BLASTX NCBI GI q2739360 BLAST score 433 E value 9.0e-43Match length 145 % identity 63 NCBI Description (AC002505) unknown protein [Arabidopsis thaliana] >gi 3075385 (AC004484) unknown protein [Arabidopsis thaliana] 236906 Seq. No. Seq. ID uC-gsronu33B008f10b1 Method BLASTX NCBI GI g2662415 BLAST score 173 E value 2.0e-12 56 Match length % identity 54 NCBI Description (U97494) metallothionein-like protein [Prunus armeniaca] Seq. No. 236907 Seq. ID uC-gsronu33B008f11b1 Method BLASTX NCBI GI q4455190 BLAST score 473 E value 2.0e-47

Match length 121 % identity

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 236908



uC-gsronu33B008h12b1 Seq. ID Method BLASTX NCBI GI g730463 BLAST score 321 E value 1.0e-29 Match length 102 60 % identity NCBI Description 60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi\_630323\_pir\_\_S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi\_484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi\_1420537\_emb\_CAA99454\_ (Z75142) ORF YOR234c [Saccharomyces cerevisiae] 236909 Seq. No. Seq. ID uC-gsronu33B009a06b1 Method BLASTX NCBI GI q2462781 BLAST score 408 3.0e-40E value Match length 95 75 % identity NCBI Description (U73175) carbamoyl phosphate synthetase small subunit [Arabidopsis thaliana] 236910 Seq. No. Seq. ID uC-gsronu33B011a09b1 BLASTX Method g2829926 NCBI GI BLAST score 186 E value 6.0e-14Match length 116 % identity 42 NCBI Description (AC002291) Hypothetical protein [Arabidopsis thaliana] Seq. No. 236911 Seq. ID uC-gsronu33B011c03b1 Method BLASTX NCBI GI q1657948 BLAST score 378 E value 2.0e-36 Match length 138 89 % identity NCBI Description (U73466) MipC [Mesembryanthemum crystallinum] 236912 Seq. No. Seq. ID uC-gsronu33B011d06b1 Method BLASTX NCBI GI g2642432 BLAST score 99 E value 6.0e-09

Match length 105 % identity 47

(AC002391) putative elicitor response element binding NCBI Description

protein (WRKY3) [Arabidopsis thaliana]

Seq. No. 236913



Seq. ID uC-gsronu33B011e07b1 Method BLASTX NCBI GI g4204297 269 BLAST score E value 2.0e-23 Match length 163 % identity 47 NCBI Description (AC003027) ADK1 [Arabidopsis thaliana] Seq. No. 236914 Seq. ID uC-gsronu33B011e08b1 Method BLASTX NCBI GI q2664210 BLAST score 476 E value 9.0e-48 Match length 100 % identity 88 NCBI Description (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis thaliana] Seq. No. 236915 Seq. ID uC-gsronu33B011e10b1 Method BLASTX NCBI GI q3334157 BLAST score 495 E value 4.0e-50 Match length 110 % identity 84 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) NCBI Description (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi\_1220142 emb CAA59468 (X85185) cyclophilin [Catharanthus roseus] Seq. No. 236916 Seq. ID uC-gsronu33B011f06b1 Method BLASTX NCBI GI q267069 BLAST score 369 E value 1.0e-35 Match length 67 % identity 97 NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi 166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >qi 166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana] Seq. No. 236917 Seq. ID uC-gsronu33B011f07b1 Method BLASTX NCBI GI g1408460 BLAST score 269

E value 1.0e-23 Match length 65 % identity

NCBI Description (U40161) type 2A protein serine/threonine phosphatase 55

kDa B regulatory subunit [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  uC-gsronu33B011h05b1
Method
                  BLASTX
NCBI GI
                  .g4204293
BLAST score
                  722
E value
                  1.0e-76
Match length
                  166
                  80
% identity
                  (AC003027) 1cl prt seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  236919
Seq. ID
                  uC-gsronu33B011h09b1
Method
                  BLASTX
NCBI GI
                  g4263711
BLAST score
                  349
E value
                  4.0e-33
                  73
Match length
                  88
% identity
                 (AC006223) putative CCR4-associated transcription factor
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  236920
Seq. ID
                  uC-gsronu33B011h10b1
Method
                  BLASTX
NCBI GI
                  g4204293
BLAST score
                  649
E value
                  1.0e-74
Match length
                  162
                  82
% identity
                  (AC003027) lcl_prt_seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
                  236921
Seq. No.
Seq. ID
                  uC-gsronu33B012a09b1
Method
                  BLASTX
NCBI GI
                  q2618688
BLAST score
                  196
E value
                  1.0e-15
Match length
                  50
% identity
NCBI Description (AC002510) putative esterase D [Arabidopsis thaliana]
Seq. No.
                  236922
Seq. ID
                  uC-gsronu33B012a10b1
Method
                  BLASTX
NCBI GI
                  q3292824
BLAST score
                  259
E value
                  2.0e-22
```

Match length 114 % identity 55

NCBI Description (AL031018) putative protein [Arabidopsis thaliana]

Seq. No. 236923

uC-gsronu33B012b09b1 Seq. ID

Method BLASTX NCBI GI g1091678

NCBI Description



```
BLAST score
                   193
                   9.0e-15
E value
Match length
                  79
% identity
                   53
NCBI Description activator-like transposable element [Pennisetum glaucum]
Seq. No.
                   236924
Seq. ID
                  uC-gsronu33B012c05b1
Method
                  BLASTX
NCBI GI
                  g2213621
BLAST score
                  196
E value
                   5.0e-15
Match length
                   50
% identity
                   72
                  (AC000103) F21J9.26 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   236925
Seq. ID
                  uC-gsronu33B012c07b1
Method
                  BLASTX
NCBI GI
                   g3928150
BLAST score
                   441
E value
                   1.0e-43
Match length
                   98
% identity
                   90
NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]
Seq. No.
                   236926
Seq. ID
                  uC-gsronu33B012c12b1
Method
                  BLASTX
NCBI GI
                   g3122673
BLAST score
                   263
E value
                   3.0e-24
Match length
                  111
% identity
                   57
NCBI Description
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                  236927
Seq. No.
Seq. ID
                  uC-gsronu33B012d03b1
                  BLASTX
Method
NCBI GI
                   g984756
BLAST score
                   147
E value
                   3.0e-09
Match length
                   90
% identity
                   47
NCBI Description
                  (Z54153) chilling-inducible protein [Oryza sativa]
                  236928
Seq. No.
Seq. ID
                  uC-gsronu33B012e02b1
Method
                  BLASTX
NCBI GI
                  g1350707
BLAST score
                  212
                   5.0e-17
E value
                   52
Match length
% identity
                  73
```

60S RIBOSOMAL PROTEIN L29 >gi\_539923\_pir\_\_JC2012 ribosomal protein 17K - mouse >gi 404766 (L08651) ribosomal protein

E value

Match length

% identity

2.0e-20

57

81



## [Mus musculus]

```
Seq. No.
                   236,929
Seq. ID
                   uC-gsronu33B012q07b1
Method
                   BLASTX
NCBI GI
                   q4388829
BLAST score
                   167
E value
                   1.0e-11
Match length
                   78
                   37
% identity
NCBI Description
                   (AC006528) putative pol polyprotein with a Zn-finger CCHC
                   type domain (prosite:QDOC50158) and a DDE integrase
                   signature motif [Arabidopsis thaliana]
Seq. No.
                   236930
Seq. ID
                   uC-gsronu33B012g10b1
Method
                   BLASTX
NCBI GI
                   g123379
BLAST score
                   141
E value
                   1.0e-08
Match length
                   31
% identity
                   HMG1/2-LIKE PROTEIN (SB11 PROTEIN) >gi_99914_pir__$22309
HMG-1-like protein - soybean >gi_18645_emb_CAA41200_
NCBI Description
                   (X58245) HMG-1 like protein gene [Glycine max]
Seq. No.
                   236931
Seq. ID
                   uC-gsronu33B014b10b1
Method
                   BLASTX
NCBI GI
                   g2982452
BLAST score
                   220
E value
                   5.0e-18
                   107
Match length
% identity
                   42
NCBI Description
                   (AL022223) receptor protein kinase-like protein
                   [Arabidopsis thaliana]
                   236932
Seq. No.
Seq. ID
                   uC-gsronu33B014e04b1
Method
                   BLASTX
NCBI GI
                   g1616614
BLAST score
                   207
E value
                   1.0e-16
Match length
                   40
% identity
                   100
NCBI Description
                   (Y08425) small GTP-binding protein [Nicotiana
                   plumbaginifolia]
Seq. No.
                   236933
Seq. ID
                   uC-gsronu33B014e05b1
Method
                   BLASTX
NCBI GI
                   g140400
                   237
BLAST score
```

NCBI Description HYPOTHETICAL 37.2 KD PROTEIN IN CHA1-PRD1 INTERGENIC REGION



>gi\_83176\_pir\_\_S19389 hypothetical protein YCL059c - yeast
(Saccharomyces cerevisiae) >gi\_5300\_emb\_CAA42386\_ (X59720)
YCL059c, len:316 [Saccharomyces cerevisiae]

Seq. No. 236934

Seq. ID uC-gsronu33B014e12b1

Method BLASTX
NCBI GI g4220472
BLAST score 225
E value 4.0e-19
Match length 64
% identity 73

NCBI Description (AC006069) similar to yeast ccc1 protein [Arabidopsis

thaliana]

Seq. No. 236935

Seq. ID uC-gsronu33B014g11b1

Method BLASTX
NCBI GI g2821957
BLAST score 141
E value 3.0e-09
Match length 56

% identity 50
NCBI Description (AB006691) spermidine synthase 2 [Hyoscyamus niger]

Seq. No. 236936

Seq. ID uC-gsronu33B015a06b1

Method BLASTX
NCBI GI g3548815
BLAST score 188
E value 4.0e-14
Match length 124
% identity 43

NCBI Description (AC005313) similar to axoneme-associated protein mst101

[Arabidopsis thaliana]

Seq. No. 236937

Seq. ID uC-gsronu33B015a07b1

Method BLASTX
NCBI GI g3924601
BLAST score 463
E value 3.0e-46
Match length 116
% identity 80

NCBI Description (AF069442) putative rac GTPase activating protein

[Arabidopsis thaliana] >gi\_4262138\_gb\_AAD14438\_ (AC005275)

putative rac GTPase-activating protein [Arabidopsis

thaliana]

Seq. No. 236938

Seq. ID uC-gsronu33B015b06b1

Method BLASTX
NCBI GI g2465923
BLAST score 388
E value 5.0e-43
Match length 144
% identity 62



NCBI Description (AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No. 236939

uC-gsronu33B015b09b1

Method BLASTX
NCBI GI g4006827
BLAST score 540
E value 2.0e-55
Match length 151
% identity 77

Seq. ID

NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 236940

Seq. ID uC-gsronu33B015c07b1

Method BLASTX
NCBI GI g3668089
BLAST score 424
E value 1.0e-41
Match length 143
% identity 56

NCBI Description (AC004667) unknown protein [Arabidopsis thaliana]

Seq. No. 236941

Seq. ID uC-gsronu33B015e03b1

Method BLASTX
NCBI GI g1172441
BLAST score 384
E value 5.0e-37
Match length 160
% identity 57

NCBI Description POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi\_99685 pir S21883

DNA-binding protein POSF21 - Arabidopsis thaliana >gi 16429 emb CAA43366 (X61031) posF21 [Arabidopsis

thaliana]

Seq. No. 236942

Seq. ID uC-gsronu33B015f02b1

Method BLASTX
NCBI GI g1401078
BLAST score 488
E value 3.0e-49
Match length 151
% identity 58

NCBI Description (U46691) putative chromatin structure regulator [Homo

sapiens]

Seq. No.

236943

Seq. ID uC-gsronu33B015f07b1

Method BLASTX
NCBI GI g3152596
BLAST score 372
E value 9.0e-36
Match length 131
% identity 63

NCBI Description (AC002986) YUP8H12R.36 [Arabidopsis thaliana]



```
Seq. No.
                  uC-gsronu33B015f10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206199
BLAST score
                  142
                  1.0e-08
E value
                  95
Match length
% identity
                  24
NCBI Description
                  (AF071527) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  236945
                  uC-gsronu33B015g02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191140
BLAST score
                  281
E value
                   6.0e-25
Match length
                  105
% identity
                   59
NCBI Description
                   (AF007269) contains weak similarity to MYB-related proteins
                   [Arabidopsis thaliana]
Seq. No.
                  236946
Seq. ID
                  uC-gsronu33B015g11b1
Method
                  BLASTX
NCBI GI
                  q3242717
BLAST score
                  145
E value
                   1.0e-13
Match length
                  124
% identity
                   36
NCBI Description
                  (AC003040) putative APG protein [Arabidopsis thaliana]
                  236947
Seq. No.
Seq. ID
                  uC-gsronu33B015h11b1
Method
                  BLASTX
NCBI GI
                  g4371280
                   395
BLAST score
E value
                  2.0e-38
Match length
                  117
% identity
                   66
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  236948
Seq. No.
Seq. ID
                  uC-gsronu33B016a03b1
Method
                  {\tt BLASTX}
NCBI GI
                  q4335745
BLAST score
                  180
E value
                   4.0e-13
Match length
                  58
                   50
% identity
```

NCBI Description (AC006284) putative hydrolase (contains an

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 236949

Seq. ID uC-gsronu33B016b04b1

Method BLASTX NCBI GI g3281846

% identity

82



```
167
BLAST score
                  1.0e-11
E value
                  58
Match length
                  59
% identity
                  (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
NCBI Description
                  236950
Seq. No.
                  uC-gsronu33B016b05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3850108
BLAST score
                  365
                  7.0e-35
E value
                  137
Match length
                  54
% identity
                  (AL033388) putative calcium-transporting atpase
NCBI Description
                   [Schizosaccharomyces pombe]
                  236951
Seq. No.
                  uC-gsronu33B016c04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4097561
BLAST score
                  564
                  3.0e-58
E value
                  119
Match length
                   90
% identity
                  (U64918) ATGP1 [Arabidopsis thaliana]
NCBI Description
                  236952
Seq. No.
                  uC-gsronu33B016c05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3924597
BLAST score
                  268
                   2.0e-23
E value
Match length
                   168
                   34
% identity
NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]
                   236953
Seq. No.
Seq. ID
                  uC-qsronu33B016d08b1
Method
                  BLASTX
NCBI GI
                   q3953471
BLAST score
                   281
                   5.0e-25
E value
                   73
Match length
                   66
% identity
NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
                   236954
                   uC-gsronu33B016d09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3150407
BLAST score
                   301
E value
                   2.0e-27
Match length
                   65
```

NCBI Description (AC004165) hypothetical protein [Arabidopsis thaliana]

Method

NCBI GI

BLASTX

g1871187



```
236955
Seq. No.
                  uC-qsronu33B016d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2632106
BLAST score
                  439
E value
                  1.0e-43
Match length
                  113
                  76
% identity
                  (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  236956
                  uC-gsronu33B016h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3176711
BLAST score
                  319
E value
                   2.0e-29
Match length
                  148
                   49
% identity
NCBI Description
                  (AC002392) bZIP-like protein [Arabidopsis thaliana]
                  236957
Seq. No.
                  uC-gsronu33B016h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q461929
BLAST score
                   526
E value
                   8.0e-54
Match length
                  118
% identity
                   54
                  PROBABLE TONOPLAST INTRINSIC PROTEIN DIP
NCBI Description
                   >gi_1076688_pir__S51781 integral membrane protein - garden
                   snapdragon >gi 414088 emb CAA49854 (X70417) integral
                  membrane protein [Antirrhinum majus]
                   236958
Seq. No.
Seq. ID
                   uC-gsronu33B017a08b1
Method
                  BLASTX
                   q4467095
NCBI GI
                   237
BLAST score
                   5.0e-20
E value
Match length
                   105
% identity
                   50
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
                   236959
Seq. No.
Seq. ID
                   uC-gsronu33B017d11b1
                  BLASTX
Method
                   g1938227
NCBI GI
                   320
BLAST score
                   1.0e-29
E value
                  130
Match length
% identity
                   53
                  (X93312) Carbonic anhydrase [Medicago sativa]
NCBI Description
                   236960
Seq. No.
Seq. ID
                   uC-gsronu33B017e03b1
```



BLAST score E value 5:0e-61 Match length 135 79 % identity NCBI Description Seq. No. 236961 Seq. ID Method BLASTX NCBI GI BLAST score 317

(U90439) unknown protein [Arabidopsis thaliana]

uC-gsronu33B017e10b1

g2281090 E value 2.0e-29 Match length 98 % identity 62

NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236962

Seq. ID uC-gsronu33B017g08b1

Method BLASTX NCBI GI g2501056 BLAST score 328 E value 4.0e-31 Match length 71 % identity 85

NCBI Description SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)

>gi\_2129737\_pir S71293 seryl-tRNA synthetase - Arabidopsis thaliana >gi\_1359497\_emb\_CAA94388\_ (Z70313) seryl-tRNA

Synthetase [Arabidopsis thaliana]

Seq. No. 236963

Seq. ID uC-gsronu33B018b01b1

Method BLASTX NCBI GI g3063396 BLAST score 384 E value 8.0e-54 Match length 118 % identity 89

NCBI Description (AB012947) vcCyP [Vicia faba]

Seq. No. 236964

Seq. ID uC-gsronu33B018c01b1

Method BLASTX NCBI GI q2738949 BLAST score 453 E value 3.0e-45Match length 93 % identity 91

NCBI Description (AF022213) cytosolic ascorbate peroxidase [Fragaria x

ananassa]

Seq. No. 236965

Seq. ID uC-gsronu33B018c12b1

Method BLASTX NCBI GI q4510376 BLAST score 296 E value 5.0e-27 Match length 87

Seq. ID



```
% identity
NCBI Description
                  (AC007017) unknown protein [Arabidopsis thaliana]
                  236966
Seq. No.
Seq. ID
                  uC-gsronu33B018d03b1
Method
                  BLASTX
NCBI GI
                  g4572674
BLAST score
                  274
                  3.0e-24
E value
Match length
                  61
                  79
% identity
NCBI Description
                  (AC006954) unknown protein [Arabidopsis thaliana]
Seq. No.
                  236967
Seq. ID
                  uC-gsronu33B018d07b1
Method
                  BLASTX
NCBI GI
                  g2827623
BLAST score
                  213
E value
                  4.0e-17
                  46
Match length
% identity
                  91
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
                  236968
Seq. No.
Seq. ID
                  uC-gsronu33B018d11b1
Method
                  BLASTX
NCBI GI
                  g1657619
BLAST score
                  404
E value
                  2.0e-39
Match length
                  164
% identity
                  46
NCBI Description
                  (U72504) G5p [Arabidopsis thaliana] >gi 3068710 (AF049236)
                  putative transmembrane protein G5p [Arabidopsis thaliana]
Seq. No.
                  236969
Seq. ID
                  uC-gsronu33B018f01b1
Method
                  BLASTX
NCBI GI
                  g3608412
BLAST score
                  334
E value
                  4.0e-31
Match length
                  99
% identity
                  65
NCBI Description
                  (AF079355) protein phosphatase-2c [Mesembryanthemum
                  crystallinum]
Seq. No.
                  236970
Seq. ID
                  uC-gsronu33B018f10b1
Method
                  BLASTX
NCBI GI
                  g3769671
BLAST score
                  350
E value
                  4.0e-33
Match length
                  81
% identity
                  78
NCBI Description
                  (AF095284) Tic22 [Pisum sativum]
Seq. No.
                  236971
```

34380

uC-gsronu33B018f12b1

Match length



```
Method
                    BLASTX
 NCBI GI
                    g2738949
 BLAST score
                    377
                    2.0e-36
 E value
 Match length
                    84
  % identity
                    85
 NCBI Description
                    (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                    ananassa]
                    236972
  Seq. No.
 Seq. ID
                    uC-gsronu33B019a03b1
                    BLASTX
 Method
 NCBI GI
                    g1710551
  BLAST score
                    281
 E value
                    5.0e-25
 Match length
                    51
  % identity
                    100
 NCBI Description 60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728
                    (X95458) ribosomal protein L39 [Zea mays]
                    236973
  Seq. No.
                    uC-gsronu33B019a04b1
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3201627
 BLAST score
                    473
 E value
                    2.0e-47
Match length
                    142
  % identity
                    64
 NCBI Description (AC004669) putative SWH1 protein [Arabidopsis thaliana]
  Seq. No.
                    236974
  Seq. ID
                    uC-gsronu33B019b07b1
 Method
                    BLASTX
 NCBI GI
                    q2425129
 BLAST score
                    234
 E value
                    1.0e-19
 Match length
                    92
  % identity
                    53
 NCBI Description (AF020280) PkgA [Dictyostelium discoideum]
  Seq. No.
                    236975
  Seq. ID
                    uC-qsronu33B019c12b1
 Method
                    BLASTX
 NCBI GI
                    g2213592
 BLAST score
                    489
 E value
                    2.0e-49
 Match length
                  . 143
  % identity
                    33
 NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]
  Seq. No.
                    236976
                    uC-gsronu33B019d03b1
  Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2341024
 BLAST score
                    177
 E value
                    8.0e-13
```



```
% identity
                  (AC000104) F19P19.1 [Arabidopsis thaliana]
NCBI Description
                  236977
Seq. No.
                  uC-gsronu33B019d04b1
Seq. ID
                  BLASTX
Method
                  q3882149
NCBI GI
BLAST score
                  296
E value
                  8.0e-27
Match length
                  116
% identity
                  43
                  (AB018257) KIAA0714 protein [Homo sapiens]
NCBI Description
Seq. No.
                  236978
                  uC-gsronu33B019d09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3913295
BLAST score
                  365
E value
                  7.0e-47
Match length
                  154
% identity
                   56
NCBI Description
                  CAFFEIC ACID 3-O-METHYLTRANSFERASE
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi 602588 emb CAA58218
                   (X83217) caffeic O-methyltransferase [Prunus dulcis]
                  236979
Seq. No.
                  uC-gsronu33B019e10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1669601
                   328
BLAST score
                   2.0e-30
E value
Match length
                  131
% identity
                   53
NCBI Description (D88747) AR401 [Arabidopsis thaliana]
                   236980
Seq. No.
Seq. ID
                   uC-gsronu33B019f12b1
Method
                   BLASTX
NCBI GI
                   g2129752
BLAST score
                   419
                   4.0e-41
E value
                   107
Match length
                   71
% identity
NCBI Description thioredoxin - Arabidopsis thaliana >gi 992964 emb CAA84612_
                   (Z35475) thioredoxin [Arabidopsis thaliana]
                   236981
Seq. No.
Seq. ID
                   uC-gsronu33B019g03b1
                   BLASTX
Method
NCBI GI
                   g4432855
```

NCBI GI g4432855
BLAST score 382
E value 6.0e-37
Match length 132
% identity 62

NCBI Description (AC006300) unknown protein [Arabidopsis thaliana]



```
236982
Seq. No.
                  uC-gsronu33B019g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g99755
BLAST score
                  341
E value
                  4.0e-32
Match length
                  103
% identity
                  61
                  RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis
NCBI Description
                  thaliana retrotransposon Ta1-1 (fragment)
                  >gi 16356 emb CAA37917 (X53973) reverse transcriptase
                  [Arabidopsis thaliana]
                  236983
Seq. No.
Seq. ID
                  uC-gsronu33B019g12b1
Method
                  BLASTX
NCBI GI
                  g3860272
BLAST score
                  150
E value
                  4.0e-10
                  32
Match length
% identity
                  88
NCBI Description
                  (AC005824) putative suppressor protein [Arabidopsis
                  thaliana] >gi 4314399 gb AAD15609 (AC006232) putative skd1
                  protein [Arabidopsis thaliana]
                  236984
Seq. No.
Seq. ID
                  uC-gsronu33B021a06b1
Method
                  BLASTX
NCBI GI
                  g401189
BLAST score
                  423
E value
                  9.0e-44
                  105
Match length
% identity
                  88
NCBI Description WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN (WSI-TIP)
                  (TURGOR-RESPONSIVE PROTEIN 7A) >gi 485511 pir S33617
                  trg-31 protein - garden pea >gi 20426 emb CAA79159_
                  (Z18288) trg-31 [Pisum sativum]
Seq. No.
                  236985
                  uC-gsronu33B021a12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662310
BLAST score
                  247
E value
                  2.0e-21
Match length
                  78
                  67
% identity
```

NCBI Description (AB009307) bpw1 [Hordeum vulgare]

Seq. No. 236986

Seq. ID uC-gsronu33B021b04b1

Method BLASTX g4376203 NCBI GI BLAST score 298 E value 7.0e-27 Match length 125 % identity

NCBI Description (U35226) putative cytochrome P-450 [Nicotiana



## plumbaginifolia]

Seq. No. 236987

Seq. ID uC-gsronu33B021c09b1

Method BLASTX
NCBI GI g1352681
BLAST score 419
E value 3.0e-41
Match length 128
% identity 65

NCBI Description PROTEIN PHOSPHATASE 2C (PP2C) >gi\_1076391\_pir\_\_S55457

phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis

thaliana >gi 633028 dbj BAA07287 (D38109) protein

phosphatase 2C [Arabidopsis thaliana]

Seq. No. 236988

Seq. ID uC-gsronu33B02ld10b1

Method BLASTX
NCBI GI g455858
BLAST score 445
E value 3.0e-44
Match length 128
% identity 66

NCBI Description (AC007138) putative polygalacturonidase [Arabidopsis

thaliana]

Seq. No. 236989

Seq. ID uC-gsronu33B021e11b1

Method BLASTX
NCBI GI g2062167
BLAST score 205
E value 4.0e-16
Match length 49
% identity 76

NCBI Description (AC001645) Proline-rich protein APG isolog [Arabidopsis

thaliana]

Seq. No. 236990

Seq. ID uC-gsronu33B021e12b1

Method BLASTX
NCBI GI g3319353
BLAST score 255
E value 4.0e-22
Match length 73
% identity 58

NCBI Description (AF077407) contains similarity to copper-binding proteins

[Arabidopsis thaliana]

Seq. No. 236991

Seq. ID uC-gsronu33B021f01b1

Method BLASTX
NCBI GI g2618686
BLAST score 189
E value 2.0e-14
Match length 89
% identity 40

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

BLAST score

E value

279 3.0e-25



```
Seq. No.
                   236992
Seq. ID
                   uC-gsronu33B021f02b1
Method
                   BLASTX
NCBI GI
                   g3608155
BLAST score
                   518
E value
                   8.0e-53
Match length
                   135
% identity
                   68
NCBI Description
                  (AC005314) putative RNA helicase [Arabidopsis thaliana]
                   236993
Seq. No.
Seq. ID
                   uC-gsronu33B021h11b1
Method
                   BLASTX
NCBI GI
                   g2880046 -
BLAST score
                   260
E value
                   2.0e-22
Match length
                   110
% identity
                   55
NCBI Description
                  (AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   236994
Seq. ID
                   uC-gsronu33B027b01b1
Method
                   BLASTX
NCBI GI
                   q405080
BLAST score
                   148
E value
                   1.0e-09
Match length
                   101
% identity
                   40
NCBI Description
                  (U01058) ABC family transporter [Entamoeba histolytica]
Seq. No.
                   236995
Seq. ID
                   uC-gsronu33B027b09b1
Method
                   BLASTX
NCBI GI
                   g2245094
BLAST score
                   178
E value
                   8.0e-13
Match length
                   102
% identity
                   43
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   236996
Seq. ID
                   uC-gsronu33B027c11b1
Method
                  BLASTX
NCBI GI
                   q3256066
BLAST score
                   288
E value
                   2.0e-37
Match length
                   95
% identity
NCBI Description
                  (Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]
Seq. No.
                  236997
Seq. ID
                  uC-gsronu33B027e04b1
Method
                  BLASTX
NCBI GI
                  g2583118
```



Match length 87 % identity 62

NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]

Seq. No. 236998

Seq. ID uC-gsronu33B027e07b1

Method BLASTX
NCBI GI g3915031
BLAST score 408
E value 4.0e-40
Match length 85

% identity 93

NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR

(STEAROYL-ACP DESATURASE) >gi\_1217628\_emb\_CAA65232

(X95988) delta 9 stearoyl-[acyl-carrier protein] desaturase

[Gossypium hirsutum]

Seq. No. 236999

Seq. ID uC-gsronu33B027e10b1

Method BLASTX
NCBI GI g100099
BLAST score 256
E value 1.0e-29
Match length 78
% identity 87

NCBI Description DNA-binding protein VBP1 - fava bean >gi 1372966 (M81827)

CREB-like protein [Vicia faba]

Seq. No. 237000

Seq. ID uC-gsronu33B027f01b1

Method BLASTX
NCBI GI g121353
BLAST score 400
E value 3.0e-39
Match length 102
% identity 76

NCBI Description GLUTAMINE SYNTHETASE LEAF ISOZYME PRECURSOR (ISOZYME DELTA)

(GLUTAMATE-AMMONIA LIGASE) >gi 68596 pir AJFBQD

glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - kidney bean >gi\_21005\_emb\_CAA31234\_ (X12738)

GS precursor protein [Phaseolus vulgaris]

Seq. No. 237001

Seq. ID uC-gsronu33B027f08b1

Method BLASTX
NCBI GI g2598589
BLAST score 463
E value 2.0e-46
Match length 125
% identity 62

NCBI Description (Y15367) MtN19 [Medicago truncatula]

Seq. No. 237002

Seq. ID uC-gsronu33B027f11b1

Method BLASTX NCBI GI g2498883 BLAST score 431



2.0e-56 E value Match length 147 74 % identity SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150) NCBI Description >gi 1173905 (U41371) spliceosome associated protein [Homo sapiens] Seq. No. 237003 Seq. ID uC-gsronu33B028c12b1 Method BLASTX g282881 NCBI GI BLAST score 510 7.0e-52 E value Match length 138 % identity 67 receptor-like protein kinase precursor - Arabidopsis NCBI Description thaliana >gi 166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana] 237004 Seq. No. Seq. ID uC-gsronu33B028h03b1 Method BLASTX NCBI GI g2342682 BLAST score 208 E value 5.0e-17 Match length 50 74 % identity NCBI Description (AC000106) Contains similarity to Rattus AMP-activated protein kinase (gb\_X95577). [Arabidopsis thaliana] 237005 Seq. No. Seq. ID uC-gsronu33B029b10b1 Method BLASTX NCBI GI g3860250 BLAST score 233 E value 8.0e-20 50 Match length 90 % identity (AC005824) putative chloroplast prephenate dehydratase NCBI Description [Arabidopsis thaliana] 237006 Seq. No. Seq. ID uC-gsronu33B029b11b1 Method BLASTX NCBI GI g4324597 BLAST score 102

Method BLASTX
NCBI GI g4324597
BLAST score 102
E value 6.0e-09
Match length 95
% identity 45

NCBI Description (AF106324) sodium proton exchanger Nhx1 [Arabidopsis

thaliana]

Seq. No. 237007

Seq. ID uC-gsronu33B029d09b1

Method BLASTX NCBI GI g171366 BLAST score 253



```
1.0e-21
E value
Match length
                  158
% identity
                   35
                  (M69294) alantoinase [Saccharomyces cerevisiae]
NCBI Description
                   237008
Seq. No.
                  uC-gsronu33B029f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1184123
BLAST score
                  228
E value
                   9.0e-19
                  79
Match length
% identity
                  (U20809) auxin-induced protein [Vigna radiata]
NCBI Description
                  237009
Seq. No.
                  uC-gsronu33B031a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3033377
BLAST score
                   410
E value
                   4.0e-40
Match length
                  137
% identity
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   237010
Seq. No.
Seq. ID
                   uC-gsronu33B031b03b1
Method
                  BLASTX
NCBI GI
                   g4103635
BLAST score
                   328
E value
                   2.0e-30
                  94
Match length
% identity
                   64
                  (AF026538) ABA-responsive protein [Hordeum vulgare]
NCBI Description
                   237011
Seq. No.
Seq. ID
                   uC-gsronu33B031b10b1
Method
                  BLASTX
NCBI GI
                   g3549660
BLAST score
                   341
E value
                   5.0e-32
Match length
                   123
% identity
                   56
NCBI Description
                   (AL031394) carbonate dehydratase - like protein
                   [Arabidopsis thaliana]
                   237012
Seq. No.
Seq. ID
                   uC-gsronu33B031e03b1
Method
                  BLASTX
NCBI GI
                   g2738949
BLAST score
                   290
E value
                   3.0e-26
Match length
                   90
% identity
NCBI Description
                   (AF022213) cytosolic ascorbate peroxidase [Fragaria x
                   ananassa]
```



```
Seq. No.
                  237013
Seq. ID
                  uC-gsronu33B031g01b1
                  BLASTX
Method
NCBI GI
                  g2384760
BLAST score
                  189
E value
                  2.0e-14
Match length
                  47
% identity
                  74
NCBI Description
                  (AF016897) GDP dissociation inhibitor protein OsGDI2 [Oryza
                  sativa]
Seq. No.
                  237014
Seq. ID
                  uC-gsronu33B031g08b1
                  BLASTX
Method
NCBI GI
                  g3548802
BLAST score
                  185
                  3.0e-14
E value
Match length
                  53
% identity
                  64
                   (AC005313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4335769 gb AAD17446 (AC006284) putative axi1 protein
                  [Nicotiana tabacum] [Arabidopsis thaliana]
Seq. No.
                  237015
                  uC-gsronu33B031h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3402704
BLAST score
                  469
E value
                  6.0e-47
Match length
                  138
% identity
                  (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  237016
Seq. ID
                  uC-gsronu33B032c03b1
Method
                  BLASTX
NCBI GI
                  q3461846
BLAST score
                  300
E value
                  1.0e-27
Match length
                  84
                  36
% identity
                  (AC005315) putative zinc-finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  237017
Seq. No.
Seq. ID
                  uC-gsronu33B032g02b1
                  BLASTX
Method
NCBI GI
                  g2129742
BLAST score
                  275
E value
                  3.0e-24
```

% identity 65 NCBI Description stress-induced protein OZI1 precursor - Arabidopsis

77

Match length

thaliana >gi\_790583 (U20347) mRNA corresponding to this gene accumulates in response to ozone stress and pathogen (bacterial) infection; putative pathogenesis-related

parameter, parameter,

Seq. No.

Seq. ID



protein [Arabidopsis thaliana] >gi\_2252869 (AF013294) No
definition line found [Arabidopsis thaliana]

Seq. No. 237018 Seq. ID uC-gsronu33B036a11b1 Method BLASTX NCBI GI q1518540 BLAST score 489 E value 2.0e-49Match length 104 % identity 92 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max] 237019 Seq. No. Seq. ID uC-gsronu33B036b01b1 Method BLASTX NCBI GI g1787721 BLAST score 163 E value 4.0e-11 Match length 144 % identity 30 NCBI Description (AE000242) putative oxidoreductase [Escherichia coli] Seq. No. 237020 Seq. ID uC-gsronu33B036b07b1 Method BLASTX NCBI GI g1652057 BLAST score 422 E value 1.0e-41Match length 121 % identity 68 NCBI Description (D90902) hypothetical protein [Synechocystis sp.] Seq. No. 237021 Seq. ID uC-gsronu33B036c05b1 Method BLASTX NCBI GI g3204129 BLAST score 321 E value 1.0e-29 Match length 78 % identity 82 NCBI Description (AJ006768) histone H2A [Cicer arietinum] Seq. No. 237022 Seq. ID uC-gsronu33B036c10b1 Method BLASTX NCBI GI g3738298 BLAST score 236 E value 1.0e-19 Match length 151 % identity 35 NCBI Description (AC005309) unknown protein [Arabidopsis thaliana] >gi 4249394 (AC006072) unknown protein [Arabidopsis thaliana]

uC-gsronu33B036d03b1



```
BLASTX
Method
NCBI GI
                  g2253583
BLAST score
                  294
E value
                  1.0e-26
                  96
Match length
% identity
                  66
NCBI Description (U78721) hypothetical protein [Arabidopsis thaliana]
                  237024
Seq. No.
Seq. ID
                  uC-gsronu33B036f08b1
Method
                  BLASTX
NCBI GI
                  g2443887
BLAST score
                  614
E value
                  5.0e-64
Match length
                  152
                  76
% identity
                  (AC002294) Similar to transcription factor
NCBI Description
                  gb_Z46606_1658307 and others [Arabidopsis thaliana]
                  237025
Seq. No.
Seq. ID
                  uC-gsronu33B036h01b1
Method
                  BLASTX
NCBI GI
                  q1170409
BLAST score
                  188 .
E value
                  4.0e-14
Match length
                  61
% identity
                  67
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22)
NCBI Description
                  >gi_549887 (U09336) homeobox protein [Arabidopsis thaliana]
                  >gi_549888 (U09337) homeobox protein [Arabidopsis thaliana]
                  >gi 4490724_emb_CAB38927.1_ (AL035709) homeobox protein
                  HAT22 [Arabidopsis thaliana]
Seq. No.
                  237026
                  uC-gsronu33B037b05b1
Seq. ID
                  {\tt BLASTX}
Method
NCBI GI
                  g881625
BLAST score
                  319
E value
                  2.0e-29
Match length
                  70
% identity
NCBI Description (U29432) 22.8 kDa protein [Ipomoea trifida]
Seq. No.
                  237027
                  uC-gsronu33B037b06b1
Seq. ID
                  BLASTX
Method
                  -q1076685
NCBI GI
BLAST score
                  358
E value
                  3.0e-34
Match length
                  103
% identity
                  44
NCBI Description SPF1 protein - sweet potato >gi 484261 dbj BAA06278
                  (D30038) SPF1 protein [Ipomoea batatas]
```

Seq. No. 237028

Seq. ID uC-gsronu33B037b10b1

Method BLASTX



NCBI GI g3738089
BLAST score 231
E value 2.0e-19
Match length 86
% identity 59
NCBI Description (AC00561

(AC005617) similar to symbiotic ammonium transporter, SAT1 [Arabidopsis thaliana] >gi\_4314372\_gb\_AAD15583\_ (AC006340) putative symbiotic ammonium transporter SAT1 [Arabidopsis thaliana]

thaliana]

Seq. No. 237029

Seq. ID uC-gsronu33B037c09b1

Method BLASTX
NCBI GI g4263722
BLAST score 312
E value 5.0e-29
Match length 90
% identity 67

NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]

Seq. No. 237030

Seq. ID uC-gsronu33B037f01b1

Method BLASTX
NCBI GI g3033380
BLAST score 430
E value 1.0e-42
Match length 102
% identity 80

NCBI Description (AC004238) putative coatomer epsilon subunit [Arabidopsis

thaliana]

Seq. No. 237031

Seq. ID uC-gsronu33B037f05b1

Method BLASTX
NCBI GI g3953471
BLAST score 222
E value 3.0e-18
Match length 53
% identity 70

NCBI Description (AC002328) F2202.16 [Arabidopsis thaliana]

Seq. No. 237032

Seq. ID uC-gsronu33B037f12b1

Method BLASTX
NCBI GI g3548802
BLAST score 372
E value 1.0e-35
Match length 141
% identity 51

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi 4335769 gb AAD17446 (AC006284) putative axi1 protein

[Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 237033

Seq. ID uC-gsronu33B037g07b1

Method BLASTX NCBI GI g3986110

Match length

% identity

120

92



```
BLAST score
                  1.0e-12
E value
Match length
                  49
                  67
% identity
NCBI Description (AB012716) heat shock protein 70 cognate [Salix gilgiana]
                  237034
Seq. No.
                  uC-gsronu33B037h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1077378
BLAST score
                  281
                  4.0e-25
E value
                  108
Match length
% identity
                  18
                  probable membrane protein YLR222c - yeast (Saccharomyces
NCBI Description
                  cerevisiae) >gi_609371 (U19027) Ylr222cp [Saccharomyces
                  cerevisiae]
Seq. No.
                  237035
                  uC-gsronu33B038b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928150
BLAST score
                  466
                  1.0e-46
E value
Match length
                  101
% identity
                  91
NCBI Description (AJ131049) hypothetical protein [Cicer arietinum]
                  237036
Seq. No.
                  uC-gsronu33B038c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3850585
BLAST score
                  426
                  3.0e-42
E value
Match length
                  131
% identity
                  68
                  (AC005278) ESTs gb H36966, gb_R65511, gb_T42324 and
NCBI Description
                  gb_T20569 come from this gene. [Arabidopsis thaliana]
                  237037
Seq. No.
                  uC-gsronu33B038c05b1
Seq. ID
                  BLASTX
Method
                  g2660674
NCBI GI
BLAST score
                  163
E value
                   4.0e-11
                  32
Match length
% identity
NCBI Description (AC002342) hypothetical protein [Arabidopsis thaliana]
                   237038
Seq. No.
                  uC-gsronu33B038d03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2213877
BLAST score
                  589
E value
                   4.0e-61
```

Seq. No.

237044



```
NCBI Description
                   (AF003197) glutamine synthetase [Hevea brasiliensis]
                    237039
 Seq. No.
 Seq. ID
                    uC-gsronu33B038e03b1
                    BLASTX
 Method
 NCBI GI
                    g1938424
 BLAST score
                    267
 E value
                    2.0e-23
                    148
 Match length
 % identity
                    39
 NCBI Description
                    (U97002) similar to acyl-CoA dehydrogenases and epoxide
                    hydrolases [Caenorhabditis elegans]
                    237040
 Seq. No.
                    uC-gsronu33B038e09b1
 Seq. ID
                    BLASTX
 Method
                    g3600033
 NCBI GI
 BLAST score
                    475
 E value
                    1.0e-47
 Match length
                    168
 % identity
                    54
                    (AF080119) contains similarity to the N terminal domain of
 NCBI Description
                    the E1 protein (Pfam: E1 N.hmm, score: 12.36) [Arabidopsis
                    thalianal
                    237041
 Seq. No.
 Seq. ID
                    uC-gsronu33B038e11b1
 Method
                    BLASTX
 NCBI GI
                    g2244868
 BLAST score
                    562
                    6.0e-58
 E value
 Match length
                    115
 % identity
                    89
                    (Z97337) cytochrome P450 [Arabidopsis thaliana]
 NCBI Description
Seq. No.
                    237042
 Seq. ID
                    uC-gsronu33B038f12b1
                    BLASTX
 Method
 NCBI GI
                    q4566614
 BLAST score
                    186
 E value
                    3.0e-14
 Match length
                    47
                    77
 % identity
                    (AF112887) actin depolymerizing factor [Populus alba x
 NCBI Description
                    Populus tremula]
                    237043
 Seq. No.
 Seq. ID
                    uC-gsronu33B038g07b1
 Method
                    BLASTX
 NCBI GI
                    q3096922
 BLAST score
                    293
                    2.0e-26
 E value
                    84
 Match length
                    69
  % identity
 NCBI Description
                    (AL023094) putative protein [Arabidopsis thaliana]
```



Seq. ID uC-gsronu33B038h03b1 Method BLASTX NCBI GI q2262113 BLAST score 238 6.0e-20 E value Match length 74 72 % identity (AC002343) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 237045 Seq. ID uC-gsronu33B038h10b1 Method BLASTX NCBI GI q1297187 BLAST score 568 E value 1.0e-58 Match length 162 69 % identity (U53501) similar to protein encoded by GenBank Accession NCBI Description Number U41815, nucleoporin 98 [Arabidopsis thaliana] 237046 Seq. No. uC-gsronu33B039f07b1 Seq. ID Method BLASTX NCBI GI g3860256 BLAST score 358 E value 2.0e-3491 Match length 71 % identity (AC005824) putative tRNA isopentenylpyrophosphate NCBI Description transferase [Arabidopsis thaliana] 237047 Seq. No. uC-gsronu33B039h03b1 Seq. ID BLASTX Method NCBI GI q4335729 BLAST score 201 E value 8.0e-16 Match length 108 % identity NCBI Description (AC006248) putative salt-inducible protein [Arabidopsis thaliana] Seq. No. 237048 Seq. ID uC-gsronu33B040a09b1 Method BLASTX NCBI GI g2459435 BLAST score 144 E value 2.0e-09 Match length 42 % identity 62 (AC002332) putative serine carboxypeptidase [Arabidopsis NCBI Description thaliana]

Seq. No. 237049

Seq. ID uC-gsronu33B040b01b1

Method BLASTX NCBI GI g3395436

```
BLAST score
                   154
E value
                   5.0e-10
Match length
                   123
% identity
                   32
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                   237050
Seq. No.
Seq. ID
                  uC-gsronu33B040c05b1
Method
                   BLASTX
NCBI GI
                   q4566505
BLAST score
                   190
E value
                   9.0e-15
Match length
                   67
                   55
% identity
NCBI Description
                   (AF102868) beta-D-glucan exohydrolase isoenzyme ExoI
                   [Hordeum vulgare]
                   237051
Seq. No.
Seq. ID
                   uC-gsronu33B040f01b1
Method
                  BLASTX
NCBI GI
                   q2911042
BLAST score
                   459
E value
                   6.0e - 46
Match length
                   129
                   74
% identity
NCBI Description
                   (AL021961) Phosphoglycerate dehydrogenase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   237052
Seq. ID
                   uC-gsronu33B041a01b1
Method
                   BLASTX
NCBI GI
                   g3023194
BLAST score
                   644
E value
                   2.0e-67
Match length
                   134
% identity
                   95
```

NCBI Description 14-3-3-LIKE PROTEIN A (SGF14A) >gi\_1575725 (U70533) SGF14A

[Glycine max]

Seq. No. 237053

Seq. ID uC-gsronu33B041e03b1

Method BLASTX
NCBI GI g3335362
BLAST score 167
E value 1.0e-11
Match length 57
% identity 54

NCBI Description (AC003028) putative ribosomal protein S31 [Arabidopsis

thaliana]

Seq. No. 237054

Seq. ID uC-gsronu33B041g06b1

Method BLASTX
NCBI GI g2245131
BLAST score 212
E value 4.0e-17
Match length 74



% identity

```
NCBI Description
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
                   237055
Seq. No.
Seq. ID
                  uC-gsronu33B041h07b1
                  BLASTX
Method
NCBI GI
                  g3850823
                  190
BLAST score
E value
                   7.0e-15
                   70
Match length
                   56
% identity
NCBI Description
                   (Y18351) U2 snRNP auxiliary factor, large subunit
                   [Nicotiana plumbaginifolia]
                   237056
Seq. No.
Seq. ID
                  uC-gsronu33B041h09b1
Method
                  BLASTX
NCBI GI
                  g1173218
BLAST score
                   326
E value
                   2.0e-30
Match length
                   62
% identity
                   100
NCBI Description
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
                   protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
                  237057
Seq. No.
Seq. ID
                  uC-gsronu33B042d02b1
Method
                  BLASTX
NCBI GI
                  g3510505
BLAST score
                  307
E value
                   4.0e-28
Match length
                  130
% identity
                   44
NCBI Description
                  (AF030881) pol polyprotein [Fugu rubripes]
Seq. No.
                  237058
Seq. ID
                  uC-gsronu33B042e04b1
Method
                  BLASTX
NCBI GI
                  g3924603
BLAST score
                  307
E value
                  1.0e-28
Match length
                  76
% identity
NCBI Description
                  (AF069442) putative WD-repeat protein [Arabidopsis
                  thaliana]
Seq. No.
                  237059
Seq. ID
                  uC-gsronu33B042f03b1
Method
                  BLASTX
NCBI GI
                  q417540
BLAST score
                  388
E value
                  2.0e-37
Match length
                  117
% identity
                  67
NCBI Description
                  PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
```

>gi 20851 emb CAA44646 (X62842) pyrroline carboxylate



reductase [Pisum sativum] >gi\_445614\_prf\_\_1909360A
pyrroline carboxylate reductase [Pisum sativum]

Seq. No. 237060

Seq. ID uC-gsronu33B042f08b1

Method BLASTX
NCBI GI g4539298
BLAST score 498
E value 2.0e-50
Match length 148
% identity 64

NCBI Description (AL049480) putative calmodulin-binding protein [Arabidopsis

thaliana]

Seq. No. 237061

Seq. ID uC-gsronu33B042f09b1

Method BLASTX
NCBI GI g294668
BLAST score 198
E value 7.0e-16
Match length 41
% identity 98

NCBI Description (L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No. 237062

Seq. ID uC-gsronu33B044a02b1

Method BLASTX
NCBI GI g4127461
BLAST score 241
E value 6.0e-21
Match length 58
% identity 81

NCBI Description (AJ011674) receptor-like protein kinase, RLK3 [Arabidopsis

thaliana

Seq. No. 237063

Seq. ID uC-gsronu33B044a09b1

Method BLASTX
NCBI GI g3193301
BLAST score 183
E value 3.0e-14
Match length 73
% identity 47

NCBI Description (AF069298) Arabidopsis putative chloroplast outer envelope

86-like protein T10P11.19 (GB: AC002330) [Arabidopsis

thaliana]

Seq. No. 237064

Seq. ID uC-gsronu33B044d03b1

Method BLASTX
NCBI GI g2995405
BLAST score 190
E value 6.0e-15
Match length 51
% identity 76

NCBI Description (Y12432) polyprotein [Ananas comosus]



```
237065
Seq. No.
Seq. ID
                  uC-gsronu33B044e12b1
Method
                  BLASTX
NCBI GI
                  g1173209
BLAST score
                  600
E value
                  2.0e-62
                  120
Match length
% identity
                  99
                  40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal
NCBI Description
                  protein S16 protein - upland cotton
                  >gi_439654_emb_CAA53567_ (X75954) RS16 protein, 40S subunit
                  [Gossypium hirsutum]
Seq. No.
                  237066
Seq. ID
                  uC-gsronu33B044g05b1
Method
                  BLASTX
NCBI GI
                  g2335101
BLAST score
                  523
E value
                  2.0e-53
Match length
                  117
                  79
% identity
NCBI Description
                  (AC002339) unknown protein [Arabidopsis thaliana]
                  237067
Seq. No.
Seq. ID
                  uC-gsronu33B046a03b1
Method
                  BLASTX
NCBI GI
                  g2465923
BLAST score
                  474
E value
                  1.0e-47
Match length
                  122
                  73
% identity
                  (AF024648) receptor-like serine/threonine kinase
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  237068
Seq. ID
                  uC-gsronu33B046c04b1
Method
                  BLASTX
NCBI GI
                  q1076275
BLAST score
                  202
                  2.0e-16
E value
Match length
                  43
                  93
% identity
NCBI Description
                  phenylanaline ammonia-lyase - muskmelon
                  >gi 735957 emb CAA53733 (X76130) phenylanaline
                  ammonia-lyase [Cucumis melo]
                  237069
Seq. No.
Seq. ID
                  uC-gsronu33B046c07b1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2739279
BLAST score 170
E value 4.0e-12
Match length 77
% identity 43

NCBI Description (AJ223177) short chain alcohol dehydrogenase [Nicotiana tabacum] >gi\_2791348\_emb\_CAA11154\_ (AJ223178) short chain

alcohol dehydrogenase [Nicotiana tabacum]



```
Seq. No.
                    237070
  Seq. ID
                    uC-gsronu33B046c09b1
  Method
                    BLASTX
NCBI GI
                    g4457221
  BLAST score
                    230
                     4.0e-19
  E value
  Match length
                     96
                     50
  % identity
NCBI Description (AF127797) putative bZIP DNA-binding protein [Capsicum
                    chinense]
  Seq. No.
                    237071
  Seq. ID
                    uC-gsronu33B046e12b1
  Method
                    BLASTX
  NCBI GI
                    g3126967
  BLAST score
                    211
  E value
                    2.0e-17
  Match length
                    45
  % identity
                    16
  NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]
                    237072
  Seq. No.
  Seq. ID
                    uC-gsronu33B046f04b1
                    BLASTX
  Method
  NCBI GI
                    q2244734
  BLAST score
                    216
  E value
                    6.0e-18
  Match length
                    40
  % identity
                    100
  NCBI Description (D88414) actin [Gossypium hirsutum]
  Seq. No.
                    237073
  Seq. ID
                    uC-qsronu33B046f05b1
  Method
                    BLASTX
  NCBI GI
                    g1587206
  BLAST score
                    491
  E value
                    1.0e-49
  Match length
                    103
  % identity
                     94
  NCBI Description T complex protein [Cucumis sativus]
  Seq. No.
                    237074
                    uC-gsronu33B046h11b1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g2981439
  BLAST score
                    205
  E value
                    1.0e-16
  Match length
                    51
  % identity
                    76
  NCBI Description (AF051853) t-SNARE SED5 [Arabidopsis thaliana]
  Seq. No.
                    237075
                    uC-gsronu33B047a11b1
```

Seq. ID

Method BLASTX NCBI GI g2924777 BLAST score 300



```
E value
                  2.0e-27
Match length
                  102
                  59
% identity
NCBI Description
                  (AC002334) putative receptor protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  237076
Seq. ID
                  uC-gsronu33B047b02b1
Method
                  BLASTX
NCBI GI
                  g2493852
BLAST score
                  291
E value
                  4.0e-26
Match length
                  63
% identity
                  84
NCBI Description CYTOCHROME C OXIDASE POLYPEPTIDE VC
                  >gi_1070356_emb_CAA92107 (Z68091) cytochrome c oxidase, Vc
                  subunit [Hordeum vulgare]
                  237077
Seq. No.
Seq. ID
                  uC-gsronu33B047b08b1
Method
                  BLASTX
NCBI GI
                  g2760327
BLAST score
                  498
E value
                  1.0e-50
Match length
                  109
% identity
                  44
NCBI Description (AC002130) F1N21.12 [Arabidopsis thaliana]
Seq. No.
                  237078
Seq. ID
                  uC-gsronu33B047e03b1
Method
                  BLASTX
                  g1076793
NCBI GI
BLAST score
                  638
E value
                  7.0e-67
Match length
                  138
% identity
                  62
NCBI Description calmodulin cam2 - maize >gi_747917_emb_CAA54583_ (X77397)
                  calmodulin [Zea mays]
                  237079
Seq. No.
Seq. ID
                  uC-gsronu33B047f02b1
Method
                  BLASTX
NCBI GI
                  g2626753
BLAST score
                  522
E value
                  4.0e-53
Match length
                  168
% identity
                  65
NCBI Description (AB008782) sulfate transporter [Arabidopsis thaliana]
                  237080
Seq. No.
Seq. ID
                  uC-gsronu33B048b01b1
```

Method BLASTX NCBI GI q4538911 BLAST score 180 E value 3.0e-13 Match length 119 % identity 32



```
NCBI Description (AL049482) hypothetical protein [Arabidopsis thaliana]
                  237081
Seq. No.
Seq. ID
                  uC-gsronu33B048e02b1
Method
                  BLASTX
NCBI GI
                  g2244749
BLAST score
                  499
E value
                  8.0e-51
Match length
                  98
% identity
                  94
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                  237082
Seq. ID
                  uC-gsronu33B048e05b1
Method
                  BLASTX
NCBI GI
                  g2098705
BLAST score
                  534
E value
                  1.0e-56
Match length
                  153
                  77
% identity
NCBI Description
                  (U82973) pectinesterase [Citrus sinensis]
Seq. No.
                  237083
Seq. ID
                  uC-gsronu33B048e08b1
Method
                  BLASTX
NCBI GI
                  q2244949
BLAST score
                  265
E value
                  2.0e-23
Match length
                  72
% identity
                  75
NCBI Description
                  (Z97339) similarity to ORF - Lilium longiflorum
                   [Arabidopsis thaliana]
Seq. No.
                  237084
Seq. ID
                  uC-gsronu33B048e12b1
                  BLASTX
Method
NCBI GI
                  g2078350
BLAST score
                  212
E value
                  5.0e-17
Match length
                  108
% identity
                  44
NCBI Description
                  (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                  237085
Seq. ID
                  uC-gsronu33B048g02b1
Method
                  BLASTX
NCBI GI
                  g3687389
BLAST score
                  339
E value
                  3.0e-32
Match length
                  78
                  85
% identity
NCBI Description (Y16124) putative cullin protein [Lycopersicon esculentum]
```

Seq. No. 237086

Seq. ID uC-gsronu33B049a03b1

Method BLASTX NCBI GI g4469025



BLAST score 317 E value 2.0e-29 Match length 76 % identity 57

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 237087

Seq. ID uC-gsronu33B049c04b1

Method BLASTX
NCBI GI g2245139
BLAST score 384
E value 3.0e-37
Match length 114
% identity 70

NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237088

Seq. ID uC-gsronu33B049e01b1

Method BLASTX
NCBI GI g1684851
BLAST score 313
E value 9.0e-29
Match length 113
% identity 57

NCBI Description (U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No. 237089

Seq. ID uC-gsronu33B049h04b1

Method BLASTX
NCBI GI g2642215
BLAST score 244
E value 6.0e-21
Match length 61
% identity 80

NCBI Description (AF030386) NOI protein [Arabidopsis thaliana]

Seq. No. 237090

Seq. ID uC-gsronu33B049h08b1

Method BLASTX
NCBI GI g4467133
BLAST score 197
E value 3.0e-15
Match length 102
% identity 49

NCBI Description (AL035540) geranylgeranyl pyrophosphate synthase-related

protein [Arabidopsis thaliana]

Seq. No. 237091

Seq. ID uC-gsronu33B050a10b1

Method BLASTX
NCBI GI g3885336
BLAST score 142
E value 1.0e-08
Match length 89
% identity 34

NCBI Description (AC005623) receptor-like protein kinase [Arabidopsis

thaliana]

```
237092
Seq. No.
                  uC-gsronu33B050c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3983665
BLAST score
                   710
                   3.0e-75
E value
                   163
Match length
                   81
% identity
                  (AB011271) importin-beta2 [Oryza sativa]
NCBI Description
Seq. No.
                   237093
Seq. ID
                   uC-gsronu33B050c09b1
                   BLASTX
Method
NCBI GI
                   g2911040
                   397
BLAST score
                   2.0e-38
E value
                   129
Match length
                   59
% identity
NCBI Description
                   (AL021961) receptor protein kinase - like protein
                   [Arabidopsis thaliana]
                  .237094
Seq. No.
                   uC-gsronu33B050d12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2262103
                   233
BLAST score
                   2.0e-19
E value
                   57
Match length
                   74
% identity
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                   237095
Seq. No.
                   uC-gsronu33B050f04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2257524
BLAST score
                   299
E value
                   5.0e-27
Match length
                   136
                   49
% identity
NCBI Description
                   (AB004537) HYPOTHETICAL 47.4KD PROTEIN IN SHP1-SEC17
                   INTERGENIC REGION [Schizosaccharomyces pombe]
Seq. No.
                   237096
                   uC-gsronu33B050f05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3288721
BLAST score
                   417
                   7.0e-41
E value
Match length
                   127
% identity
                   62
                  (AB015872) chalcone synthase [Vitis vinifera]
NCBI Description
                   237097
Seq. No.
                   uC-gsronu33B050g02b1
Seq. ID
```

34404

BLASTX

g3451074

Method NCBI GI



```
BLAST score
                  379
                  2.0e-36 ·
E value
Match length
                  149
                  53
% identity
                 (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  237098
Seq. ID
                  uC-gsronu33B051c03b1
Method
                  BLASTX
NCBI GI
                  g2244841
BLAST score
                  199
E value
                  1.0e-15
Match length
                  49
% identity
                  80
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                  237099
Seq. No.
Seq. ID
                  uC-gsronu33B051f01b1
Method
                  BLASTX
NCBI GI
                  g2370459
BLAST score
                  256
                  2.0e-23
E value
                  77
Match length
                  75
% identity
NCBI Description (Y11987) FPF1 protein [Sinapis alba]
Seq. No.
                  237100
Seq. ID
                  uC-gsronu33B055a09b1
Method
                  BLASTX
NCBI GI
                  g3080401
BLAST score
                  207
                  6.0e-17
E value
Match length
                  46
                  80
% identity
                  (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4455265_emb_CAB36801.1_ (AL035527) putative protein
                  [Arabidopsis thaliana]
Seq. No.
                  237101
                  uC-gsronu33B055b08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1149569
BLAST score
                  299
E value
                  2.0e-27
Match length
                  87
                  72
% identity
NCBI Description (Z50851) HD-zip [Arabidopsis thaliana]
Seq. No.
                  237102
Seq. ID
                  uC-gsronu33B055d05b1
                  BLASTX
Method
```

Method BLASTX
NCBI GI g4056506
BLAST score 309
E value 1.0e-28
Match length 82
% identity 73

NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]



```
Seq. No.
                  237103
                  uC-gsronu33B055d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4049401
BLAST score
                  185
E value
                  5.0e-14
Match length
                  51
% identity
                  67
                  (AJ131580) glutathione transferase AtGST 10 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No. Seq. ID
                  237104
                  uC-gsronu33B055d09b1
                  BLASTX
Method
NCBI GI
                  g1169200
BLAST score
                  313
E value
                  2.0e-29
Match length
                  73
                  79
% identity
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR
NCBI Description
                  >gi_421829_pir__S33706 DNA-damage resistance protein -
                  Arabidopsis thaliana >gi_166694 (M98455) [Arabidopsis
                  thaliana recombination and DNA-damage resistance protein
                   (DRT111) mRNA, complete cds.], gene product [Arabidopsis
                  thaliana]
                  237105
Seq. No.
Seq. ID
                  uC-gsronu33B055e08b1
Method
                  BLASTX
NCBI GI
                  g1019946
BLAST score
                  149
E value
                  4.0e-10
Match length
                  33
% identity
                  82
NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]
                  237106
Seq. No.
Seq. ID
                  uC-gsronu33B055f08b1
                  BLASTX
Method
NCBI GI
                  g730456
BLAST score
                  309
E value
                  1.0e-28
Match length
                  68
% identity
                  81
NCBI Description 40S RIBOSOMAL PROTEIN S19
Seq. No.
                  237107
```

Seq. ID uC-gsronu33B055h04b1

Method BLASTX
NCBI GI g4468805
BLAST score 256
E value 2.0e-22
Match length 84
% identity 56

NCBI Description (AL035601) auxin-responsive GH3-like protein [Arabidopsis

thaliana]



```
Seq. No.
                   237108
                   uC-gsronu33B057a11b1
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g2224897
BLAST score
                   275
E value
                   2.0e-24
                   118
Match length
                   53
 % identity
                  (U67132) DNA-binding protein PcMYB1 [Petroselinum crispum]
NCBI Description
Seq. No.
                   237109
Seq. ID
                   uC-gsronu33B057b08b1
Method
                   BLASTX
NCBI GI
                   g2984292
BLAST score
                   184
E value
                   2.0e-17
Match length
                   108
% identity
                   48
                  (AE000771) GTP-binding protein [Aquifex aeolicus]
NCBI Description
Seq. No.
                   237110
Seq. ID
                   uC-gsronu33B057d12b1
Method
                   BLASTX
NCBI GI
                   q4539348
BLAST score
                   136
E value
                   1.0e-17
Match length
                   95
                   52
% identity
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]
Seq. No.
                   237111
Seq. ID
                   uC-gsronu33B057f05b1
Method
                   BLASTX
NCBI GI
                   q4510345
BLAST score
                   222
E value
                   1.0e-18
Match length
                   48
 % identity
NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
Seq. No.
                   237112
Seq. ID
                   uC-gsronu33B057g04b1
```

Method BLASTX
NCBI GI g1352186
BLAST score 325
E value 2.0e-30
Match length 89
% identity 70

NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)

(CYTOCHROME P450 74)  $>gi_404866$  (U00428) allene oxide

synthase [Linum usitatissimum]

Seq. No. 237113

Seq. ID uC-gsronu33B057g08b1

Method BLASTX NCBI GI g529353



```
BLAST score
                   9.0e-18
E value
                   125
Match length
                   51
% identity
                  (U12757) diphenol oxidase [Acer pseudoplatanus]
NCBI Description
Seq. No.
                   237114
Seq. ID
                   uC-gsronu33B057h03b1
Method
                   BLASTX
NCBI GI
                   q2665890
BLAST score
                   358
E value
                   4.0e-34
Match length
                   86
                   78
% identity
                  (AF035944) calcium-dependent protein kinase [Fragaria x
NCBI Description
                   ananassa]
                   237115
Seq. No.
Seq. ID
                  uC-gsronu33B057h10b1
                  BLASTX
Method
NCBI GI
                   g2194115
BLAST score
                  197
E value
                  1.0e-15
                  70
Match length
                   56
% identity
NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]
Seq. No.
                  237116
Seq. ID
                  uC-gsronu33B058a07b1
Method
                  BLASTX
NCBI GI
                  g2827141
BLAST score
                  158
E value
                   1.0e-10
Match length
                   36
% identity
                   78
NCBI Description
                  (AF027173) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                   237117
Seq. ID
                  uC-gsronu33B058a09b1
Method
                  BLASTX
NCBI GI
                  g2465008
BLAST score
                   459
                   6.0e-46
E value
Match length
                  140
% identity
                   63
NCBI Description
                  (AJ001445) ripening-induced protein [Fragaria vesca]
Seq. No.
                  237118
Seq. ID
                  uC-gsronu33B058a10b1
Method
                  BLASTX
NCBI GI
                  g3122386
```

Method BLASTX
NCBI GI g3122386
BLAST score 656
E value 5.0e-69
Match length 130
% identity 47

NCBI Description WD-40 REPEAT PROTEIN MSI1 >gi 2394227 (AF016845) WD-40



## repeat protein [Lycopersicon esculentum]

Seq. No. 237119 Seq. ID uC-gsronu33B058c08b1 Method BLASTX NCBI GI g2137156 BLAST score 142 7.0e-09 E value 92 Match length 45 % identity apoptosis protein MA-3 - mouse >gi 1384078 dbj BAA09056 NCBI Description (D50465) apoptosis-inducible [Mus musculus] 237120 Seq. No. Seq. ID uC-gsronu33B058c10b1 BLASTX Method NCBI GI g3582333 BLAST score 236 9.0e-20 E value Match length 133 % identity 37 (AC005496) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 237121 Seq. ID uC-gsronu33B058e03b1 Method BLASTX NCBI GI g4455356 BLAST score 550 E value 1.0e-56 Match length 144 74 % identity NCBI Description (AL035524) putative protein [Arabidopsis thaliana] Seq. No. 237122 uC-gsronu33B058f12b1 Seq. ID BLASTX Method NCBI GI q4314396 BLAST score 153 E value 4.0e-10 Match length 54 % identity 57 NCBI Description (AC006232) putative flavonol sulfotransferase [Arabidopsis thaliana] Seq. No. 237123 Seq. ID uC-gsronu33B058g09b1 Method BLASTX NCBI GI q4006878 BLAST score 484 E value 7.0e-49 Match length 124 % identity NCBI Description (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]

Seq. No. 237124

Seq. ID uC-gsronu33B058h03b1

Method BLASTX

34409



```
NCBI GI
                   q4262236
BLAST score
                   151
E value
                   3.0e-10
                   57
Match length
                   61
% identity
NCBI Description
                   237125
Seq. No.
```

(AC006200) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

uC-gsronu33B060c07b1 Seq. ID

Method BLASTX NCBI GI q441457 BLAST score 178 3.0e-22 E value 74 Match length 78 % identity

NCBI Description (X73419) ubiquitin conjugating enzyme E2 [Lycopersicon

esculentum]

Seq. No.

237126

Seq. ID uC-gsronu33B061a01b1 BLASTX Method NCBI GI g2495256 BLAST score 616 3.0e-64E value 137 Match length 82 % identity

NCBI Description STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 HOMOLOG (HMG

PROTEIN) >gi\_481756\_pir\_\_S39242 HMG protein - Madagascar periwinkle >gi\_433872\_emb\_CAA82251\_ (Z28410) HMG protein

[Catharanthus roseus]

Seq. No. 237127

uC-gsronu33B061a08b1 Seq. ID

BLASTX Method q3915961 NCBI GI BLAST score 564 E value 3.0e-58 Match length 124 90 % identity

HYPOTHETICAL 267 KD PROTEIN (ORF 2280) NCBI Description

> >gi 2924274 emb CAA77427 (Z00044) Ycf2 protein [Nicotiana tabacum] >qi 2924285 emb CAA77438 (Z00044) hypothetical

protein [Nicotiana tabacum]

Seq. No. 237128

Seq. ID uC-gsronu33B061b06b1

Method BLASTX NCBI GI g2129772 BLAST score 173 1.0e-12 E value Match length 39 % identity 74

NCBI Description xyloglucan endotransglycosylase-related protein XTR-7 -

Arabidopsis thaliana >gi 1244760 (U43489) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  uC-gsronu33B061c01b1
Method
                  BLASTX
NCBI GI
                  g4309698
BLAST score
                  153
                  2.0e-10
E value
Match length
                  58
% identity
                  53
                  (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  237130
Seq. No.
Seq. ID
                  uC-gsronu33B061c02b1
Method
                  BLASTX
NCBI GI
                  g4455322
BLAST score
                  423
E value
                  5.0e-54
Match length
                  127
% identity
                  89
NCBI Description
                  (AL035525) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  237131
Seq. ID
                  uC-gsronu33B061d10b1
Method
                  BLASTX
NCBI GI
                  g1657617
BLAST score
                  175
E value
                   3.0e-23
Match length
                  72
% identity
                  81
NCBI Description
                  (U72503) G2p [Arabidopsis thaliana] >gi 3068707 (AF049236)
                  putative nuclear DNA-binding protein G2p [Arabidopsis
                  thaliana]
                  237132
Seq. No.
Seq. ID
                  uC-gsronu33B061e01b1
Method
                  BLASTX
NCBI GI
                  g3334320
BLAST score
                  160
E value
                   6.0e-11
                  30
Match length
                  100
% identity
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 2444420 (AF020553)
                  ribosome-associated protein p40 [Glycine max]
Seq. No.
                  237133
                  uC-gsronu33B061f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2864616
BLAST score
                  212
```

E value 5.0e-17 Match length 65 % identity

NCBI Description (AL021811) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237134

uC-gsronu33B061f10b1 Seq. ID

Method BLASTX

% identity

88



```
NCBI GI
                   g2583131
BLAST score
                   186
E value
                   2.0e-14
Match length
                   52
% identity
NCBI Description
                  (AC002387) putative pectinesterase [Arabidopsis thaliana]
                  237135
Seq. No.
Seq. ID
                  uC-qsronu33B062a03b1
Method
                  BLASTX
NCBI GI
                  q2894599
BLAST score
                   210
                   2.0e-17
E value
Match length
                   52
% identity
                   71
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
                  237136
Seq. No.
Seq. ID
                  uC-gsronu33B062b06b1
Method
                  BLASTX
NCBI GI
                   q2829899
BLAST score
                   179
E value
                   3.0e-13
Match length
                  80
                   45
% identity
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                   gp X91961 1107495 [Arabidopsis thaliana]
Seq. No.
                   237137
                  uC-gsronu33B062b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3688186
BLAST score
                  150
E value
                   7.0e-10
Match length
                   40
% identity
                   68
NCBI Description
                  (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                   237138
Seq. ID
                  uC-gsronu33B062d12b1
                  BLASTX
Method
NCBI GI
                   g3717946
BLAST score
                   294
E value
                   2.0e-26
Match length
                  72
% identity
                   81
NCBI Description
                  (AJ005901) vag1 [Arabidopsis thaliana]
                   237139
Seq. No.
Seq. ID
                  uC-gsronu33B062f08b1
Method
                  BLASTX
NCBI GI
                  g3023194
BLAST score
                  147
E value
                  7.0e-10
Match length
                   40
```



NCBI Description 14-3-3-LIKE PROTEIN A (SGF14A) >gi\_1575725 (U70533) SGF14A [Glycine max]

Seq. No. 237140

Seq. ID uC-gsronu33B072c10b1

Method BLASTX
NCBI GI g3776559
BLAST score 220
E value 2.0e-18
Match length 57
% identity 70

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi\_3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb\_AC003970. ESTs gb\_Z35332 and gb\_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 237141

Seq. ID uC-gsronu33B074a06b1

Method BLASTX
NCBI GI g1171577
BLAST score 138
E value 7.0e-09
Match length 41
% identity 68

NCBI Description (X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No. 237142

Seq. ID uC-gsronu33B074f02b1

Method BLASTX
NCBI GI g2914700
BLAST score 147
E value 6.0e-10
Match length 46
% identity 67

NCBI Description (AC003974) tRNA-processing protein SEN3-like [Arabidopsis

thaliana]

Seq. No. 237143

Seq. ID uC-gsronu33B076a02b1

Method BLASTX
NCBI GI g3004547
BLAST score 153
E value 3.0e-10
Match length 35
% identity 86

NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]

>gi\_4185150 (AC005724) unknown protein [Arabidopsis

thalianal

Seq. No. 237144

Seq. ID uC-gsronu33B076a04b1

Method BLASTX
NCBI GI g2500649
BLAST score 210
E value 5.0e-17
Match length 87
% identity 47



NCBI Description PROBABLE RNA 3'-TERMINAL PHOSPHATE CYCLASE (RNA-3'-PHOSPHATE CYCLASE) (RNA CYCLASE)

Seq. No. 237145

Seq. ID uC-gsronu33B076c03b1

Method BLASTX
NCBI GI g1469930
BLAST score 181
E value 1.0e-13
Match length 45
% identity 82

NCBI Description (U48777) fiber-specific acyl carrier protein [Gossypium

hirsutum]

Seq. No. 237146

Seq. ID uC-gsronu33B076c12b1

Method BLASTX
NCBI GI g548770
BLAST score 159
E value 4.0e-11
Match length 36
% identity 83

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal

protein L3 - rice >gi\_303853\_dbj\_BAA02155 (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 237147

Seq. ID uC-gsronu33B076f02b1

Method BLASTX
NCBI GI g3098571
BLAST score 232
E value 2.0e-19
Match length 82
% identity 51

NCBI Description (AF049028) BURP domain containing protein [Brassica napus]

Seq. No. 237148

Seq. ID uC-gsronu33B076g03b1

Method BLASTX
NCBI GI g3193234
BLAST score 156
E value 2.0e-10
Match length 43
% identity 67

NCBI Description (AF068690) peroxisomal targeting signal-1 receptor

[Citrullus lanatus]

Seq. No. 237149

Seq. ID uC-gsronu33B077a08b1

Method BLASTX
NCBI GI g2058280
BLAST score 198
E value 7.0e-16
Match length 37
% identity 97

NCBI Description (X97381) atran3 [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  uC-gsronu33B077b04b1
Method
                  BLASTX
NCBI GI
                  g4415908
BLAST score
                  420
E value
                  2.0e-41
Match length
                  110
                  65
% identity
NCBI Description (AC006282) unknown protein [Arabidopsis thaliana]
Seq. No.
                  237151
Seq. ID
                  uC-gsronu33B077c01b1
Method
                  BLASTX
NCBI GI
                  g1620371
BLAST score
                  511
E value
                  6.0e-52
Match length
                  118
                  77
% identity
NCBI Description (Y08782) peroxidase ATP23a [Arabidopsis thaliana]
Seq. No.
                  237152
Seq. ID
                  uC-gsronu33B077c10b1
Method
                  BLASTX
NCBI GI
                  g4038030
BLAST score
                  441
E value
                  1.0e-43
Match length
                  125
% identity
                  63
                  (AC005936) putative protein kinase, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  237153
Seq. ID
                  uC-gsronu33B077c12b1
Method
                  BLASTX
NCBI GI
                  q3242717
BLAST score
                  400
                  4.0e-39
E value
Match length
                  93
% identity
NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana]
Seq. No.
                  237154
Seq. ID
                  uC-gsronu33B077e04b1
Method
                  BLASTX
NCBI GI
                  g3269301
BLAST score
                  516
E value
                  1.0e-52
Match length
                  143
% identity
                  63
NCBI Description
                 (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                  237155
Seq. ID
                  uC-gsronu33B077e11b1
```

Method BLASTX NCBI GI g1171579 BLAST score 250 E value 2.0e-21



```
Match length
% identity
                   36
NCBI Description
                  (X95342) cytochrome P450 [Nicotiana tabacum]
                   237156
Seq. No.
Seq. ID
                  uC-gsronu33B077f03b1
Method
                  BLASTX
NCBI GI
                  g3549666
BLAST score
                   300
E value
                   3.0e-27
                  79
Match length
% identity
                   76
NCBI Description
                  (AL031394) putative protein [Arabidopsis thaliana]
Seq. No.
                   237157
Seq. ID
                  uC-gsronu33B077f09b1
Method
                  BLASTX
NCBI GI
                  g3913425
BLAST score
                  277
E value
                  1.0e-24
Match length
                   62
% identity
                  77
NCBI Description
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
                  HELICASE >gi 2275203 (AC002337) RNA helicase isolog
                   [Arabidopsis thaliana]
Seq. No.
                  237158
Seq. ID
                  uC-gsronu33B077g06b1
Method
                  BLASTX
NCBI GI
                  g2459431
BLAST score
                  166
E value
                  1.0e-11
Match length
                  102
                  45
% identity
NCBI Description
                  (AC002332) unknown protein [Arabidopsis thaliana]
                  237159
Seq. No.
Seq. ID
                  uC-gsronu33B077h03b1
Method
                  BLASTX
NCBI GI
                  g3080401
BLAST score
                  524
E value
                  2.0e-53
Match length
                  117
% identity
NCBI Description
                  (AL022603) putative protein [Arabidopsis thaliana]
                  >gi 4455265 emb CAB36801.1 (AL035527) putative protein
                   [Arabidopsis thaliana]
Seq. No.
                  237160
Seq. ID
                  uC-gsronu33B078a02b1
Method
                  BLASTX
NCBI GI
                  g3334405
BLAST score
                  395
E value
                  2.0e-38
```

Match length 108 % identity

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)



>gi\_2267583 (AF009338) vacuolar H+-ATPase subunit E
[Gossypium hirsutum]

Seq. No. 237161

Seq. ID uC-gsronu33B078a10b1

Method BLASTX
NCBI GI g2833390
BLAST score 367
E value 2.0e-35
Match length 80
% identity 80

NCBI Description GLYCOGEN (STARCH) SYNTHASE PRECURSOR (GBSSII)

(GRANULE-BOUND STARCH SYNTHASE II) >gi\_887649\_emb\_CAA61241\_(X87988) glycogen (starch) synthase [Solanum tuberosum]

Seq. No. 237162

Seq. ID uC-gsronu33B078b12b1

Method BLASTX
NCBI GI g1669601
BLAST score 541
E value 2.0e-55
Match length 149
% identity 67

NCBI Description (D88747) AR401 [Arabidopsis thaliana]

Seq. No. 237163

Seq. ID uC-gsronu33B078c02b1

Method BLASTX
NCBI GI g3811293
BLAST score 149
E value 2.0e-09
Match length 55
% identity 64

NCBI Description (AF032465) putative serine/threonine protein kinase

[Nicotiana tabacum] >gi 4098172 (U73938) PK11-C1 [Nicotiana

tabacum]

Seq. No. 237164

Seq. ID uC-gsronu33B078c06b1

Method BLASTX
NCBI GI g1523800
BLAST score 340
E value 4.0e-32
Match length 103
% identity 56

NCBI Description (Y07694) MAP kinase kinase alpha protein kinase

[Arabidopsis thaliana]

Seq. No. 237165

Seq. ID uC-gsronu33B078c07b1

Method BLASTX
NCBI GI g3176715
BLAST score 504
E value 4.0e-51
Match length 114
% identity 83

NCBI Description (AC002392) putative receptor-like protein kinase



```
[Arabidopsis thaliana]
                  237166
Seq. No.
Seq. ID
                  uC-gsronu33B078c08b1
                  BLASTX
Method
NCBI GI
                  g3080437
BLAST score
                  283
                  3.0e-25
E value
                  69
Match length
                  75
% identity
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]
Seq. No.
                  237167
Seq. ID
                  uC-gsronu33B078c12b1
                  BLASTX
Method
NCBI GI
                  g2104536
BLAST score
                  575
E value
                  2.0e-59
```

Match length 121 79 % identity (AF001308) predicted glycosyl transferase [Arabidopsis NCBI Description

237168 Seq. No.

Seq. ID uC-gsronu33B078d02b1

thaliana]

BLASTX Method NCBI GI g4098272 BLAST score 253 E value 7.0e-22 50 Match length 98 % identity

NCBI Description (U76558) alpha-tubulin [Triticum aestivum]

237169 Seq. No.

Seq. ID uC-gsronu33B078d09b1

BLASTX Method NCBI GI q4056457 BLAST score 331 E value 7.0e-31 92 Match length % identity 68

NCBI Description (AC005990) ESTs gb 234051 and gb F13722 come from this

gene. [Arabidopsis thaliana]

237170 Seq. No.

uC-gsronu33B078f06b1 Seq. ID

Method BLASTX q4335773 NCBI GI BLAST score 259 2.0e-22 E value Match length 93 % identity 63

NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]

Seq. No. 237171

Seq. ID uC-gsronu33B078f10b1

Method BLASTX

34418

Method

NCBI GI

E value

BLAST score



```
NCBI GI
                  g3236261
                  243
BLAST score
                  5.0e-32
E value
                  133
Match length
                  52
% identity
                  (AC004684) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  237172
Seq. No.
                  uC-gsronu33B078g04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q548852
BLAST score
                  361
                  2.0e-34
E value
                  82
Match length
                  80
% identity
                  40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal
NCBI Description
                  protein S21 - rice >gi 303839 dbj BAA02158 (D12633) 40S
                  subunit ribosomal protein [Oryza sativa]
                  237173
Seq. No.
                  uC-gsronu33B078h10b1
Seq. ID
                  {\tt BLASTX}
Method
                  g3927825
NCBI GI
BLAST score
                  280
E value
                   5.0e-25
Match length
                  61
% identity
                  85
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                  237174
Seq. No.
Seq. ID
                  uC-gsronu33B078h12b1
                  BLASTX
Method
                  q3228668
NCBI GI
                  169
BLAST score
                   6.0e-12
E value
                  77
Match length
                   44
% identity
NCBI Description (AF069988) nitrilase 1 [Mus musculus]
                   237175
Seq. No.
Seq. ID
                  uC-gsronu33B079a04b1
Method
                  BLASTX
NCBI GI
                   g2505870
BLAST score
                  163
                   2.0e-11
E value
Match length
                   86
                   47
% identity
NCBI Description (Y12227) hypothetical protein [Arabidopsis thaliana]
                   237176
Seq. No.
Seq. ID
                   uC-gsronu33B079b12b1
```

34419

BLASTX

316 3.0e-29

g1169009



```
Match length
% ~identity
                  81
                  CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                  (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                  3-O-METHYLTRANSFERASE) (COMT) >gi_542009_pir__S40146
                  catechol O-methyltransferase (EC 2.1.1.6) - cider tree
                  >gi_437777_emb_CAA52814_ (X74814) 0-Methyltransferase
                  [Eucalyptus gunnii]
                  237177
Seq. No.
Seq. ID
                  uC-gsronu33B079c09b1
                  BLASTX
Method
NCBI GI
                  g136644
BLAST score
                  247
E value
                  5.0e-21
                  59
Match length
                  80
% identity
NCBI Description
                  UBIQUITIN-CONJUGATING ENZYME E2-23 KD (UBIQUITIN-PROTEIN
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 100765 pir A34506
                  23K ubiquitin carrier protein E2 - wheat >gi_170782
                  (M28059) ubiquitin carrier protein [Triticum vulgare]
                  237178
Seq. No.
Seq. ID
                  uC-gsronu33B079c11b1
Method
                  BLASTX
NCBI GI
                  g3319353
BLAST score
                  225
E value
                  1.0e-18
Match length
                  74
                  64
% identity
NCBI Description
                  (AF077407) contains similarity to copper-binding proteins
                  [Arabidopsis thaliana]
                  237179
Seq. No.
                  uC-gsronu33B079e03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3668118
BLAST score
                  378
E value
                  1.0e-36
Match length
                  93
% identity
NCBI Description (AJ224078) hypothetical protein [Brassica napus]
Seq. No.
                  237180
Seq. ID
                  uC-gsronu33B079e10b1
Method
                  BLASTX
NCBI GI
                  q1076627
BLAST score
                  414
```

E value 8.0e-41 Match length 91 % identity 88

NCBI Description inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco

>gi 790479 emb CAA58701 (X83730) inorganic pyrophosphatase

[Nicotiana tabacum]

Seq. No. 237181

Seq. ID uC-gsronu33B079e11b1

34420



Method BLASTX
NCBI GI g2804280
BLAST score 340
E value 6.0e-32
Match length 91
% identity 68
NCBI Description (AB003687

NCBI Description (AB003687) 6-4 photolyase [Arabidopsis thaliana] >gi\_3929918\_dbj\_BAA34711\_ (AB017331) 6-4 photolyase

[Arabidopsis thaliana]

Seq. No. 237182

Seq. ID uC-gsronu33B079g04b1

Method BLASTX
NCBI GI g2443473
BLAST score 286
E value 9.0e-26
Match length 90
% identity 64

NCBI Description (AF001035) ASF/SF2 homolog [Arabidopsis thaliana]

Seq. No. 237183

Seq. ID uC-gsronu33B080a02b1

Method BLASTX
NCBI GI g2500380
BLAST score 566
E value 2.0e-58
Match length 105
% identity 99

NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi\_2119128\_pir\_\_JC4923 ribosomal

protein RL44 - upland cotton >gi\_1553129 (U64677) ribosomal

protein L44 isoform a [Gossypium hirsutum] >gi\_1553131 (U64678) ribosomal protein L44 isoform b [Gossypium

hirsutum]

Seq. No. 237184

Seq. ID uC-gsronu33B080a05b1

Method BLASTX
NCBI GI g1518540
BLAST score 458
E value 6.0e-46
Match length 99
% identity 91

NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No. 237185

Seq. ID uC-gsronu33B080b05b1

Method BLASTX
NCBI GI 93452091
BLAST score 439
E value 1.0e-43
Match length 98
% identity 83

NCBI Description (AJ004899) rudimentary enhancer [Glycine max]

Seq. No. 237186

Seq. ID uC-gsronu33B080b11b1

Method BLASTX



```
NCBI GI
                  g3445397
BLAST score
                  167
E value
                  9.0e-12
                  78
Match length
                  40
% identity -
                 (AJ010166) S-domain receptor-like protein kinase [Zea mays]
NCBI Description
Seq. No.
                  237187
Seq. ID
                  uC-gsronu33B080c06b1
                  BLASTX
Method
NCBI GI
                  q1170689
BLAST score
                  550
E value
                  1.0e-56
                  133
Match length
                  79
% identity
                  SERINE/THREONINE-PROTEIN KINASE ATPK1/ATPK6
NCBI Description
                  >gi 625979 pir A54141 ribosomal protein S6 kinase (EC
                  2.7.1.-) Atpk1 - Arabidopsis thaliana
                  >gi 2129542 pir S68462 ATPK6 protein - Arabidopsis
                  thaliana >gi 914080 bbs 160873 ATPK6=ribosomal-protein S6
                  kinase homolog [Arabidopsis thaliana, Peptide, 465 aa]
                  >gi 508308 (L29030) protein-serine kinase [Arabidopsis
                  thaliana] >gi 867997 dbj BAA07656 (D42056)
                  risosomal-protein S6 kinase homolog [Arabidopsis thaliana]
                  237188
Seq. No.
Seq. ID
                  uC-gsronu33B080d12b1
Method
                  BLASTX
NCBI GI
                  q3702327
BLAST score
                  365
E value
                  8.0e-35
Match length
                  151
% identity
NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]
                  237189
Seq. No.
Seq. ID
                  uC-gsronu33B080e09b1
Method
                  BLASTX
NCBI GI
                  g3080438
BLAST score
                  292
E value
                  3.0e-26
Match length
                  141
% identity
NCBI Description (AL022605) putative protein [Arabidopsis thaliana]
                  237190
Seq. No.
                  uC-gsronu33B080e10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023818
```

BLAST score 699 E value 5.0e-74Match length 145 % identity 92

NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM

> PRECURSOR (G6PD) >gi 1197385 emb CAA58775 (X83923) glucose-6-phosphate dehydrogenase [Solanum tuberosum]



```
Seq. No.
                  237191
Seq. ID
                  uC-gsronu33B080e11b1
Method
                  BLASTX
NCBI GI
                  g3158474
BLAST score
                  635
E value
                  2.0e-66
Match length
                  137
                  89
% identity
NCBI Description (AF067184) aquaporin 1 [Samanea saman]
                  237192
Seq. No.
Seq. ID
                  uC-gsronu33B080e12b1
Method
                  BLASTX
NCBI GI
                  q3355468
BLAST score
                  522
E value
                  3.0e-53
Match length
                  120
                  89
% identity
NCBI Description
                  (AC004218) putative ribosomal protein L35 [Arabidopsis
                  thaliana]
                  237193
Seq. No.
Seq. ID
                  uC-gsronu33B080f12b1
                  BLASTX
Method
NCBI GI
                  q4559346
BLAST score
                  242
                  2.0e-20
E value
Match length
                  91
% identity
                  45
NCBI Description (AC006585) early nodulin 16 [Arabidopsis thaliana]
Seq. No.
                  237194
Seq. ID
                  uC-gsronu33B080g03b1
                  BLASTX
Method
NCBI GI
                  q1563719
BLAST score
                  324
E value
                  4.0e-30
Match length
                  68
% identity
                  88
NCBI Description (Y08320) cyclophylin [Digitalis lanata]
                  237195
Seq. No.
Seq. ID
                  uC-gsronu33B080h03b1
Method
                  BLASTX
                  q4572679
NCBI GI
BLAST score
                  280
E value
                  3.0e-25
Match length
                  71
% identity
                  77
NCBI Description
                  (AC006954) RSZp22 splicing factor; contains RNA recognition
                  motif [Arabidopsis thaliana]
```

Seq. No. 237196

Seq. ID uC-gsronu33B080h08b1

Method BLASTX NCBI GI q3850816 BLAST score 235

BLAST score

Match length

E value

378

129

2.0e-36



```
E value
                   6.0e-20
Match length
                   42
% identity
                   98
NCBI Description
                   (Y18348) U2 snRNP auxiliary factor, small subunit [Oryza
                   sativa]
Seq. No.
                   237197
Seq. ID
                   uC-gsronu33B081a10b1
Method
                   BLASTX
NCBI GI
                   g3776559
BLAST score
                   242
E value
                   1.0e-20
Match length
                   86
% identity
                   65
NCBI Description
                   (AC005388) Strong similarity to gene F14J9.26 gi 3482933
                   cdc2 protein kinase homolog from A. thaliana BAC
                   gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   237198
Seq. ID
                   uC-gsronu33B081b06b1
Method
                   BLASTX
NCBI GI
                   g3355480
BLAST score
                   279
E value
                   1.0e-24
Match length
                   124
% identity
                   42
NCBI Description
                  (AC004218) Medicago nodulin N21-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   237199
Seq. ID
                  uC-gsronu33B081b07b1
Method
                  BLASTX
NCBI GI
                   g4508068
BLAST score
                   225
E value
                   2.0e-18
Match length
                  114
% identity
                   49
NCBI Description
                  (AC005882) 3063 [Arabidopsis thaliana]
Seq. No.
                   237200
Seq. ID
                  uC-gsronu33B081c02b1
Method
                  BLASTX
NCBI GI
                   q4580523
BLAST score
                  143
E value
                   2.0e-09
Match length
                  35
% identity
NCBI Description (AF036305) scarecrow-like 8 [Arabidopsis thaliana]
Seq. No.
                  237201
Seq. ID
                  uC-gsronu33B081d02b1
Method
                  BLASTX
NCBI GI
                  q2088653
```



```
% identity
NCBI Description
                   (AF002109) Hs1pro-1 related protein isolog [Arabidopsis
                  thaliana]
                  237202
Seq. No.
Seq. ID
                  uC-gsronu33B081g11b1
Method
                  BLASTX
NCBI GI
                  g4098129
BLAST score
                  224
E value
                  1.0e-18
Match length
                  43
                  100
% identity
NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]
                  237203
Seq. No.
Seq. ID
                  uC-gsronu33B081h02b1
Method
                  BLASTX
NCBI GI
                  g1168609
BLAST score
                  191
                  7.0e-15
E value
Match length
                  54
                  70
% identity
NCBI Description
                  AUXIN-RESISTANCE PROTEIN AXR1 >qi 479664 pir $35071
                  auxin-resistance protein AXR1 - Arabidopsis thaliana
                  >gi 304104 (L13922) ubiquitin-activating enzyme E1
                  [Arabidopsis thaliana] >gi 2388579 (AC000098) Match to
                  Arabidopsis AXR1 (gb ATHAXR1122). [Arabidopsis thaliana]
                  >gi 448755 prf 1917\overline{3}37A ubiquitin-activating enzyme E1
                  [Arabidopsis thaliana]
                  237204
Seq. No.
Seq. ID
                  uC-gsronu33B082a04b1
Method
                  BLASTX
NCBI GI
                  q4220462
BLAST score
                  173
                  1.0e-12
E value
Match length
                  34
% identity
NCBI Description
                  (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)
                  gene from Arabidopsis thaliana containing Homeobox PF_00046
                  and bZIP PF 00170 domains. [Arabidopsis thaliana]
Seq. No.
                  237205
                  uC-gsronu33B082b01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2580440
BLAST score
                  187
E value
                  5.0e-14
Match length
                  60
% identity
                  67
                  (D87261) PCF2 [Oryza sativa]
NCBI Description
```

Seq. No. 237206

Seq. ID uC-gsronu33B082b02b1

Method BLASTX
NCBI GI g2388575
BLAST score 255



E value 6.0e-22 Match length 144 % identity 39 (AC000098) YUP8H12.18 [Arabidopsis thaliana] NCBI Description 237207 Seq. No. uC-gsronu33B082c10b1 Seq. ID Method BLASTX NCBI GI a2979544 BLAST score 369 E value 2.0e-35 Match length 108 % identity 64 NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana] 237208 Seq. No. uC-gsronu33B082d11b1 Seq. ID Method BLASTX NCBI GI q3420906 BLAST score 364 E value 1.0e-34 Match length 112 % identity 41 NCBI Description (AF080595) zinc finger protein; WRKY1 [Pimpinella brachycarpa] 237209 Seq. No. Seq. ID uC-gsronu33B082f08b1 Method BLASTX NCBI GI q1518540 BLAST score 838 E value 3.0e-90 Match length 167 % identity NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max] Seq. No. 237210 uC-gsronu33B082f10b1 Seq. ID Method BLASTX NCBI GI q3858935 BLAST score 243 E value 1.0e-20 Match length 83 % identity 58 (AL021636) synaptobrevin-like protein [Arabidopsis NCBI Description thaliana] >gi 4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

237211 Seq. No.

Seq. ID uC-gsronu33B082h12b1

Method BLASTX NCBI GI g2252847 BLAST score 161 E value 3.0e-11 Match length 84 % identity 42

34426



```
(AF013293) No definition line found [Arabidopsis thaliana]
  NCBI Description
                     237212
  Seq. No.
                     uC-gsronu33B086d12b1
  Seq. ID
                     BLASTX
  Method
                     g4185819
  NCBI GI
                     192
  BLAST score
  E value
                     5.0e-15
  Match length
                     47
  % identity
                     68
                     (AF116845) metallothionein-like type 1 protein [Ipomoea
  NCBI Description
                     batatas]
                     237213
  Seq. No.
                     uC-gsronu33B086e02b1
  Seq. ID
  Method
                     BLASTX
                     g2959781
  NCBI GI
  BLAST score
                     180
  E value
                     9.0e-14
                     39
  Match length
                     87
  % identity
                    (AJ223508) Zwille protein [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                     237214
  Seq. ID
                     uC-gsronu33B086g12b1
                     BLASTX
  Method
                     g2244898
  NCBI GI
                     220
  BLAST score
                     2.0e-18
  E value
  Match length
                     45
                     96
  % identity
                    (Z97338) strong similarity to protein phosphatase 2A
  NCBI Description
                     regulatory chain, 74K [Arabidopsis thaliana]
                     237215
  Seq. No.
                     uC-gsronu33B086h10b1
  Seq. ID
                     BLASTX
  Method
                     g99749
  NCBI GI
  BLAST score
                     204
  E value
                     1.0e-16
                     38
  Match length
                     95
  % identity
                    probable serine/threonine-specific protein kinase ATPK64
  NCBI Description
                     (EC 2.7.1.-) - Arabidopsis thaliana
                     >gi 217843_dbj_BAA01731_ (D10937) protein kinase
                     [Arabidopsis thaliana]
                     237216
  Seq. No.
                     uC-gsronu33B087c05b1
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     q4008072
  BLAST score
                     164
  E value
                     1.0e-11
                     66
  Match length
% identity
                     45
```

NCBI Description (AF105425) chitinase [Cynodon dactylon]

```
Seq. No.
                  uC-gsronu33B087f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1168408
BLAST score
                  161
                  2.0e-11
E value
Match length
                  38
% identity
                  82
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1
NCBI Description
                  >gi 2118268 pir__S58168 fructose-bisphosphate aldolase (EC
                  4.1.2.13) - garden pea >gi_927507_emb_CAA61946 (X89828)
                  fructose-1,6-bisphosphate aldolase [Pisum sativum]
                  237218
Seq. No.
                  uC-gsronu33B087f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3420008
BLAST score
                  238
E value
                  5.0e-20
Match length
                  106
% identity
                   42
NCBI Description
                  (AF000307) steroid sulfotransferase 3 [Brassica napus]
Seq. No.
                  237219
Seq. ID
                  uC-gsronu33B087h07b1
Method
                  BLASTX
NCBI GI
                  q3482929
BLAST score
                  147
E value
                   9.0e-10
Match length
                  28
% identity
                  93
NCBI Description
                  thaliana]
```

(AC003970) Putative transcription factor [Arabidopsis

Seq. No. 237220

Seq. ID uC-gsronu33B089b08b1

BLASTX Method NCBI GI g2462828 BLAST score 247 2.0e-21 E value 87 Match length % identity

(AF000657) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 237221

uC-gsronu33B089b11b1 Seq. ID

Method BLASTX NCBI GI q4115377 BLAST score 169 6.0e-12 E value 53 Match length % identity 75

(AC005967) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 237222

uC-gsronu33B089c05b1 Seq. ID

Method BLASTX



a416650 NCBI GI 400 BLAST score 6.0e-39 E value Match length 112 % identity 68

PROBABLE GLUTATHIONE S-TRANSFERASE (AUXIN-INDUCED PROTEIN NCBI Description

PGNT35/PCNT111) >gi\_100304\_pir\_\_S16268 auxin-induced

protein (clone pGNT35) - common tobacco >gi 19797 emb CAA39706 (X56265) auxin-induced protein [Nicotiana tabacum] >gi 19801 emb CAA39710 (X56269)

auxin-induced protein [Nicotiana tabacum]

237223 Seq. No.

uC-gsronu33B089d08b1 Seq. ID

BLASTX Method NCBI GI q3395440 339 BLAST score 1.0e-44E value 135 Match length 64 % identity

(AC004683) hypothetical protein [Arabidopsis thaliana] NCBI Description

237224 Seq. No.

uC-gsronu33B089e01b1 Seq. ID

Method BLASTX q1168470 NCBI GI BLAST score 570 6.0e-59 E value 121 Match length 89 % identity

PROTEIN KINASE APK1A >gi 282877 pir S28615 protein kinase, NCBI Description

tyrosine/serine/threonine-specific (EC 2.7.1.-) -

Arabidopsis thaliana >gi\_217829 dbj BAA02092 (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis

thaliana]

Seq. No. 237225

uC-gsronu33B089f09b1 Seq. ID

BLASTX Method q1946329 NCBI GI BLAST score 446 E value 2.0e-44 123 Match length % identity

(U69154) prohibitin [Nicotiana tabacum] NCBI Description

Seq. No. 237226

uC-gsronu33B089h12b1 Seq. ID

Method BLASTX NCBI GI q125606 BLAST score 141 8.0e-09 E value Match length 55 56 % identity

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 100463\_pir\_\_S12248

pyruvate kinase (EC 2.7.1.40) - potato

>gi 22576 emb CAA37727\_ (X53688) pyruvate kinase [Solanum

% identity



## tuberosum]

```
237227
Seq. No.
                  uC-gsronu33B090b11b1
Seq. ID
                  BLASTX
Method
                  g2961346
NCBI GI
                  495
BLAST score
E value
                  4.0e-50
                  144
Match length
% identity
                  65
                  (AL022140) pectinesterase like protein [Arabidopsis
NCBI Description
                  thaliana]
                  237228
Seq. No.
                  uC-gsronu33B090e06b1
Seq. ID
                  BLASTX
Method
                  g2909781
NCBI GI
                  261
BLAST score
                  1.0e-22
E value
                  120
Match length
                  47
% identity
                  (AF020288) MgATP-energized glutathione S-conjugate pump
NCBI Description
                  [Arabidopsis thaliana]
                  237229
Seq. No.
                  uC-gsronu33B090e07b1
Seq. ID
                  BLASTX
Method
                  g4512698
NCBI GI
                  325
BLAST score
                  4.0e-30
E value
                  150
Match length
                  39
% identity
                 (AC006569) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  237230
Seq. No.
                  uC-gsronu33B090f06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4056456
BLAST score
                  177
                  8.0e-13
E value
                  101
Match length
                   46
% identity
                  (AC005990) Strong similarity to gb_U20808 auxin-induced
NCBI Description
                   protein from Vigna radiata and a member of the zinc-binding
                   dehydrogenase family PF 00107. ESTs gb T43674, gb H77006
                   and gb AA395179 come from this gene. [Arabidopsis thaliana]
                   237231
Seq. No.
                   uC-gsronu33B096e09b1
Seq. ID
                   BLASTX
Method
                   g3033397
NCBI GI
BLAST score
                   136
E value
                   1.0e-08
                   26
Match length
```

NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]



```
Seq. No.
                    237232
                    uC-gsronu33B096g02b1
Seq. ID
Method
                    BLASTX
                    q3860250
NCBI GI
                    543
BLAST score
                    7.0e-56
E value
                    118
Match length
                    89
% identity
                   (AC005824) putative chloroplast prephenate dehydratase
NCBI Description
                    [Arabidopsis thaliana]
                    237233
Seq. No.
                   uC-gsronu33B098a02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                    q1168727
BLAST score
                    167
E value
                    5.0e-12
Match length
                    42
% identity
                    86
                   CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD)
NCBI Description
                   >gi_474300_dbj_BAA03099_ (D13991) cinnamyl alcohol
dehydrogenase [Aralia cordata] >gi_745086_prf__2015401A
                    cinnamoyl alcohol dehydrogenase [Aralia cordata]
                    237234
Seq. No.
Seq. ID
                   uC-qsronu33B098a04b1
Method
                   BLASTX
NCBI GI
                    g1076609
BLAST score
                    243
                    8.0e-21
E value
                    50
Match length
                    86
% identity
NCBI Description NTL1 protein - curled-leaved tobacco
                    237235
Seq. No.
                    uC-gsronu33B098a11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                    g4455159
{\tt BLAST\cdot score}
                    283
                    3.0e - 32
E value
Match length
                    86
                    79
% identity
NCBI Description (AL021687) putative protein [Arabidopsis thaliana]
Seq. No.
                    237236
Seq. ID
                    uC-gsronu33B098e05b1
Method
                    BLASTX
NCBI GI
                    q4158219
BLAST score
                    484
E value
                    8.0e-49
Match length
                    138
                    67
% identity
NCBI Description (Y18623) amylogenin [Oryza sativa]
```

34431

237237

BLASTX

uC-gsronu33B098h04b1

Seq. No. Seq. ID

Method

NCBI GI

```
NCBI GI
                    g2765748
 BLAST score
                    180
 E value
                    3.0e-13
 Match length
                    41
 % identity
 NCBI Description (Z93764) PaMip-2 [Picea abies]
 Seq. No.
                   237238
 Seq. ID
                   uC-gsronu33B099a06b1
 Method
                   BLASTX
 NCBI GI
                   q1915974
 BLAST score
                   160
 E value
                   3.0e-11
 Match length
                   45
 % identity
NCBI Description (U62329) fructokinase [Lycopersicon esculentum] >gi_2102693
                   (U64818) fructokinase [Lycopersicon esculentum]
 Seq. No.
                   237239
Seq. ID
                   uC-gsronu33B099a07b1
Method
                   BLASTX
NCBI GI
                   q3193310
BLAST score
                   303
E value
                   1.0e-27
Match length
                   113
% identity
                   55
NCBI Description (AF069300) contains similarity to Nicotiana tabacum hin1
                   (GB:Y07563) [Arabidopsis thaliana]
Seq. No.
                   237240
Seq. ID
                   uC-gsronu33B099b08b1
Method
                   BLASTX
NCBI GI
                   q1084455
BLAST score
                   170
E value
                   2.0e-12
Match length
                   38
% identity
                   89
NCBI Description peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                   >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   237241
Seq. ID
                   uC-gsronu33B099c03b1
Method
                   BLASTX
NCBI GI
                   q3142300
BLAST score
                   389
E value
                   1.0e-37
Match length
                   118
% identity
                   64
NCBI Description
                  (AC002411) Contains similarity to pre-mRNA processing
                  protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb R64908
                   and gb\_T88158, g\overline{b}\_N38703 and gb\_AA651043 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  237242
Seq. ID
                  uC-gsronu33B099c09b1
Method
                  BLASTX
```

34432

g2811025



BLAST score 612 E value 7.0e-64 Match length 136 % identity 82

NCBI Description ASPARTIC PROTEINASE PRECURSOR >gi\_1944181\_dbj\_BAA19607\_(AB002695) aspartic endopeptidase [Cucurbita pepo]

Seq. No. 237243

Seq. ID uC-gsronu33B099d02b1

Method BLASTX
NCBI GI 94200165
BLAST score 721
E value 1.0e-76
Match length 145
% identity 86

NCBI Description (Y16262) neutral invertase [Daucus carota]

Seq. No. 237244

Seq. ID uC-gsronu33B099d05b1

Method BLASTX
NCBI GI g3540207
BLAST score 344
E value 2.0e-32
Match length 102
% identity 71

NCBI Description (AC004260) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 237245

Seq. ID uC-gsronu33B099d10b1

Method BLASTX
NCBI GI g642339
BLAST score 199
E value 2.0e-15
Match length 99
% identity 47

NCBI Description (X83226) peroxisome biogenesis invlved proteind

[Saccharomyces cerevisiae]

Seq. No. 237246

Seq. ID uC-gsronu33B099e07b1

Method BLASTX
NCBI GI g1172571
BLAST score 517
E value 9.0e-53
Match length 126
% identity 97

NCBI Description PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)

>gi\_1076277\_pir\_\_S52637 phosphoenolpyruvate carboxykinase

(ATP) (EC 4.1.1.49) - cucumber >gi\_567102 (L31899) phosphoenolpyruvate carboxykinase [Cucumis sativus]

Seq. No. 237247

Seq. ID uC-gsronu33B099e11b1

Method BLASTX
NCBI GI g2632105
BLAST score 586
E value 9.0e-61



Match length 148 % identity 77

NCBI Description (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]

>gi\_4539426\_emb\_CAB38959.1\_ (AL049171) arginyl-tRNA

synthetase [Arabidopsis thaliana]

Seq. No. 237248

Seq. ID uC-gsronu33B099e12b1

Method BLASTX
NCBI GI g1346763
BLAST score 330
E value 2.0e-31
Match length 65
% identity 88

NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP1

>gi\_1084363\_pir\_\_S46282 phosphoprotein phosphatase 1 - Alfalfa >gi\_575672\_emb\_CAA56766\_ (X80788) potentially catalitic subunit of the ser /thr protein phosphatase 1

[Medicago sativa subsp. X varia]

Seq. No. 237249

Seq. ID uC-gsronu33B099f04b1

Method BLASTX
NCBI GI g1076758
BLAST score 236
E value 2.0e-20
Match length 50
% identity 90

NCBI Description heat-shock protein precursor - rye >gi 2130093 pir S65776

heat-shock protein, 82K, precursor - rye

>gi\_556673\_emb\_CAA82945\_ (Z30243) heat-shock protein

[Secale cereale]

Seq. No. 237250

Seq. ID uC-gsronu33B099f09b1

Method BLASTX
NCBI GI g1350944
BLAST score 300
E value 2.0e-27
Match length 79
% identity 77

NCBI Description 40S RIBOSOMAL PROTEIN S17

Seq. No. 237251

Seq. ID uC-gsronu33B099g01b1

Method BLASTX
NCBI GI g4262236
BLAST score 509
E value 8.0e-52
Match length 123
% identity 82

NCBI Description (AC006200) putative ribose 5-phosphate isomerase

[Arabidopsis thaliana]

Seq. No. 237252

Seq. ID uC-gsronu33B099g04b1

Method BLASTX

NCBI GI

E value

BLAST score

q4521249

4.0e-41

417

```
NCBI GI
                   g2880049
BLAST score
                   208
E value
                   2.0e-16
Match length
                   44
% identity
                   91
NCBI Description (AC002340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  237253
Seq. ID
                  uC-gsronu33B099h06b1
Method
                  BLASTX
NCBI GI
                  g4539423
BLAST score
                  270
E value
                   9.0e-24
Match length
                  77
% identity
                  71
NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
                   [Arabidopsis thaliana]
Seq. No.
                  237254
Seq. ID
                  uC-gsronu33B099h09b1
Method
                  BLASTX
NCBI GI
                  g2707336
BLAST score
                  291
E value
                  4.0e-26
Match length
                  81
% identity
                  69
NCBI Description (AF037442) histone acetyltransferase [Arabidopsis thaliana]
Seq. No.
                  237255
Seq. ID
                  uC-gsronu33B100c05b1
Method
                  BLASTX
NCBI GI
                  g2443329
BLAST score
                  149
                  4.0e-10
E value
Match length
                  36
% identity
                  83
NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]
Seq. No.
                  237256
Seq. ID
                  uC-gsronu33B100d11b1
Method
                  BLASTX
NCBI GI
                  g4263517
BLAST score
                  142
E value
                  3.0e-09
Match length
                  78
% identity
                  46
NCBI Description (AC004044) similar to PHZF, catalyzing the hydroxylation of
                  phenazine-1-carboxylic acid to
                  2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis
                  thaliana]
Seq. No.
                  237257
Seq. ID
                  uC-gsronu33B100g02b1
Method
                  BLASTX
```

Match length 121 % identity 68 NCBI Description (AB013912) DNA helicase [Mus musculus] Seq. No. 237258 Seq. ID uC-gsronu33B100g05b1 Method BLASTX NCBI GI g2462751 BLAST score 168 E value 4.0e-12 Match length 36 % identity 92 NCBI Description (AC002292) nearly identical to rice water stress induced protein gp D26537 537404 [Arabidopsis thaliana] Seq. No. 237259 Seq. ID uC-gsronu33B100g12b1 Method BLASTX NCBI GI g2911799 BLAST score 214 E value 9.0e-18 Match length 48 % identity 90 NCBI Description (AF008184) 4-coumarate:CoA ligase 1 [Populus balsamifera subsp. trichocarpa X Populus deltoides] Seq. No. 237260 Seq. ID uC-gsronu33B101a03b1 Method BLASTX NCBI GI q4038035 BLAST score 231 E value 9.0e-20 Match length 60 % identity 82 (AC005936) putative DNA-binding protein [Arabidopsis NCBI Description thaliana] Seq. No. 237261 Seq. ID uC-gsronu33B101f02b1 Method BLASTX NCBI GI g4567312 BLAST score 464 E value 1.0e-46 Match length 113 % identity 75 NCBI Description (AC005956) hypothetical protein [Arabidopsis thaliana] Seq. No. 237262 Seq. ID

uC-gsronu33B103a02b1

Method BLASTX NCBI GI g3164115 BLAST score 228 E value 7.0e-19 Match length 114 % identity 40

NCBI Description (AJ224145) major latex-like protein [Rubus idaeus]



```
Seq. No.
                   237263
Seq. ID
                   uC-gsronu33B103b01b1
Method
                   BLASTX
NCBI GI
                   g2244876
BLAST score
                   363
E value
                   1.0e-34
Match length
                   93
% identity
                   70
NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   237264
Seq. ID
                   uC-gsronu33B103d06b1
Method
                   BLASTX
NCBI GI
                   g2464901
BLAST score
                   211
E value
                   4.0e-17
Match length
                  86
% identity
                   47
NCBI Description (299708) putative protein [Arabidopsis thaliana]
Seq. No.
                   237265
Seq. ID
                   uC-gsronu33B103d07b1
Method
                  BLASTX
NCBI GI
                  g2924515
BLAST score
                   243
E value
                   1.0e-20
Match length
                  108
% identity
                   44
NCBI Description (AL022023) putative protein [Arabidopsis thaliana]
Seq. No.
                   237266
Seq. ID
                  uC-gsronu33B103e06b1
Method
                  BLASTX
NCBI GI
                  g4510347
BLAST score
                  428
E value
                  2.0e-42
Match length
                  117
% identity
                  69
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  237267
Seq. ID
                  uC-gsronu33B103g01b1
Method
                  BLASTX
NCBI GI
                  q3033375
BLAST score
                  208
E value
                  1.0e-16
                  66
Match length
% identity
NCBI Description (AC004238) putative berberine bridge enzyme [Arabidopsis
                  thaliana]
```

Seq. No.

237268

Seq. ID

uC-gsronu33B104a01b1

Method BLASTX NCBI GI g124429 BLAST score 667 E value 3.0e-70



```
Match length 143
% identity 86
NCBI Description 37
(E3
pre
```

37 KD CHLOROPLAST INNER ENVELOPE MEMBRANE PROTEIN PRECURSOR

(E37) >gi\_99543\_pir\_\_S14409 membrane protein, 37K, precursor, chloroplast inner envelope - spinach >gi\_21228\_emb\_CAA40283\_ (X56963) 37 kD inner envelope

membrane polypeptide [Spinacia oleracea]

Seq. No. 237269

Seq. ID uC-gsronu33B104a07b1

Method BLASTX
NCBI GI 94432841
BLAST score 477
E value 6.0e-48
Match length 132
% identity 67

NCBI Description (AC006283) hypothetical protein [Arabidopsis thaliana]

Seq. No.

237270

Seq. ID uC-gsronu33B104a09b1

Method BLASTX
NCBI GI g2623295
BLAST score 359
E value 4.0e-34
Match length 84
% identity 79

NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]

Seq. No.

237271

Seq. ID uC-gsronu33B104b06b1

Method BLASTX
NCBI GI g2749982
BLAST score 233
E value 2.0e-19
Match length 113
% identity 47

NCBI Description (AF036705) Similar to phytoene desaturase; coded for by C.

elegans cDNA CEESX74F; coded for by C. elegans cDNA

yk303f4.3; coded for by C. elegans cDNA yk257d4.3; coded for by C. elegans cDNA yk303f4.5; coded for by C. elegans

cDNA yk257d4.5;

Seq. No. 237272

Seq. ID uC-gsronu33B104b07b1

Method BLASTX
NCBI GI g4574139
BLAST score 140
E value 9.0e-09
Match length 29
% identity 93

NCBI Description (AF073697) cysteine synthase [Oryza sativa]

Seq. No.

237273

Seq. ID uC-gsronu33B104c08b1

Method BLASTX NCBI GI g4191796 BLAST score 509

% identity

48

NCBI Description (U72725) retrofit [Oryza longistaminata]

```
E value
                     1.0e-51
 Match length
                     152
% identity
                    59
 NCBI Description
                     (AC005917) putative senescence-associated protein 5
                     [Arabidopsis thaliana]
                    237274
 Seq. No.
 Seq. ID
                    uC-gsronu33B104c11b1
 Method
                    BLASTX
 NCBI GI
                    g3292817
 BLAST score
                    433
 E value
                    7.0e-43
 Match length
                    128
                    70
  % identity
 NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]
                    237275
 Seq. No.
                    uC-gsronu33B104d10b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2088648
 BLAST score
                    268
 E value
                    9.0e-24
 Match length
                    84
  % identity
                    65
 NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]
                    237276
 Seq. No.
 Seq. ID
                    uC-gsronu33B104e05b1
 Method
                    BLASTX
 NCBI GI
                    g4262233
 BLAST score
                    233
 E value
                    1.0e-19
 Match length
                    98
  % identity
                    53
 NCBI Description (AC006200) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    237277
 Seq. ID
                    uC-gsronu33B104e11b1
 Method
                    BLASTX
 NCBI GI
                    g4090259
 BLAST score
                    213
 E value
                    3.0e-17
 Match length
                    56
 % identity
                    66
 NCBI Description (AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga
                    menziesii]
                    237278
 Seq. No.
 Seq. ID
                    uC-gsronu33B104f04b1
 Method
                    BLASTX
 NCBI GI
                    q2586082
 BLAST score
                    238
 E value
                    1.0e-29
 Match length
                    156
```



```
Seq. No.
                   237279
Seq. ID
                   uC-gsronu33B104f05b1
Method
                  BLASTX
NCBI GI
                   g3776025
BLAST score
                   620
                   9.0e-65
E value
Match length
                  144
% identity
                  83
NCBI Description (AJ010474) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  237280
Seq. ID
                  uC-gsronu33B104f09b1
Method
                  BLASTX
                  g1813891
NCBI GI
BLAST score
                  152
E value
                  4.0e-10
Match length
                  38
% identity
                  87
NCBI Description (Y10749) 1-aminocyclopropane-1-carboxylate oxidase [Betula
                  pendula]
Seq. No.
                  237281
Seq. ID
                  uC-gsronu33B104h01b1
Method
                  BLASTX
                  g1706282
NCBI GI
BLAST score
                  355
E value
                  1.0e-33
Match length
                  101
% identity
                  64
NCBI Description DISEASE RESISTANCE RESPONSE PROTEIN 206 >gi 508844 (U11716)
                  disease resistance response protein 206-d [Pisum sativum]
Seq. No.
                  237282
Seq. ID
                  uC-gsronu33B106b08b2
Method
                  BLASTX
NCBI GI
                  q2760844
BLAST score
                  224
E value
                  3.0e-18
Match length
                  68
% identity
                  59
NCBI Description (AC003105) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  237283
Seq. ID
                  uC-gsronu33B106b09b2
Method
                  BLASTX
NCBI GI
                  q2244996
                  572
```

BLAST score E value 5.0e-59 Match length 136 % identity 79

(Z97341) similarity to a membrane-associated salt-inducible NCBI Description

protein [Arabidopsis thaliana]

Seq. No. 237284

Seq. ID uC-gsronu33B106b12b2

Method BLASTX NCBI GI q4432836

```
BLAST score
E value
                   3.0e-09
Match length
                   59
% identity
                   51
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                   237285
Seq. ID
                   uC-gsronu33B106d07b2
                  BLASTX
Method
NCBI GI
                  g3023961
BLAST score
                   202
E value
                   3.0e - 31
Match length
                  76
% identity
                  91
NCBI Description HOMEOBOX PROTEIN KNOTTED-1-LIKE >gi 1946222 emb CAA96512
                  (Z71980) knotted1-like homeobox protein [Malus domestica]
Seq. No.
                   237286
Seq. ID
                  uC-gsronu33B106e07b2
Method
                  BLASTX
NCBI GI
                  g3080451
BLAST score
                  492
E value
                  9.0e-50
Match length
                  111
% identity
                  80
NCBI Description (AL022605) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  237287
Seq. ID
                  uC-gsronu33B106e09b2
Method
                  BLASTX
                  g1778376
NCBI GI
BLAST score
                  274
E value
                  3.0e-24
Match length
                  68
% identity
                  78
NCBI Description (U81288) PsRT17-1 [Pisum sativum]
Seq. No.
                  237288
Seq. ID
                  uC-gsronu33B106e12b2
Method
                  BLASTX
NCBI GI
                  q4432823
BLAST score
                  234
E value
                  2.0e-19
Match length
                  100
% identity
NCBI Description (AC006593) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  237289
Seq. ID
                  uC-gsronu33B106f03b2
Method
                  BLASTX
NCBI GI
                  q3292849
BLAST score
                  612
E value
                  8.0e-64
Match length
                  149
% identity
                  (AJ007582) arginine methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
```

34441

Seq. No.

```
Seq. No.
                   237290
Seq. ID
                   uC-gsronu33B106g06b2
Method
                   BLASTX
NCBI GI
                   g2935521
BLAST score
                   263
E value
                   7.0e-23
Match length
                   127
% identity
                   46
NCBI Description (AF049065) germin-like protein [Pinus radiata]
Seq. No.
                   237291
Seq. ID
                   uC-gsronu33B106g09b2
Method
                   BLASTX
NCBI GI
                   q4102600
BLAST score
                   328
E value
                   2.0e-30
Match length
                   62
% identity
                   97
NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.
                   237292
Seq. ID
                   uC-gsronu33B106h02b2
Method
                   BLASTX
NCBI GI
                   q2506931
BLAST score
                   332
E value
                   6.0e-31
Match length
                   148
% identity
                   45
NCBI Description APYRASE PRECURSOR (ATP-DIPHOSPHATASE) (ADENOSINE
                   DIPHOSPHATASE) (ADPASE) (ATP-DIPHOSPHOHYDROLASE)
                   >gi_2129977_pir__JC4616 apyrase (EC 3.6.1.5) - potato
                   >gi_1381633 (U58597) ATP-diphosphohydrolase [Solanum
                   tuberosum]
Seq. No.
                   237293
Seq. ID
                  uC-gsronu33B107a06b1
Method
                  BLASTX
NCBI GI
                  g2943792
BLAST score
                  304
E value
                  1.0e-34
Match length
                  104
% identity
                  63
NCBI Description
                 (AB006809) PV72 [Cucurbita sp.]
Seq. No.
                  237294
Seq. ID
                  uC-gsronu33B107b12b1
Method
                  BLASTX
NCBI GI
                  g4455223
BLAST score
                  343
                  1.0e-32
E value
Match length
                  98
% identity
NCBI Description
                  (AL035440) putative DNA binding protein [Arabidopsis
                  thaliana]
```

```
Seq. ID
                   uC-gsronu33B107c01b1
Method
                   BLASTX
NCBI GI
                   q2952338
BLAST score
                   284
                   3.0e-25
E value ·
Match length
                   61
% identity
NCBI Description
                  (AF050200) submergence induced protein 2 [Oryza sativa]
Seq. No.
                   237296
Seq. ID
                   uC-gsronu33B107e04b1
Method
                   BLASTX
NCBI GI
                   q2660670
BLAST score
                   268
                   2.0e-23
E value
Match length
                   118
% identity
                   38
NCBI Description
                   (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
                   thaliana]
                   237297
Seq. No.
Seq. ID
                   uC-gsronu33B107e05b1
Method
                   BLASTX
                   g2499606
NCBI GI
BLAST score
                   556
E value
                   3.0e-75
Match length
                   146
% identity
                   95
NCBI Description
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2 (MAP KINASE 2)
                   (ATMPK2) >gi_533281_dbj_BAA03536_ (D14714) ATMPK2
                   [Arabidopsis thaliana]
Seq. No.
                   237298
Seq. ID
                   uC-gsronu33B107e09b1
Method
                  BLASTX
NCBI GI
                   g4235430
BLAST score
                   154
E value
                   2.0e-10
Match length
                   63
% identity
NCBI Description (AF098458) latex-abundant protein [Hevea brasiliensis]
                   237299
Seq. No.
Seq. ID
                  uC-gsronu33B107f03b1
Method
                  BLASTX
NCBI GI
                  g2459442
BLAST score
                  155
E value
                  3.0e-10
Match length
                  66
% identity
                  52
NCBI Description
                  (AC002332) putative DNA-binding protein PD1 [Arabidopsis
```

thaliana]

Seq. No. 237300

Seq. ID uC-gsronu33B107f10b1

Method BLASTX NCBI GI g2244822



```
BLAST score
E value
                   2.0e-18
Match length
                  66
% identity
                   62
NCBI Description (Z97336) RNA polymerase II fifth largest subunit homolog
                  [Arabidopsis thaliana]
Seq. No.
                  237301
Seq. ID
                  uC-gsronu33B107f11b1
Method
                  BLASTX
NCBI GI
                  q3831451
BLAST score
                  442
E value
                  4.0e-44
Match length
                  111
                  77
% identity
NCBI Description (AC005700) putative O-GlcNAc transferase [Arabidopsis
                  thaliana]
Seq. No.
                  237302
Seq. ID
                  uC-gsronu33B107g02b1
Method
                  BLASTX
NCBI GI
                  g4490330
BLAST score
                  692
E value
                  3.0e-73
Match length
                  132
                  93
% identity
NCBI Description (AL035656) splicing factor-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  237303
Seq. ID
                  uC-gsronu33B107h12b1
Method
                  BLASTX
NCBI GI
                  g1706958
BLAST score
                  429
E value
                  1.0e-42
Match length
                  92
% identity
                  83
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  237304
Seq. ID
                  uC-gsronu33B108a05b1
Method
                  BLASTX
NCBI GI
                  q4406759
BLAST score
                  174
E value
                  1.0e-12
Match length
                  66
% identity
```

NCBI Description (AC006836) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237305

Seq. ID uC-gsronu33B108b08b1

Method BLASTX NCBI GI g3033389 BLAST score 140 E value 1.0e-08 Match length 67 % identity 9



NCBI Description (AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq. No. 237306

Seq. ID uC-gsronu33B108c03b1

Method BLASTX
NCBI GI g3915023
BLAST score 481
E value 2.0e-48
Match length 145
% identity 67

NCBI Description SUCROSE-PHOSPHATE SYNTHASE 1

(UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi\_2588888\_dbj\_BAA23213 (AB005023) sucrose-phosphate

synthase [Citrus unshiu]

Seq. No. 237307

Seq. ID uC-gsronu33B108c05b1

Method BLASTX
NCBI GI g4467128
BLAST score 572
E value 4.0e-59
Match length 137
% identity 74

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 237308

Seq. ID uC-gsronu33B108c10b1

Method BLASTX
NCBI GI g729723
BLAST score 188
E value 4.0e-14
Match length 118
% identity 33

NCBI Description PEROXISOMAL FARNESYLATED PROTEIN 33 D HOUSEKEEPING PROTEIN) >gi\_551250\_emb\_CAA53225\_(X75535) house keeping

PROTEIN) >gi\_551250\_emb\_CAA53225 (%75535) house keeping gene 33 [Homo sapiens] >gi\_2570023\_emb\_CAA70257\_ (Y09048) PxF protein [Homo sapiens] >gi\_4521235\_dbj\_BAA76291.1

(AB018541) PEX19 [Homo sapiens]

>gi\_4506339\_ref\_NP\_002848.1\_pPXF\_ peroxisomal farnesylated

protein

Seq. No. 237309

Seq. ID uC-gsronu33B108e04b1

Method BLASTX
NCBI GI g3461820
BLAST score 481
E value 2.0e-48
Match length 143
% identity 71

NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]

Seq. No. 237310

Seq. ID uC-gsronu33B108e12b1

Method BLASTX
NCBI GI g1263291
BLAST score 477
E value 4.0e-48



Match length 112 77

NCBI Description (U49452) alcohol dehydrogenase 2b [Gossypium hirsutum]

Seq. No.

237311

Seq. ID

uC-gsronu33B108g07b1

Method BLASTX
NCBI GI g2443329
BLAST score 188
E value 5.0e-14
Match length 159

% identity 30

NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.

237312

Seq. ID uC-gsronu33B108h04b1

Method BLASTX
NCBI GI g2583108
BLAST score 263
E value 6.0e-23
Match length 110
% identity 48

NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.

237313

Seq. ID uC-gsronu33B108h05b1

Method BLASTX
NCBI GI g3850113
BLAST score 351
E value 4.0e-33
Match length 154
% identity 49

NCBI Description (AL033388) hypothetical integral membrane protein

[Schizosaccharomyces pombe]

Seq. No.

Seq. ID uC-gsronu33B108h10b1

237314

Method BLASTX
NCBI GI 94539545
BLAST score 738
E value 2.0e-78
Match length 158
% identity 90

NCBI Description (Y16644) PRCI [Nicotiana tabacum]

Seq. No. 237315

Seq. ID uC-gsronu33B109a04b1

Method BLASTX
NCBI GI 9730449
BLAST score 361
E value 2.0e-34
Match length 125
% identity 57

NCBI Description 60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A)

>gi\_480647\_pir\_\_S37132 ribosomal protein L13.A - rape
>gi\_398918\_emb\_CAA80341\_ (Z22618) cold induced protein

(BnC24A) [Brassica napus]

Seq. No. 237316 Seq. ID uC-gsronu33B109d04b1 Method BLASTX NCBI GI g3033375 BLAST score 343 E value 3.0e-32 Match length 139 % identity (AC004238) putative berberine bridge enzyme [Arabidopsis NCBI Description thaliana] Seq. No. 237317 Seq. ID uC-gsronu33B109e08b1 Method BLASTX NCBI GI g4508079 BLAST score 258 E value 2.0e-22 Match length 98 % identity 50 NCBI Description (AC005882) 66284 [Arabidopsis thaliana] Seq. No. 237318 Seq. ID uC-gsronu33B109e09b1 Method BLASTX NCBI GI g1703200 BLAST score 323 E value 6.0e-30 Match length 98 % identity 66 NCBI Description PROTEIN KINASE AFC2 >gi\_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi\_642130\_dbj\_BAA08214\_ (D45353) protein kinase [Arabidopsis thaliana] >gi\_4220516\_emb\_CAA22989\_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana] Seq. No. 237319 Seq. ID uC-gsronu33B109f08b1 Method BLASTX NCBI GI g4218187 BLAST score 196 5.0e-15 E value Match length 55 % identity NCBI Description (AJ010165) leghemoglobin activating factor [Glycine max] Seq. No. 237320 Seq. ID uC-gsronu33B109q07b1 Method BLASTX NCBI GI g3157933 BLAST score 565 E value 3.0e-58 Match length 141 % identity NCBI Description (AC002131) Contains similarity to box helicases gb U29097 from C. elegans and to the ENBP1 gene product gb  $\bar{\text{X95995}}$ 

34447

from Vicia sativa. [Arabidopsis thaliana]



```
Seq. No.
                  237321
Seq. ID
                  uC-gsronu33B109g11b1
Method
                  BLASTX
NCBI GI
                  g2494844
BLAST score
                  209
E value
                  1.0e-16
Match length
                  52
% identity
                  81
NCBI Description LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE)
                   (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE
                  MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE)
                  >gi_2129930_pir__S62723 lactoylglutathione lyase (EC
                  4.4.1.5) - tomato >gi 1177314 emb CAA88233 (Z48183)
                  glyoxalase-I [Lycopersicon esculentum]
Seq. No.
                  237322
Seq. ID
                  uC-gsronu33B109h12b1
Method
                  BLASTX
NCBI GI
                  g629602
BLAST score
                  238
E value
                  5.0e-20
Match length
                  122
% identity
                  41
NCBI Description
                  probable imbibition protein - wild cabbage
                  >gi_488787_emb_CAA55893_ (X79330) putative imbibition
                  protein [Brassica oleracea]
Seq. No.
                  237323
Seq. ID
                  uC-gsronu33B110a03b1
Method
                  BLASTX
NCBI GI
                  g1710590
BLAST score
                  152
E value
                  4.0e-12
Match length
                  47
% identity
                  85
NCBI Description 60S ACIDIC RIBOSOMAL PROTEIN P1 (L12) >gi 1209701 (U40147)
                  ribosomal protein L12 [Zea mays]
Seq. No.
                  237324
Seq. ID
                  uC-gsronu33B110a12b1
Method
                  BLASTX
NCBI GI
                  g126985
BLAST score
                  339
E value
                  5.0e-32
Match length
                  78
% identity
                  81
NCBI Description MERI-5 PROTEIN >gi_166778 (M63166) meri-5 [Arabidopsis
                  thaliana]
```

Seq. No. 237325

Seq. ID uC-gsronu33B110b12b1

Method BLASTX
NCBI GI g3482977
BLAST score 349
E value 5.0e-33
Match length 129



```
% identity
NCBI Description (AL031369) putative protein [Arabidopsis thaliana]
                  237326
Seq. No.
                  uC-gsronu33B110c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510401
BLAST score
                  153
E value
                  5.0e-10
Match length
                  37
                  76
% identity
NCBI Description (AC006587) putative general negative regulator of
                  transcription [Arabidopsis thaliana]
                  237327
Seq. No.
Seq. ID
                  uC-gsronu33B110c11b1
Method
                  BLASTX
NCBI GI
                  g1632831
BLAST score
                  251
E value
                  6.0e-22
                  54
Match length
                  87
% identity
NCBI Description (Z49698) orf [Ricinus communis]
Seq. No.
                  237328
Seq. ID
                  uC-gsronu33B110d06b1
Method
                  BLASTX
NCBI GI
                  g4105794
BLAST score
                  215
                  2.0e-17
E value
Match length
                  71
% identity
                  54
NCBI Description (AF049928) PGP224 [Petunia x hybrida]
Seq. No.
                  237329
                  uC-gsronu33B110e04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982303
BLAST score
                  244
E value
                  3.0e-21
Match length
                  68
                  69
% identity
NCBI Description (AF051236) hypothetical protein [Picea mariana]
Seq. No.
                  237330
Seq. ID
                  uC-gsronu33B110e06b1
                  BLASTX
Method
NCBI GI ...
                  q3283433
BLAST score
                  177
                  8.0e-13
E value
```

Match length 73 % identity

(AF069494) cytochrome P450 [Sinapis alba] NCBI Description

Seq. No. 237331 Seq. ID

uC-gsronu33B110g07b1

Method BLASTX

% identity

```
NCBI GI
                   g3122367
BLAST score
                   151
E value
                   6.0e-10
Match length
                   98
% identity
                   36
NCBI Description LIGATIN >gi_1377880 (U58337) ligatin [Mus musculus]
Seq. No.
                   237332
Seq. ID
                  uC-gsronu33B110h10b1
Method
                  BLASTX
NCBI GI
                  q951427
BLAST score
                   434
E value
                   5.0e-43
Match length
                  109
% identity
                   73
NCBI Description (M59857) stearoyl-acyl-carrier protein desaturase [Ricinus
                  communis]
Seq. No.
                  237333
Seq. ID
                  uC-gsronu33B111a07b1
Method
                  BLASTX
NCBI GI
                  q3549666
BLAST score
                  144
E value
                  4.0e-09
Match length
                  40
                  70
% identity
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
Seq. No.
                  237334
Seq. ID
                  uC-gsronu33B111b03b1
Method
                  BLASTX
NCBI GI
                  g1345644
BLAST score
                  439
                  1.0e-43
E value
Match length
                  116
% identity
                  72
NCBI Description CYTOCHROME P450 86A1 (CYPLXXXVI) >gi 940446 emb CAA62082
                  (X90458) cytochrome p450 [Arabidopsis thaliana]
Seq. No.
                  237335
Seq. ID
                  uC-gsronu33B111c04b1
Method
                  BLASTX
NCBI GI
                  g2344887
BLAST score
                  207
E value
                  2.0e-16
Match length
                  57
% identity
                  70
NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.
                  237336
Seq. ID
                  uC-gsronu33B111c09b1
Method
                  BLASTX
NCBI GI
                  q4206208
BLAST score
                  231
E value
                  4.0e-19
Match length
                  97
```



237338

NCBI Description (AF071527) hypothetical protein [Arabidopsis thaliana] >gi\_4263041\_gb\_AAD15310\_ (AC005142) hypothetical protein [Arabidopsis thaliana] Seq. No. 237337 Seq. ID uC-gsronu33B111d09b1 Method BLASTX NCBI GI g4220489 BLAST score 155 E value 3.0e-10Match length 71

% identity 52 NCBI Description (AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. ID uC-gsronu33B111e08b1 Method BLASTX NCBI GI g4249382 BLAST score 163 E value 9.0e-12Match length 40 % identity 70

Seq. No.

NCBI Description (AC005966) Strong similarity to gi\_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC

gb AC004481. [Arabidopsis thaliana]

Seq. No. 237339 Seq. ID uC-gsronu33B111f07b1 Method BLASTX

NCBI GI q4512685 BLAST score 154 E value 9.0e-11 Match length 39 % identity 62

(AC006931) hypothetical protein [Arabidopsis thaliana] NCBI Description

>gi\_4559325\_gb\_AAD22987.1 AC007087 6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237340

Seq. ID uC-gsronu33B111q01b1

Method BLASTX NCBI GI g2499710 BLAST score 326 E value 1.0e-30 Match length 69 % identity

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)

>gi\_1438075 (L33686) phospholipase D [Ricinus communis]

Seq. No. 237341

Seq. ID uC-gsronu33B111q10b1

Method BLASTX NCBI GI g3513737 BLAST score 182 E value 2.0e-13 Match length 46

```
% identity
   NCBI Description
                     (AF080118) contains similarity to C3HC4-type zinc fingers
                      (Pfam:zf-C3HC4.hmm, score: 34.87) [Arabidopsis thaliana]
   Seq. No.
                     237342
   Seq. ID
                     uC-gsronu33B111h04b1
  Method
                     BLASTX
   NCBI GI
                     g3559814
   BLAST score
                     665
  E value
                     5.0e-70
  Match length
                     151
   % identity
                     83
  NCBI Description (Y15781) transketolase 1 [Capsicum annuum]
  Seq. No.
                     237343
  Seq. ID
                     uC-gsronu33B111h06b1
  Method
                     BLASTX
  NCBI GI
                     g2191191
  BLAST score
                     160
  E value
                     7.0e-11
  Match length
                     51
  % identity
                     59
  NCBI Description (AF007271) A_TM021B04.14 gene product [Arabidopsis
                     thaliana]
  Seq. No.
                     237344
  Seq. ID
                     uC-gsronu33B113a08b1
  Method
                     BLASTX
 NCBI GI
                     g2662343
BLAST score
                     577
  E value
                     9.0e-60
  Match length
                     110
  % identity
                     100
  NCBI Description (D63581) EF-1 alpha [Oryza sativa]
  Seq. No.
                     237345
  Seq. ID
                     uC-gsronu33B113b01b1
  Method
                     BLASTX
  NCBI GI
                     g4545262
  BLAST score
                     215
  E value
                     3.0e-17
  Match length
                     48
  % identity
```

Seq. No. 237346

NCBI Description

Seq. ID uC-gsronu33B113c06b1

Method BLASTX
NCBI GI g4454484
BLAST score 216
E value 9.0e-18
Match length 56
% identity 71

NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis

thalianal

hirsutum]

(AF118230) metallothionein-like protein [Gossypium

NCBI GI

BLAST score

q417073

518

```
Seq. No.
                   237347
Seq. ID
                   uC-gsronu33B113c08b1
Method
                   BLASTX
NCBI GI
                   g1407705
BLAST score
                   593
E value
                   1.0e-61
Match length
                   145
% identity
                   75
NCBI Description (U60202) lipoxygenase [Solanum tuberosum]
                   237348
Seq. No.
Seq. ID
                   uC-gsronu33B113c12b1
Method
                   BLASTX
NCBI GI
                   g3786012
BLAST score
                   366
E value
                   5.0e-35
Match length
                  130
% identity
                   52
NCBI Description (AC005499) putative acid phosphatase [Arabidopsis thaliana]
                   237349
Seq. No.
Seq. ID
                  uC-gsronu33B113d10b1
Method
                  BLASTX
NCBI GI
                   g1086147
BLAST score
                   331
E value
                   6.0e-31
Match length
                  80
                   72
% identity
NCBI Description protein S2 - Phalaris coerulescens >gi_556833_emb_CAA57520_
                   (X81992) S2 [Phalaris coerulescens]
Seq. No.
                   237350
Seq. ID
                  uC-gsronu33B113e01b1
Method
                  BLASTX
NCBI GI
                  g4539369
BLAST score
                  290
E value
                  3.0e-26
Match length
                  85
% identity
NCBI Description (AL049525) putative protein [Arabidopsis thaliana]
Seq. No.
                  237351
Seq. ID
                  uC-gsronu33B113f01b1
Method
                  BLASTX
NCBI GI
                  g3757514
BLAST score
                  408
E value
                  6.0e-40
Match length
                  80
% identity
NCBI Description
                  (AC005167) putative plasma membrane intrinsic protein
                  [Arabidopsis thaliana]
Seq. No.
                  237352
Seq. ID
                  uC-gsronu33B113f03b1
Method
                  BLASTX
```



E value 6.0e-53 Match length 116 % identity 84

NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi\_484529 pir\_JQ1977 glutamate synthase (NADH) (EC

1.4.1.14) - alfalfa >gi\_166412 (L01660) NADH-glutamate

synthase [Medicago sativa]

Seq. No. 237353

Seq. ID uC-gsronu33B113f10b1

Method BLASTX
NCBI GI g3367593
BLAST score 198
E value 3.0e-15
Match length 56
% identity 59

NCBI Description (AL031135) putative protein [Arabidopsis thaliana]

>gi\_3805841\_emb\_CAA21461\_ (AL031986) putative protein

[Arabidopsis thaliana]

Seq. No. 237354

Seq. ID uC-gsronu33B113f11b1

Method BLASTX
NCBI GI g2500380
BLAST score 572
E value 4.0e-59
Match length 105
% identity 100

NCBI Description 60S RIBOSOMAL PROTEIN L44 >gi\_2119128\_pir\_\_JC4923 ribosomal

protein RL44 - upland cotton >gi\_1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi 1553131

(U64678) ribosomal protein L44 isoform b [Gossypium

hirsutum]

Seq. No. 237355

Seq. ID uC-gsronu33B113g07b1

Method BLASTX
NCBI GI g1706282
BLAST score 434
E value 6.0e-43
Match length 127
% identity 61

NCBI Description DISEASE RESISTANCE RESPONSE PROTEIN 206 >gi\_508844 (U11716)

disease resistance response protein 206-d [Pisum sativum]

Seq. No. 237356

Seq. ID uC-gsronu33B113g08b1

Method BLASTX
NCBI GI g861170
BLAST score 699
E value 5.0e-74
Match length 145
% identity 97

NCBI Description (X03697) heat shock protein 70 [Zea mays]

Seq. No. 237357

Seq. ID uC-gsronu33B113q11b1

```
Method
                   BLASTX
NCBI GI
                   q2119353
BLAST score
                   316
E value
                   4.0e-29
Match length
                  115
% identity
                   33
NCBI Description calmodulin - moss (Physcomitrella patens)
Seq. No.
                   237358
Seq. ID
                  uC-gsronu33B114b11b1
Method
                  BLASTX
                  q4049353
```

NCBI GI BLAST score 511 E value 6.0e-52 Match length 131 % identity 71

NCBI Description (AL034567) putative protein [Arabidopsis thaliana]

Seq. No. Seq. ID uC-gsronu33B114c03b1 Method BLASTX NCBI GI q4567226 BLAST score 166 E value 2.0e-11 Match length 46 % identity 65

NCBI Description (AC007119) unknown protein [Arabidopsis thaliana]

Seq. No. 237360 Seq. ID uC-gsronu33B114c07b1 Method BLASTX NCBI GI q3879150 BLAST score 197 E value 4.0e-15

237359

Match length 75 % identity 55

NCBI Description (Z70686) Similarity to Yeast hypothetical protein YKEO (SW:YKE0 YEAST); cDNA EST yk254g6.3 comes from this gene; cDNA EST yk254g6.5 comes from this gene [Caenorhabditis

elegans]

237361 Seq. No.

Seq. ID uC-gsronu33B114c10b1

Method BLASTX NCBI GI g1563719 BLAST score 473 E value 2.0e-47 Match length 100 % identity 88

NCBI Description (Y08320) cyclophylin [Digitalis lanata]

Seq. No. 237362

Seq. ID uC-gsronu33B114d06b1

Method BLASTX NCBI GI g3821280 BLAST score 614 E value 3.0e-66

```
Match length
                   136
% identity
                   82
NCBI Description
                  (AJ009952) asparagine synthetase type II [Phaseolus
                   vulgaris]
Seq. No.
                   237363
Seq. ID
                  uC-gsronu33B114e12b1
Method
                  BLASTX
NCBI GI
                  g1082766
BLAST score
                  167
E value
                   1.0e-11
Match length
                  52
                  58
% identity
NCBI Description ribosomal protein L29 - human >gi 793843 emb CAA89008
                   (Z49148) ribosomal protein L29 [Homo sapiens]
Seq. No.
                  237364
Seq. ID
                  uC-gsronu33B114f06b1
Method
                  BLASTX
NCBI GI
                  g3269288
BLAST score
                  621
E value
                  7.0e-65
                  151
Match length
% identity
                  78
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                  237365
Seq. ID
                  uC-gsronu33B114g05b1
Method
                  BLASTX
NCBI GI
                  g2191145
BLAST score
                  181
                  3.0e-13
E value
Match length
                  119
% identity
                  39
NCBI Description (AF007269) A_IG002N01.4 gene product [Arabidopsis thaliana]
Seq. No.
                  237366
Seq. ID
                  uC-gsronu33B114g08b1
Method
                  BLASTX
NCBI GI
                  g2569940
BLAST score
                  455
E value
                  2.0e-45
Match length
                  125
% identity
```

NCBI Description (Y15194) GRS protein [Arabidopsis thaliana]

Seq. No. 237367

Seq. ID uC-gsronu33B114h12b1

Method BLASTX
NCBI GI g3415117
BLAST score 291
E value 2.0e-26
Match length 101
% identity 55

NCBI Description (AF081203) villin 3 [Arabidopsis thaliana]

Seq. No. 237368

% identity

```
Seq. ID
                   uC-gsronu33B116a05b1
Method
                   BLASTX
NCBI GI
                   g1212759
BLAST score
                   254
E value
                   8.0e-22
Match length
                   47
% identity
                   89
NCBI Description (X89192) DNA binding protein [Arabidopsis thaliana]
Seq. No.
                   237369
Seq. ID
                   uC-gsronu33B116a06b1
Method
                   BLASTX
NCBI GI
                   q4455293
BLAST score
                   359
E value
                   4.0e-34
Match length
                   133
% identity
                   60
NCBI Description (AL035528) putative protein [Arabidopsis thaliana]
Seq. No.
                   237370
Seq. ID
                   uC-gsronu33B116b08b1
Method
                   BLASTX
NCBI GI
                   g3395441
BLAST score
                   247
E value
                   4.0e-21
Match length
                   65
% identity
                   68
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   237371
Seq. ID
                   uC-gsronu33B116c01b1
Method
                   BLASTX
NCBI GI
                   g1001649
BLAST score
                   229
E value
                   5.0e-19
                   116
Match length
% identity
                   47
NCBI Description
                  (D64002) DNA gyrase A subunit [Synechocystis sp.]
Seq. No.
                   237372
Seq. ID
                   uC-gsronu33B116c04b1
Method
                  BLASTX
NCBI GI
                  g336392
BLAST score
                  271
                   7.0e-24
E value
Match length
                  89
% identity
                   66
NCBI Description
                  (J05215) ribosomal protein S17 [Arabidopsis thaliana]
Seq. No.
                  237373
Seq. ID
                  uC-gsronu33B116c05b1
Method
                  BLASTX
NCBI GI
                  g4455330
BLAST score
                  323
E value
                  6.0e-30
Match length
                  149
```

% identity

78

```
(NI 035525) contains FST chem44002 (Amehidan-ia-th-2)
```

```
NCBI Description (AL035525) contains EST gb:T44002 [Arabidopsis thaliana]
Seq. No.
                   237374
Seq. ID
                   uC-gsronu33B116e06b1
Method
                   BLASTX
NCBI GI
                   g3540201
BLAST score
                   688
E value
                   1.0e-72
Match length
                   141
                   90
% identity
NCBI Description (AC004260) Putative nuclear protein [Arabidopsis thaliana]
Seq. No.
                   237375
Seq. ID
                   uC-gsronu33B116e11b1
Method
                   BLASTX
NCBI GI
                   g421843
BLAST score
                   250
E value
                   2.0e-21
Match length
                   71
% identity
                   68
NCBI Description protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana
                   >gi_217861_dbj_BAA01715_ (D10909) serine/threonine protein
                   kinase [Arabidopsis thaliana]
Seq. No.
                   237376
Seq. ID
                   uC-gsronu33B116e12b1
Method
                   BLASTX
NCBI GI
                   g2982444
BLAST score
                   509
E value
                   8.0e-52
Match length
                  134
% identity
                   72
NCBI Description (AL022224) CLV1 receptor kinase like protein [Arabidopsis
                   thaliana]
Seq. No.
                   237377
Seq. ID
                  uC-gsronu33B116f01b1
Method
                  BLASTX
NCBI GI
                  g1171707
BLAST score
                  250
E value
                  2.0e-21
Match length
                  66
% identity
                  70
NCBI Description
                  NITRATE REDUCTASE (NR) >gi_1086084 pir S52301 nitrate
                  reductase (NADH) (EC 1.6.6.1) - chicory
                  >gi_662902_emb_CAA58909 (X84103) nitrate reductase (NADH)
                  [Cichorium intybus]
Seq. No.
                  237378
Seq. ID
                  uC-gsronu33B116f05b1
Method
                  BLASTX
NCBI GI
                  g4185509
BLAST score
                  412
E value
                  1.0e-43
Match length
                  111
```

NCBI Description (AF102821) actin depolymerizing factor 3 [Arabidopsis

Seq. ID



## thaliana]

```
237379
Seq. No.
Seq. ID
                   uC-gsronu33B116g03b1
Method
                   BLASTX
NCBI GI
                   g3176072
BLAST score
                   133
                   4.0e-16
E value
Match length
                   52
% identity
                   88
NCBI Description
                   (AJ002485) protein phosphatase 1, catalytic beta subunit
                   [Medicago sativa]
                   237380
Seq. No.
Seq. ID
                   uC-gsronu33B116g04b1
Method
                   BLASTX
                   q3786011
NCBI GI
BLAST score
                   678
E value
                   2.0e-71
Match length
                   149
% identity
                   85
NCBI Description
                   (AC005499) putative elongation factor [Arabidopsis
                   thaliana]
Seq. No.
                   237381
Seq. ID
                   uC-gsronu33B116h01b1
Method
                   BLASTX
NCBI GI
                   g2809262
BLAST score
                   257
E value
                   2.0e-22
Match length
                   109
% identity
                   46
NCBI Description
                  (AC002560) F21B7.31 [Arabidopsis thaliana]
Seq. No.
                   237382
Seq. ID
                   uC-gsronu33B117a07b1
Method
                   BLASTX
NCBI GI
                   q3831471
BLAST score
                   178
E value
                   4.0e-13
Match length
                   57
% identity
NCBI Description (AC005700) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   237383
Seq. ID
                   uC-gsronu33B117a10b1
Method
                   BLASTX
NCBI GI
                   g3818624
BLAST score
                   765
E value
                   1.0e-81
Match length
                   154
% identity
                   96
NCBI Description
                  (AF095912) actin related protein 2; ARP2 [Arabidopsis
                   thaliana]
Seq. No.
                   237384
```

uC-gsronu33B117c04b1

Match length

% identity

41

93

```
Method
                   BLASTX
NCBI GI
                   g2262113
BLAST score
                   191
E value
                   2.0e-14
Match length
                  147
% identity
                   40
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                  237385
Seq. ID
                  uC-gsronu33B117c09b1
Method
                  BLASTX
NCBI GI
                  g3924597
BLAST score
                  145
E value
                   4.0e-09
Match length
                  53
                   57
% identity
NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  237386
Seq. ID
                  uC-gsronu33B117d08b1
Method
                  BLASTX
NCBI GI
                  q404688
BLAST score
                  188
E value
                  2.0e-14
Match length
                  74
% identity
                  47
NCBI Description (L19074) cytochrome P450 [Catharanthus roseus]
Seq. No.
                  237387
Seq. ID
                  uC-gsronu33B117d11b1
Method
                  BLASTX
NCBI GI
                  g4490303
BLAST score
                  249
E value
                  3.0e-21
Match length
                  53
% identity
                  87
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
                  237388
Seq. No.
Seq. ID
                  uC-gsronu33B117e03b1
Method
                  BLASTX
NCBI GI
                  g3831441
BLAST score
                  155
E value
                  3.0e-10
Match length
                  49
% identity
                  78
NCBI Description (AC005819) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  237389
Seq. ID
                  uC-gsronu33B117e04b1
Method
                  BLASTX
NCBI GI
                  g1351014
BLAST score
                  206
E value
                  1.0e-16
```

NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902\_dbj BAA07207 (D38010)



## ribosomal protein S8 [Oryza sativa]

```
237390
Seq. No.
Seq. ID
                  uC-gsronu33B117h03b1
Method
                   BLASTX
NCBI GI
                   q2443836
BLAST score
                   206
E value
                   2.0e-16
Match length
                   57
% identity
                   60
NCBI Description
                  (AF020793) tonoplast intrinsic protein homolog MSMCP1
                   [Medicago sativa]
                   237391
Seq. No.
Seq. ID
                  uC-gsronu33B121h01b1
Method
                  BLASTX
NCBI GI
                   q3914449
BLAST score
                   336
E value
                   7.0e-32
Match length
                  72
% identity
                   89
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
                   7) >gi_3172331 (AF041258) 26S proteasome subunit 7 [Prunus
                  persica]
Seq. No.
                   237392
Seq. ID
                  uC-gsronu33B124a03b1
Method
                  BLASTX
NCBI GI
                   g1279640
BLAST score
                   452
E value
                   5.0e-45
Match length
                  134
% identity
                   62
NCBI Description (X92204) NAM [Petunia x hybrida]
Seq. No.
                  237393
Seq. ID
                  uC-gsronu33B124a06b1
Method
                  BLASTX
NCBI GI
                  q3935183
BLAST score
                  249
E value
                   2.0e-21
Match length
                  113
% identity
                   49
NCBI Description (AC004557) F17L21.26 [Arabidopsis thaliana]
Seq. No.
                  237394
Seq. ID
                  uC-gsronu33B124b01b1
Method
                  BLASTX
NCBI GI
                  g3540181
BLAST score
                  230
E value
                  5.0e-19
Match length
                  123
% identity
                   46
NCBI Description
                  (AC004122) Unknown protein [Arabidopsis thaliana]
```

Seq. No. 237395

Seq. ID uC-gsronu33B124b11b1

% identity

```
Method
                    BLASTX
 NCBI GI
                    g3096945
 BLAST score
                    435
~ E value
                    4.0e-43
 Match length
                    107
                    80
  % identity
 NCBI Description (AL023094) putative auxin-regulated protein [Arabidopsis
                    thaliana]
                    237396
  Seq. No.
 Seq. ID
                    uC-gsronu33B124c08b1
 Method
                    BLASTX
 NCBI GI
                    g3927830
 BLAST score
                    336
 E value
                    2.0e-31
 Match length
                    128
  % identity
                    52
 NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    237397
 Seq. ID
                    uC-gsronu33B124e06b1
 Method
                    BLASTX
 NCBI GI
                    g1706958
 BLAST score
                    716
 E value
                    5.0e-76
 Match length
                    135
                    99
 % identity
 NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]
                    237398
 Seq. No.
 Seq. ID
                    uC-gsronu33B124e09b1
 Method
                    BLASTX
 NCBI GI
                    g4510345
 BLAST score
                    282
 E value
                    4.0e-25
 Match length
                    63
 % identity
                    78
 NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    237399
 Seq. ID
                    uC-gsronu33B124e10b1
 Method
                    BLASTX
 NCBI GI
                    g4107276
 BLAST score
                    151
 E value
                    8.0e-10
 Match length
                    36
% identity
 NCBI Description (X98506) acetyl-CoA synthetase [Solanum tuberosum]
 Seq. No.
                    237400
 Seq. ID
                    uC-gsronu33B124f08b1
 Method
                    BLASTX
 NCBI GI
                    g122781
 BLAST score
                    352
 E value
                    3.0e-33
 Match length
                    66
```



NCBI Description POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229) >gi 82210 pir A05198 hypothetical protein 229 - common tobacco chloroplast >gi 11844 emb CAA77364 (Z00044) hypothetical protein [Nicotiana tabacum] >gi 225212 prf\_\_1211235AT ORF 229 [Nicotiana tabacum] Seq. No. 237401 Seq. ID uC-gsronu33B124g02b1 Method BLASTX NCBI GI g2500036 BLAST score 542 E value 1.0e-55 Match length 124 % identity 82 NCBI Description DIHYDROOROTASE PRECURSOR (DHOASE) >gi\_2121273 (AF000146) dihydroorotase [Arabidopsis thaliana] >gi 3292818 emb CAA19808 (AL031018) dihydroorotase [Arabidopsis thaliana] Seq. No. 237402 Seq. ID uC-gsronu33B124g12b1 Method BLASTX NCBI GI q123534 BLAST score 532 E value 2.0e-54 Match length 133 77 % identity NCBI Description 17.3 KD CLASS I HEAT SHOCK PROTEIN (HSP 17.3) >gi\_71493\_pir\_HHSY17 heat shock protein 17 - soybean >gi\_18656\_emb\_CAA25578\_ (X01104) heat shock protein 6871 (aa 1-153) [Glycine max] >gi\_224205\_prf\_\_1012218B protein 6871, heat shock [Glycine max] Seq. No. 237403 Seq. ID uC-gsronu33B125b03b1 Method BLASTX NCBI GI g2330651 BLAST score 172 E value 3.0e-12 90 Match length % identity 52 NCBI Description (Y14559) topoisomerase II [Pisum sativum] Seq. No. 237404 Seq. ID uC-gsronu33B125c02b1 BLASTX

Method NCBI GI g2293566 BLAST score 278 E value 1.0e-24

Match length 53 % identity

NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No. 237405

Seq. ID uC-gsronu33B125c05b1

Method BLASTX NCBI GI g1762436

BLAST score

Match length

E value

214

89

2.0e-17

```
BLAST score
                   279
E value
                   2.0e-25
Match length
                   65
% identity
                   80
NCBI Description
                  (U60277) acyl-acyl carrier protein desaturase [Asclepias
                   syriaca]
                   237406
Seq. No.
Seq. ID
                   uC-gsronu33B125d01b1
Method
                   BLASTX
NCBI GI
                   g3763916
BLAST score
                   203
E value
                   4.0e-16
Match length
                   79
% identity
                   52
NCBI Description
                   (AC004450) unknown protein [Arabidopsis thaliana]
                   >gi 4531439 gb AAD22124.1 AC006224 6 (AC006224) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   237407
Seq. ID
                   uC-gsronu33B125d10b1
Method
                   BLASTX
NCBI GI
                   q4432866
BLAST score
                   140
E value
                   2.0e-09
Match length
                   123
% identity
                   31
                   (AC006300) putative reverse transcriptase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   237408
Seq. ID
                   uC-gsronu33B125f11b1
Method
                   BLASTX
NCBI GI
                   q2677828
BLAST score
                   483
E value
                   1.0e-48
Match length
                   135
% identity
NCBI Description
                  (U93166) cysteine protease [Prunus armeniaca]
Seq. No.
                   237409
Seq. ID
                   uC-gsronu33B125g01b1
Method
                   BLASTX
NCBI GI
                   g2738982
BLAST score
                   169
E value
                   6.0e-13
Match length
                   100
% identity
                   43
NCBI Description
                  (AF022157) CYP71A10 [Glycine max]
Seq. No.
                   237410
Seq. ID
                   uC-gsronu33B125g05b1
Method
                   BLASTX
NCBI GI
                   g2648273
```



% identity 47

NCBI Description (AE000949) argininosuccinate synthetase (argG)

[Archaeoglobus fulgidus]

Seq. No. 237411

Seq. ID uC-gsronu33B125g06b1

Method BLASTX
NCBI GI g3236255
BLAST score 373
E value 8.0e-36
Match length 127
% identity 59

NCBI Description (AC004684) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237412

Seq. ID uC-gsronu33B125h03b1

Method BLASTX
NCBI GI g3510260
BLAST score 373
E value 7.0e-36
Match length 100
% identity 72

NCBI Description (AC005310) putative AP2 domain containing protein

[Arabidopsis thaliana] >gi\_3522951 (AC004411) putative AP2

domain containing protein [Arabidopsis thaliana]

Seq. No. 237413

Seq. ID uC-gsronu33B125h07b1

Method BLASTX
NCBI GI g3033381
BLAST score 149
E value 2.0e-09
Match length 39
% identity 67

NCBI Description (AC004238) putative UDP-galactose-4-epimerase [Arabidopsis

thaliana]

Seq. No. 237414

Seq. ID uC-gsronu33B125h10b1

Method BLASTX
NCBI GI g2129495
BLAST score 334
E value 3.0e-31
Match length 91
% identity 70

NCBI Description fiber protein E6 (clone SIE6-2A) - sea-island cotton

>gi\_1000088 (U30507) E6 [Gossypium barbadense] >gi\_1000090

(U30508) E6 [Gossypium barbadense]

Seq. No. 237415

Seq. ID uC-gsronu33B126a03b1

Method BLASTX
NCBI GI g1350720
BLAST score 265
E value 1.0e-23
Match length 68
% identity 74



## NCBI Description 60S RIBOSOMAL PROTEIN L32

Seq. No. 237416

Seq. ID uC-gsronu33B126b01b1

Method BLASTX
NCBI GI g1174592
BLAST score 535
E value 5.0e-55
Match length 103
% identity 97

NCBI Description TUBULIN ALPHA-1 CHAIN >gi\_2119270\_pir\_\_S60233 alpha-tubulin

- garden pea >gi\_525332 (U12589) alpha-tubulin [Pisum

sativum]

Seq. No. 237417

Seq. ID uC-gsronu33B126b11b1

Method BLASTX
NCBI GI g4455338
BLAST score 538
E value 3.0e-55
Match length 114
% identity 91

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 237418

Seq. ID uC-gsronu33B126c09b1

Method BLASTX
NCBI GI g3269287
BLAST score 344
E value 1.0e-32
Match length 85
% identity 79

NCBI Description (AL030978) GH3 like protein [Arabidopsis thaliana]

Seq. No. 237419

Seq. ID uC-gsronu33B126d08b1

Method BLASTX
NCBI GI 93249068
BLAST score 263
E value 9.0e-23
Match length 128
% identity 42

NCBI Description (AC004473) Contains similarity to zinc-binding protein

(PWA33) gb\_L04190 from Pleurodeles waltlii. [Arabidopsis

thaliana]

Seq. No. 237420

Seq. ID uC-gsronu33B126d09b1

Method BLASTX
NCBI GI g1420887
BLAST score 189
E value 3.0e-14
Match length 69
% identity 48

NCBI Description (U34334) non-specific lipid transfer-like protein

[Phaseolus vulgaris]



```
Seq. No. .
                  uC-gsronu33B126e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510346
BLAST score
                  147
                  6.0e-10
E value
                  40
Match length
% identity
                  68
NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]
                  237422
Seq. No.
                  uC-gsronu33B126e06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173223
BLAST score
                  171
                  2.0e-12
E value
Match length
                  36
% identity
                  94
NCBI Description 40S RIBOSOMAL PROTEIN S11 >gi_454848 (L28831) ribosomal
                  protein S11 [Glycine max]
Seq. No.
                  237423
                  uC-gsronu33B126f04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4378848
BLAST score
                  415
                  1.0e-40
E value
                  139
Match length
                  56
% identity
NCBI Description (AF124349) hydrolase [Zymomonas mobilis]
                  237424
Seq. No.
Seq. ID
                  uC-gsronu33B126f10b1
                  BLASTX
Method
NCBI GI
                  g3478637
BLAST score
                  282
E value
                  3.0e-25
Match length
                  123
                  41
% identity
NCBI Description (AC005546) R29425_1 [Homo sapiens]
                  237425
Seq. No.
Seq. ID
                  uC-gsronu33B126g06b1
Method
                  BLASTX
NCBI GI
                  q3885334
BLAST score
                  209
E value
                  6.0e-28
Match length
                  121
% identity
                   65
NCBI Description (AC005623) putative argonaute protein [Arabidopsis
                  thaliana]
```

Method BLASTX NCBI GI g283503 BLAST score 138

```
THE YOR
```

E value 8.0e-09 Match length 43 70

NCBI Description tubulin alpha chain - Euplotes vannus (SGC9)

>gi\_9327\_emb\_CAA77816\_ (Z11769) alpha-Tubulin [Euplotes

vannus]

237427

Seq. No.

Seq. ID uC-gsronu33B127a01b1

Method BLASTX
NCBI GI g2252866
BLAST score 308
E value 3.0e-28
Match length 88
% identity 80

NCBI Description (AF013294) contains region of similarity to SYT

[Arabidopsis thaliana]

Seq. No.

Seq. ID uC-gsronu33B127a03b1

237428

Method BLASTX
NCBI GI g4455207
BLAST score 270
E value 3.0e-30
Match length 88
% identity 82

NCBI Description (AL035440) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No. 237429

Seq. ID uC-gsronu33B127a06b1

Method BLASTX
NCBI GI g2443887
BLAST score 222
E value 2.0e-18
Match length 61
% identity 74

NCBI Description (AC002294) Similar to transcription factor

gb\_Z46606\_1658307 and others [Arabidopsis thaliana]

Seq. No. 237430

Seq. ID uC-gsronu33B127a07b1

Method BLASTX
NCBI GI g130771
BLAST score 173
E value 2.0e-12
Match length 82
% identity 41

NCBI Description PHOSPHATIDYLINOSITOL TRANSFER PROTEIN ALPHA ISOFORM (PTDINS

TRANSFER PROTEIN ALPHA) (PTDINSTP) (PI-TP-ALPHA)

>gi\_92602\_pir\_\_A34391 phosphatidylinositol transfer protein - rat >gi\_206495 (M25758) phosphatidylinositol transfer

protein [Rattus norvegicus]

Seq. No. 237431

Seq. ID uC-gsronu33B127a08b1

Method BLASTX NCBI GI g2662343



```
BLAST score
                   2.0e-53
E value
                   104
Match length
% identity
                   97
NCBI Description
                   237432
```

(D63581) EF-1 alpha [Oryza sativa]

Seq. No.

uC-gsronu33B127d12b1 Seq. ID

Method BLASTX NCBI GI g2832777 BLAST score 281 E value 4.0e-25 104 Match length 50 % identity

(AL021086) 1-evidence=predicted by match; NCBI Description

1-match\_accession=SWISS-PROT:P53624;

1-match\_description=MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113)

(MAN(9)-ALPHA-MANNOSIDASE).; 1-match\_species=DROSOPHILA

Seq. No. 237433

uC-gsronu33B127f02b1 Seq. ID

Method BLASTX NCBI GI g2293360 235 BLAST score 9.0e-20 E value 84 Match length % identity 58

(D87670) polyphenol oxidase [Malus domestica] NCBI Description

Seq. No. 237434

uC-gsronu33B127h03b1 Seq. ID

Method BLASTX NCBI GI g4151068 BLAST score 546 E value 3.0e-56Match length 114

90 % identity

(Y10862) ribonucleotide reductase [Nicotiana tabacum] NCBI Description

Seq. No. 237435

Seq. ID uC-gsronu33B129a01b1

Method BLASTX NCBI GI g4544369 BLAST score 386 E value 3.0e - 37Match length 150 51 % identity

(AC006920) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 237436

Seq. ID uC-gsronu33B129b04b1

Method BLASTX NCBI GI g549010 BLAST score 376 E value 4.0e-36 Match length 80



```
% identity
                    EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)
NCBI Description
                    (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG)
                    >gi 322554_pir__S31328 omnipotent suppressor protein SUP1
                    homolog (clone G18) - Arabidopsis thaliana
                    >gi_16514_emb_CAA49172_ (X69375) similar to yeast
                    omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis
                    thaliana] >gi 1495249 emb CAA66118 (X97486) eRF1-3
                    [Arabidopsis thaliana]
                    237437
Seq. No.
Seq. ID
                    uC-gsronu33B129b05b1
Method
                    BLASTX
NCBI GI
                    g2244834
BLAST score
                    287
E value
                    1.0e-25
Match length
                    164
% identity
                    36
NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]
                   237438
Seq. No.
Seq. ID
                    uC-gsronu33B129b12b1
Method
                    BLASTX
NCBI GI
                    q88079
BLAST score
                    427
E value
                    3.0e-42
Match length
                    113
% identity
                    68
NCBI Description ribosomal protein L10, cytosolic - human (fragment)
                    >qi 249371 bbs 103310 (S35960) laminin receptor homolog
                    [human, Peptide Partial, 153 aa] [Homo sapiens]
Seq. No.
                    237439
Seq. ID
                    uC-gsronu33B129c12b1
                    BLASTX
Method
NCBI GI
                    g2317729
BLAST score
                    738
E value
                    1.0e-78
                    146
Match length
                    92
% identity
NCBI Description (AF013627) reversibly glycosylated polypeptide-1
                    [Arabidopsis thaliana]
                    237440
Seq. No.
                    uC-gsronu33B129d11b1
Seq. ID
                    BLASTX
                    g2384696
                    284
                    3.0e-25
```

Method NCBI GI BLAST score E value

Match length 132 % identity

NCBI Description (AF013216) acyl-CoA oxidase [Myxococcus xanthus]

237441 Seq. No.

uC-gsronu33B129f07b1 Seq. ID



```
BLASTX
Method
                  q4467158
NCBI GI
                  293
BLAST score
                  2.0e-26
E value
                  148
Match length
                  50
% identity
NCBI Description (AL035540) putative protein [Arabidopsis thaliana]
Seq. No.
                  237442
                  uC-gsronu33B129g05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1805254
BLAST score
                  409
                  5.0e-40
E value
                  89
Match length
                  83
% identity
                  (U62622) monogalactosyldiacylglycerol synthase [Cucumis
NCBI Description
                  sativus]
                  237443
Seq. No.
Seq. ID
                  uC-gsronu33B129g09b1
Method
                  BLASTX
NCBI GI
                  g1352442
BLAST score
                  307
                  6.0e-28
E value
Match length
                  75
                  75
% identity
NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E)
                  (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD
                  SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi 1002917 (U34598) p28
                  [Oryza sativa]
                  237444
Seq. No.
                  uC-gsronu33B129h05b1
Seq. ID
                  BLASTX
Method
                  q4545262
NCBI GI
BLAST score
                  215
                  3.0e-17
E value
Match length
                  48
                  85
% identity
                  (AF118230) metallothionein-like protein [Gossypium
NCBI Description
                  hirsutum]
                  237445
Seq. No.
                  uC-gsronu33B129h06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4454484
BLAST score
                  383
                  8.0e-37
E value
Match length
                  120
                   62
% identity
```

NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis

thaliana]

Seq. No. 237446

Seq. ID uC-qsronu33B130e03b1

Method BLASTX



```
NCBI GI
                   q629483
BLAST score
                   279
                   9.0e-25
E value
Match length
                  106
% identity
                   55
                  gene 1-Sc3 protein - European white birch
NCBI Description
                  >gi_534898_emb_CAA54696_ (X77601) 1 Sc-3 [Betula pendula]
                  >gi_1584322_prf__2122374C allergen Bet v 1-Sc3 [Betula
                  pendula]
Seq. No.
                  237447
                  uC-gsronu33B130e05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   a3157949
BLAST score
                  170
                   6.0e-12
E value
                   41
Match length
                   63
% identity
                   (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase
NCBI Description
                   precursor gb_Z28697 from Nicotiana tabacum. ESTs gb Z18185
                  and gb AA605362 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   237448
Seq. ID
                  uC-gsronu33B130e06b1
Method
                  BLASTX
NCBI GI
                   q4510383
BLAST score
                   347
                   1.0e-32
E value
                   111
Match length
% identity
                   65
NCBI Description
                  (AC007017) unknown protein [Arabidopsis thaliana]
Seq. No.
                   237449
Seq. ID
                   uC-gsronu33B130e08b1
Method
                  BLASTX
NCBI GI
                   q4138583
BLAST score
                   330
E value
                   3.0e - 31
Match length
                  73
% identity
NCBI Description
                  (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
                   237450
Seq. No.
Seq. ID
                  uC-gsronu33B130e10b1
Method
                  BLASTX
NCBI GI
                   g1652327
BLAST score
                   267
E value
                   3.0e-23
                  134
Match length
                   46
% identity
NCBI Description
                  (D90904) hypothetical protein [Synechocystis sp.]
```

237451 Seq. No.

Seq. ID uC-gsronu33B130f01b1

Method BLASTX NCBI GI g1345793 BLAST score 318



```
E value
                    6.0e-30
Match length
                   63
% identity
                   97
NCBI Description
                   CHALCONE SYNTHASE 3 (NARINGENIN-CHALCONE SYNTHASE 3)
                   >gi_1084446_pir__S55464 chalcone synthase 3 - gerbera
                   hybrid >gi_1362143_pir__ S56701 chalcone synthase 3 - gerbera hybrid >gi_853932_emb_CAA86220_ (Z38098) chalcone
                   synthase [Gerbera hybrida]
Seq. No.
                   237452
Seq. ID
                   uC-gsronu33B130f10b1
Method
                   BLASTX
NCBI GI
                   q4249388
BLAST score
                   326
E value
                   2.0e-30
Match length
                   87
% identity
                   71
NCBI Description
                   (AC005966) Similar to gb AF025438 Opa-interacting protein
                    (OIP2) from Homo sapiens. [Arabidopsis thaliana]
Seq. No.
                   237453
Seq. ID
                   uC-gsronu33B130h04b1
Method
                   BLASTX
NCBI GI
                   q2191175
BLAST score
                   266
E value
                   2.0e-23
Match length
                   113
% identity
                   50
NCBI Description
                   (AF007270) A IG002P16.24 gene product [Arabidopsis
                   thaliana]
                   237454
Seq. No.
Seq. ID
                   uC-gsronu33B130h10b1
Method
                   BLASTX
NCBI GI
                   q3738297
BLAST score
                   156
E value
                   6.0e-11
Match length
                   43
% identity
                   13
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                   237455
Seq. ID
                   uC-gsronu33B132a08b1
                   BLASTX
Method
NCBI GI
                   g3661610
BLAST score
                   138
E value
                   7.0e-09
Match length
                   60
% identity
                   43
                   (AF092565) splicing factor Prp8 [Homo sapiens]
NCBI Description
```

237456

Seq. No.

Seq. ID uC-gsronu33B132b09b1

Method BLASTX NCBI GI g100226 BLAST score 182 E value 3.0e-16



Match length 142 % identity 39 NCBI Description hyp

hypothetical protein - tomato >gi\_19275\_emb\_CAA78112\_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi\_445619\_prf\_ 1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No. 237457

Seq. ID uC-gsronu33B132b10b1

Method BLASTX
NCBI GI g4455159
BLAST score 337
E value 7.0e-32
Match length 95
% identity 64

NCBI Description (AL021687) putative protein [Arabidopsis thaliana]

Seq. No. 237458

Seq. ID uC-gsronu33B132e02b1

Method BLASTX
NCBI GI g3128203
BLAST score 488
E value 3.0e-49
Match length 138
% identity 68

NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]

Seq. No. 237459

Seq. ID uC-gsronu33B132f06b1

Method BLASTX
NCBI GI g1351279
BLAST score 497
E value 2.0e-50
Match length 116
% identity 84

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

>gi\_602590\_emb\_CAA58230\_ (X83227) triosephosphate isomerase

[Petunia x hybrida]

Seq. No. 237460

Seq. ID uC-gsronu33B132f12b1

Method BLASTX
NCBI GI g3738285
BLAST score 301
E value 2.0e-27
Match length 64
% identity 83

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 237461

Seq. ID uC-gsronu33B132g02b1

Method BLASTX
NCBI GI g4567226
BLAST score 183
E value 2.0e-13
Match length 73
% identity 55



```
(AC007119) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  237462
                  uC-gsronu33B132g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3157936
BLAST score
                  174
E value
                  2.0e-12
Match length
                  90
                  37
% identity
                  (AC002131) Contains similarity to NFATc3 gb U28807 from Mus
NCBI Description
                  musculus. [Arabidopsis thaliana]
                  237463
Seq. No.
                  uC-gsronu33B132h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4545262
BLAST score
                  159
E value
                  1.0e-10
Match length
                  44
% identity
NCBI Description
                  (AF118230) metallothionein-like protein [Gossypium
                  hirsutum]
Seq. No.
                  237464
                  uC-gsronu33B134b02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982431
BLAST score
                  240
E value
                  3.0e-20
Match length
                  121
% identity
                  3
                  (AL022224) leucine rich repeat-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  237465
Seq. No.
Seq. ID
                  uC-gsronu33B134b04b1
                  BLASTX
Method
NCBI GI
                  g3335363
                  504
BLAST score
E value
                   3.0e-51
                  131
Match length
                   37
% identity
NCBI Description
                  (AC003028) hypothetical protein [Arabidopsis thaliana]
                  237466
Seq. No.
Seq. ID
                  uC-gsronu33B134b08b1
Method
                  BLASTX
NCBI GI
                  g4138137
BLAST score
                   284
E value
                  2.0e-25
Match length
                   61
% identity
                  (AJ012796) ss-galactosidase [Lycopersicon esculentum]
NCBI Description
```

34475

237467

uC-gsronu33B134c01b1

Seq. No.

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  q1777443
BLAST score
                  407
E value
                  8.0e-40
Match length
                  91
% identity
                  (U28422) CCA1 [Arabidopsis thaliana] >gi 3510263 (AC005310)
NCBI Description
                  DNA-binding protein CCA1 [Arabidopsis thaliana] >gi 4090569
                  (U79156) CCA1 [Arabidopsis thaliana]
Seq. No.
                  237468
                  uC-gsronu33B134c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3461835
BLAST score
                  502
                  5.0e-51
E value
Match length
                  123
                  79
% identity
NCBI Description
                  (AC005315) putative protein kinase [Arabidopsis thaliana]
                  >gi 3927840 (AC005727) putative protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  237469
Seq. ID .
                  uC-gsronu33B134d09b1
Method
                  BLASTX
NCBI GI
                  q266989
BLAST score
                  289
E value
                  5.0e-26
Match length
                  93
% identity
                   62
                  GTP-BINDING PROTEIN SAR1B >gi 322517 pir S28603
NCBI Description
                  GTP-binding protein - Arabidopsis thaliana >gi_166734
                   (M95795) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                  237470
                  uC-gsronu33B134e05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3395756
                  168
BLAST score
E value
                   3.0e-18
                  91
Match length
                   56
% identity
                   (U76297) plantacyanin [Arabidopsis thaliana] >gi_3461812
NCBI Description
                   (AC004138) putative basic blue protein [Arabidopsis
                  thaliana]
                  237471
Seq. No.
```

uC-gsronu33B134e08b1 Seq. ID

BLASTX Method NCBI GI g3702343 BLAST score 271 5.0e-24E value Match length 114 53 % identity

(AC005397) putative homeotic gene regulator [Arabidopsis NCBI Description

thaliana |



```
Seq. No.
                   237472
Seq. ID
                  uC-gsronu33B134f04b1
Method
                   BLASTX
NCBI GI
                   g1173223
BLAST score
                   353
                   2.0e-33
E value
Match length
                   70
                   94
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S11 >gi 454848 (L28831) ribosomal
                  protein S11 [Glycine max]
                   237473
Seq. No.
                   uC-gsronu33B136a02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3420054
BLAST score
                   217
E value
                   1.0e-17
Match length
                   120
                   42
% identity
                  (AC004680) unknown protein [Arabidopsis thaliana]
NCBI Description
                   237474
Seq. No.
Seq. ID
                   uC-gsronu33B136b01b1
Method
                   BLASTX
NCBI GI
                   q100226
BLAST score
                   154
                   4.0e-10
E value
Match length
                   83
                   45
% identity
NCBI Description
                   hypothetical protein - tomato >gi 19275_emb_CAA78112_
                   (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi_445619_prf__1909366A Leu zipper protein
                   [Lycopersicon esculentum]
Seq. No.
                   237475
                   uC-gsronu33B136c04b1
Seq. ID
                   BLASTX
Method
                   q4468979
NCBI GI
BLAST score
                   248
                   3.0e-21
E value
Match length
                   73
% identity
                   68
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
                   237476
Seq. No.
Seq. ID
                   uC-gsronu33B136c12b1
Method
                   BLASTX
NCBI GI
                   g4115383
BLAST score
                   143
                   3.0e-13
E value
Match length
                   104
% identity
                   48
                   (AC005967) receptor-like protein kinase [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 237477

Seq. ID uC-gsronu33B136d05b1

BLAST score

Match length

E value

192

47

2.0e-14



```
Method
                   BLASTX
NCBI GI
                   g2281090
BLAST score
                   458
                   7.0e-46
E value
Match length
                   132
                   70
% identity
NCBI Description
                   (AC002333) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   237478
                   uC-gsronu33B136d06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4006896
BLAST score
                   280
                   4.0e-25
E value
                   113
Match length
                   60
% identity
                  (Z99708) SCARECROW-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   237479
                   uC-gsronu33B136e12b1
Seq. ID
Method
                   BLASTX
                   g2760839
NCBI GI
                   333
BLAST score
                   4.0e-31
.E value
Match length
                   134
% identity
                   51
NCBI Description
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
                   237480
Seq. No.
                   uC-gsronu33B136f02b1
Seq. ID
Method
                   {\tt BLASTX}
NCBI GI
                   g4185819
BLAST score
                   192
                   7.0e-15
E value
                   47
Match length
% identity
                   68
NCBI Description
                   (AF116845) metallothionein-like type 1 protein [Ipomoea
                   batatas]
                   237481
Seq. No.
                   uC-gsronu33B136f04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2911799
BLAST score
                   494
E value
                   6.0e - 50
Match length
                   121
% identity
                   83
NCBI Description
                   (AF008184) 4-coumarate: CoA ligase 1 [Populus balsamifera
                   subsp. trichocarpa X Populus deltoides]
Seq. No.
                   237482
Seq. ID
                   uC-gsronu33B136f09b1
Method
                   BLASTX
NCBI GI
                   g4185819
```

Match length

% identity

102



```
% identity
                   (AF116845) metallothionein-like type 1 protein [Ipomoea
NCBI Description
                   batatas]
                   237483
Seq. No.
                   uC-gsronu33B136g01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3046700
BLAST score
                   211
E value
                   3.0e-17
Match length
                   65
% identity
                   66
                   (AJ005261) cytidine deaminase [Arabidopsis thaliana]
NCBI Description
                   >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase
[Arabidopsis thaliana] >gi_4191787 (AC005917) putative
                   cytidine deaminase [Arabidopsis thaliana]
                   237484
Seq. No.
                   uC-gsronu33B136g02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q267124
BLAST score
                   221
                   1.0e-23
E value
                   79
Match length
% identity
                   57
                   THIOREDOXIN H-TYPE 1 (TRX-H1) >gi 100387 pir S16590
NCBI Description
                   thioredoxin h1 - common tobacco >gi 20047 emb CAA41415
                   (X58527) thioredoxin [Nicotiana tabacum]
Seq. No.
                   237485
                   uC-gsronu33B136g09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4079637
BLAST score
                   644
E value
                   1.0e-67
Match length
                   123
                   97
% identity
                  (X12769) beta-tubulin [Tetrahymena pyriformis]
NCBI Description
Seq. No.
                   237486
                   uC-gsronu33B136h11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2245125
BLAST score
                   161
E value
                   5.0e-11
Match length
                   45
                   62
% identity
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                   237487
Seq. No.
Seq. ID
                   uC-gsronu33B137a03b1
                   BLASTX
Method
NCBI GI
                   g1619300
BLAST score
                   273
E value
                   5.0e-24
```

NCBI GI

BLAST score



```
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
                  237488
Seq. No.
Seq. ID
                  uC-gsronu33B137a06b1
                  BLASTX
Method
NCBI GI
                  g2781345
BLAST score
                  507
E value
                  2.0e-51
                  149
Match length
% identity
                  62
                  (AC003113) F2401.2 [Arabidopsis thaliana]
NCBI Description
                  237489
Seq. No.
                  uC-gsronu33B137b02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2995405
BLAST score
                  268
E value
                  2.0e-23
                  75
Match length
                  65
% identity
                  (Y12432) polyprotein [Ananas comosus]
NCBI Description
                  237490
Seq. No.
                  uC-gsronu33B137b08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3183640
BLAST score
                  191
                  9.0e-15
E value
                  35
Match length
% identity
                  97
                 (AJ005869) transmembrane channel protein [Cicer arietinum]
NCBI Description
Seq. No.
                  237491
Seq. ID
                  uC-gsronu33B137c06b1
Method
                  BLASTX
NCBI GI
                  g3292823
                  175
BLAST score
E value
                  1.0e-12
                  105
Match length
% identity
                  36
                 (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                  237492
Seq. No.
Seq. ID
                  uC-gsronu33B137c07b1
Method
                  BLASTX
NCBI GI
                  g1840045
BLAST score
                  148
                  2.0e-09
E value
                  153
Match length
% identity
                  28
NCBI Description (U49082) transporter protein [Homo sapiens]
Seq. No.
                  237493
Seq. ID
                  uC-gsronu33B137c08b1
Method
                  BLASTX
```

34480

g4538920

```
3.0e-24
E value
                   76
Match length
                   38
% identity
                   (AL049483) nitrogen fixation like protein [Arabidopsis
NCBI Description
                   thaliana]
                   237494
Seq. No.
                   uC-gsronu33B137e04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3643602
BLAST score
                   399
                   9.0e-39
E value
                   133
Match length
                   62
% identity
                    (AC005395) putative tonoplast intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
                   237495
Seq. No.
                   uC-gsronu33B137e10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3894157
                   366
BLAST score
                   6.0e-35
E value
                   158
Match length
% identity
                    (AC005312) putative protein kinase, 3' partial [Arabidopsis
NCBI Description
                   thaliana]
                   237496
Seq. No.
                   uC-gsronu33B137e11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                    g115607
                    452
BLAST score
E value
                    5.0e-45
                    156
Match length
% identity
                    PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE) (PEPC)
NCBI Description
                    >gi 68033 pir QYEC phosphoenolpyruvate carboxylase (EC
                    4.1.1.31) - Escherichia coli >gi_4558284 pdb 1FIY
                    Three-Dimensional Structure Of Phosphoenolpyruvate
                    Carboxylase From Escherichia Coli At 2.8 A Resolution.
                    >gi_48\overline{6}66_emb_CAA29332_ (X05903) PEP carboxylase (AA 1-883) [Escherichia coli] >gi_396303 (U00006) phosphoenolpyruvate
                    carboxylase [Escherichia coli] >gi_1790393 (AE000469)
                    phosphoenolpyruvate carboxylase [Escherichia coli]
                    >qi 352091 prf 1005219A carboxylase,phosphoenolpyruvate
                    [Escherichia coli]
                    237497
Seq. No.
                    uC-qsronu33B137f04b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2789660
                    334
BLAST score
                    3.0e-31
E value
                    137
Match length
% identity
```

34481

NCBI Description (AF040102) p105 [Arabidopsis thaliana]

Method

NCBI GI

BLASTX

g1514649



```
237498
Seq. No.
                  uC-gsronu33B137g05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3024017
                   326
BLAST score
                   2.0e-30
E value
                   79
Match length
                   85
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)
NCBI Description
                   (EIF-4C) >gi_2565421 (AF026804) eukaryotic translation
                   initiation factor eIF-1A [Onobrychis viciifolia]
                   237499
Seq. No.
                  uC-gsronu33B137g08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2980790
BLAST score
                   144
                   3.0e-09
E value
Match length
                   43
% identity
                   56
                  (AL022197) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   237500
Seq. No.
                   uC-gsronu33B137g11b1
Seq. ID
Method
                   BLASTX
                   q3258571
NCBI GI
BLAST score
                   522
                   3.0e-53
E value
                   139
Match length
% identity
                   79
NCBI Description
                  (U89959) Hypothetical protein [Arabidopsis thaliana]
                   237501
Seq. No.
Seq. ID
                   uC-gsronu33B137h11b1
Method
                   BLASTX
NCBI GI
                   g1332579
BLAST score
                   709
E value
                   4.0e-75
Match length
                   143
% identity
                   10
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
Seq. No.
                   237502
                   uC-gsronu33B138a02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3264611
                   254
BLAST score
                   7.0e-22
E value
                   52
Match length
% identity
                   90
NCBI Description
                  (AF061511) seven in absentia homolog [Zea mays]
                   237503
Seq. No.
Seq. ID
                   uC-gsronu33B138a03b1
```



```
BLAST score
                  2.0e-32
E value
                  154
Match length
                  49
% identity
                  (X86021) potassium channel [Solanum tuberosum]
NCBI Description
Seq. No.
                  237504
Seq. ID
                  uC-gsronu33B138b02b1
                  BLASTX
Method
NCBI GI
                  g3193316
BLAST score
                  569
                  8.0e-59
E value
Match length
                  140
                  80
% identity
                  (AF069299) contains similarity to nucleotide sugar
NCBI Description
                  epimerases [Arabidopsis thaliana]
                  237505
Seq. No.
                  uC-gsronu33B138b06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2462753
BLAST score
                  391
E value
                   3.0e - 38
                  82
Match length
% identity
                  83
                  (AC002292) putative polygalacturonase [Arabidopsis
NCBI Description
                  thaliana]
                  237506
Seq. No.
Seq. ID
                  uC-gsronu33B138b11b1
                  BLASTX
Method
NCBI GI
                  g2088648
BLAST score
                  191
E value
                   8.0e-15
                   80
Match length
% identity
                   50
NCBI Description (AF002109) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   237507
                  uC-gsronu33B138e05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2982331
BLAST score
                   316
                   3.0e-29
E value
Match length
                   64
% identity
NCBI Description (AF051251) TAT-binding protein homolog [Picea mariana]
Seq. No.
                   237508
                  uC-gsronu33B138f04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827002
BLAST score
                   255
E value
                   3.0e-22
Match length
                   51
% identity
                   100
```

NCBI Description (AF005993) HSP70 [Triticum aestivum]

```
237509
Seq. No.
                  uC-gsronu33B138f05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1063276
                  389
BLAST score
E value
                  1.0e-37
                  99
Match length
                  79
% identity
                   (X92893) geranylgeranyl pyrophosphate synthase
NCBI Description
                   [Catharanthus roseus]
Seq. No.
                  237510
                  uC-gsronu33B138f07b1
Seq. ID
                  BLASTX
Method
                  g3097300
NCBI GI
                  199
BLAST score
                  2.0e-15
E value
Match length
                  114
                  35
% identity
                  (AB006754) acid alpha glucosidase [Coturnix japonica]
NCBI Description
                  237511
Seq. No.
Seq. ID
                  uC-gsronu33B138g07b1
Method
                  BLASTX
NCBI GI
                  q939726
BLAST score
                   562
                   6.0e-58
E value
Match length
                  133
                   78
% identity
                  (U31370) cyclophilin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   237512
Seq. ID
                  uC-gsronu33B138g09b1
Method
                  BLASTX
NCBI GI
                   g3142300
BLAST score
                   336
                   1.0e-31
E value
Match length
                  104
% identity
                   63
                  (AC002411) Contains similarity to pre-mRNA processing
NCBI Description
                   protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb R64908
                   and gb T88158, gb N38703 and gb AA651043 come from this
                   gene. [Arabidopsis thaliana]
                   237513
Seq. No.
                   uC-gsronu33B138g11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2980806
BLAST score
                   276
E value
                   2.0e-24
```

Match length 70 % identity

NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

237514 Seq. No.

uC-gsronu33B138h05b1 Seq. ID

```
BLASTX
Method
NCBI GI
                   q3024505
                   551
BLAST score
                   1.0e-56
E value
                   119
Match length
                   89
% identity
                   RAS-RELATED PROTEIN RAB11D >gi 623580 (L29270) putative
NCBI Description
                   [Nicotiana tabacum]
                   237515
Seq. No.
                   uC-gsronu33B138h12b1
Seq. ID
Method
                   BLASTX
                   g3024689
NCBI GI
                   404
BLAST score
                   1.0e-39
E value
Match length
                   110
                   17
 % identity
                   TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT
NCBI Description
                   (TAFII-100) (TAFII100) >gi_1491718_emb_CAA64777_ (X95525)
                   hTAFII100 [Homo sapiens]
                   237516
 Seq. No.
                   uC-gsronu33B139a10b1
 Seq. ID
                   BLASTX
Method
                   g4454482
NCBI GI
                   205
 BLAST score
                   2.0e-16
 E value
 Match length
                   91
                   54
 % identity
                   (AC006234) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                   237517
 Seq. No.
                   uC-gsronu33B139b12b1
 Seq. ID
                   BLASTX
 Method
                   g2505870
 NCBI GI
                   469
 BLAST score
 E value
                    4.0e-47
 Match length
                   102
                    88
 % identity
                   (Y12227) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    237518
 Seq. No.
                   uC-gsronu33B139c02b1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    q2498329
```

Method BLASTX
NCBI GI g2498329
BLAST score 173
E value 2.0e-12
Match length 63
% identity 62

NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi\_2129665\_pir\_\_S65571 pattern-formation protein GNOM - Arabidopsis thaliana >gi 1209633 (U36433) GNOM gene product [Arabidopsis

thaliana] >gi\_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi\_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession

Number J03918 [Arabidopsis thaliana]



```
237519
Seq. No.
                  uC-gsronu33B139c10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3121739
BLAST score
                  311
                  2.0e-28
E value
Match length
                  144
                  16
% identity
                  ANGIO-ASSOCIATED MIGRATORY CELL PROTEIN
NCBI Description
                  >gi_2134759_pir__I39383 angio-associated migratory cell
                  protein - human >gi 870803 (M95627) angio-associated
                  migratory cell protein [Homo sapiens]
                  >gi 4557229_ref_NP_001078.1_pAAMP_ angio-associated,
                  migratory cell protein
                  237520
Seq. No.
                  uC-gsronu33B139c11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2702272
BLAST score
                  197
                  3.0e-15
E value
                   69
Match length
                  17
% identity
                  (AC003033) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   237521
                  uC-gsronu33B139d06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738327
BLAST score
                   292
                   2.0e-26
E value
Match length
                   97
                   65
% identity
                   (AC005170) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                   thaliana]
                   237522
Seq. No.
                   uC-gsronu33B139e08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3201680
BLAST score
                   499
                   1.0e-50
E value
Match length
                   140
                   67
% identity
NCBI Description
                  (AF060941) extra-large G-protein [Arabidopsis thaliana]
Seq. No.
                   237523
Seq. ID
                   uC-qsronu33B139f12b1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g4538929
BLAST score 394
E value 3.0e-38
Match length 155
% identity 59

NCBI Description (AL049483) putative nucleic acid binding protein

[Arabidopsis thaliana]

```
237524
Seq. No.
                  uC-gsronu33B139g10b1
Seq. ID
                  BLASTX
Method
                  g585338
NCBI GI
                  224
BLAST score
                  2.0e-18
E value
                  54
Match length
                  81
% identity
                  ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza
                   sativa]
                   237525
Seq. No.
                   uC-gsronu33B141a06b1
Seq. ID
                   BLASTX
Method
                   q3023816
NCBI GI
                   284
BLAST score
                   2.0e-25
E value
                   56
Match length
                   96
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi 968996 (U31676) glyceraldehyde-3-phosphate
                   dehydrogenase [Oryza sativa]
                   237526
Seq. No.
                   uC-gsronu33B141b06b1
Seq. ID
                   BLASTX
Method
                   q4056506
NCBI GI
                   219
BLAST score
                   1.0e-17
E value
Match length
                   135
                   34
% identity
                  (AC005896) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   237527
Seq. No.
Seq. ID
                   uC-qsronu33B141b09b1
                   BLASTX
Method
                   q2832642
NCBI GI
                   171
BLAST score
                   4.0e-12
E value
Match length
                   137
% identity
                  (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
                   237528
Seq. No.
Seq. ID
                   uC-gsronu33B141d12b1
Method
                   BLASTX
NCBI GI
                   g1706958
                   733
BLAST score
                   6.0e-78
E value
Match length
                   154
 % identity
                   90
```

34487

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

uC-gsronu33B141e05b1

237529

Seq. No.

Seq. ID

```
Method
                  BLASTX
NCBI GI
                  q4309734
BLAST score
                  716
                  6.0e-76
E value
                  171
Match length
                  80
% identity
                  (AC006439) putative 26S proteosome regulatory subunit 8
NCBI Description
                  [Arabidopsis thaliana]
                  237530
Seq. No.
Seq. ID
                  uC-gsronu33B141e09b1
                  BLASTX
Method
NCBI GI
                  g3548818
BLAST score
                  254
                  6.0e-22
E value
                  66
Match length
                  73
% identity
NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]
                  237531
Seq. No.
                  uC-qsronu33B141e11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q81857
BLAST score
                  241
                  2.0e-20
E value
                  49
Match length
                  90
% identity
NCBI Description IgE-dependent histamine-releasing factor homolog - alfalfa
                  (fragment) >gi 19658 emb CAA45349 (X63872) translationally
                  controlled tumor protein [Medicago sativa]
                  237532
Seq. No.
Seq. ID
                  uC-gsronu33B141g08b1
                  BLASTX
Method
NCBI GI
                  q3024706
BLAST score
                  200
                  2.0e-15
E value
Match length
                  69
% identity
                  55
NCBI Description TRANSCRIPTION INITIATION FACTOR TFIID 18 KD SUBUNIT
                  (TAFII-18) (TAFII18) >gi_1362894_pir__S54782 PolII
                  transcription factor TFIID chain hTAFII18 - human
                  >gi 791053 emb CAA58827 (X84003) PolII transcription
                  factor TFIID [Homo sapiens]
                  237533
Seq. No.
Seq. ID
                  uC-gsronu33B141h05b1
                  BLASTX
Method
NCBI GI
                  g228403
                  226
BLAST score
E value
                  1.0e-18
Match length
                  113
                  51
% identity
NCBI Description glycolate oxidase [Lens culinaris]
```

34488

237534

uC-gsronu33B141h11b1

Seq. No. Seq. ID



```
Method
                   BLASTX
NCBI GI
                   g81857
BLAST score
                   340
                   7.0e-32
E value
Match length
                   71
                   90
% identity
                   IgE-dependent histamine-releasing factor homolog - alfalfa
NCBI Description
                   (fragment) >gi_19658_emb_CAA45349_ (X63872) translationally
                   controlled tumor protein [Medicago sativa]
Seq. No.
                   237535
Seq. ID
                   uC-gsronu33B143a12b1
Method
                   BLASTX
NCBI GI
                   q4454043
BLAST score
                   499
E value
                   1.0e-50
Match length
                   151
                   64
% identity
NCBI Description
                  (AL035394) putative receptor kinase [Arabidopsis thaliana]
                   237536
Seq. No.
                   uC-gsronu33B143c03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3426039
BLAST score
                   447
E value
                   1.0e-44
Match length
                   126
                   66
% identity
NCBI Description
                  (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                   237537
                   uC-gsronu33B143c06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3643607
BLAST score
                   326
E value
                   1.0e-30
Match length
                   83
% identity
                   40
                  (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   237538
Seq. ID
                   uC-gsronu33B143c07b1
Method
                   BLASTX
NCBI GI
                   g2191165
BLAST score
                   209
E value
                   1.0e-16
Match length
                   82
                   50
% identity
                  (AF007270) A IG002P16.14 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   237539
Seq. No.
```

Seq. ID uC-gsronu33B143d02b1

Method BLASTX
NCBI GI g3548801
BLAST score 188
E value 2.0e-14

Match length 48 75 % identity NCBI Description (AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi\_4335768\_gb\_AAD17445\_ (AC006284) putative integral membrane protein [Arabidopsis thaliana] Seq. No. 237540 Seq. ID uC-gsronu33B143d07b1 BLASTX Method NCBI GI g3023651 BLAST score 153 E value 4.0e-10 Match length 69 % identity 49 NCBI Description D-LACTATE DEHYDROGENASE [CYTOCHROME] PRECURSOR (D-LACTATE FERRICYTOCHROME C OXIDOREDUCTASE) (D-LCR) >gi\_1076962\_pir\_\_S51528 D-lactate dehydrogenase (cytochrome) (EC 1.1.2.4) - yeast (Kluyveromyces marxianus var. lactis) >gi\_602029\_emb\_CAA50635\_ (X71628) D-lactate dehydrogenase (cytochrome) [Kluyveromyces lactis] Seq. No. 237541 Seq. ID uC-gsronu33B143e07b1 Method BLASTX NCBI GI g2558664 BLAST score 240 E value 3.0e-20Match length 81 % identity 59 NCBI Description (AC002354) hypothetical protein [Arabidopsis thaliana] Seq. No. 237542 Seq. ID uC-gsronu33B143f09b1 Method BLASTX NCBI GI g1170660 BLAST score 191 1.0e-14 E value Match length 89 % identity 52 NCBI Description MEVALONATE KINASE (MK) >gi\_541880 pir S42088 mevalonate kinase (EC 2.7.1.36) - Arabidopsis thaliana >gi\_456614\_emb\_CAA54820\_ (X77793) mevalonate kinase [Arabidopsis thaliana] Seq. No. 237543 Seq. ID uC-gsronu33B143g05b1 Method BLASTX

NCBI GI q2388689 BLAST score 220 6.0e-18 E value Match length 85 % identity

NCBI Description (AF016633) GH1 protein [Glycine max]

Seq. No. 237544

Seq. ID uC-gsronu33B143q09b1

Method BLASTX

BLAST score

E value

318

2.0e-29



```
NCBI GI
                    g4539465
 BLAST score
                    144
 E value
                    7.0e-09
 Match length
                    89
 % identity
                    39
 NCBI Description (AL049500) putative protein [Arabidopsis thaliana]
 Seq. No.
                   237545
 Seq. ID
                   uC-gsronu33B144a04b1
Method
                   BLASTX
 NCBI GI
                   g4545262
BLAST score
                   250
E value
                   2.0e-21
Match length
                   61
 % identity
                   72
NCBI Description
                   (AF118230) metallothionein-like protein [Gossypium
                   hirsutum]
Seq. No.
                   237546
Seq. ID
                   uC-gsronu33B144a11b1
Method
                   BLASTX
NCBI GI
                   g1199772
BLAST score
                   170
E value
                   4.0e-12
Match length
                   34
% identity
                   85
NCBI Description
                   (D83226) extensin like protein [Populus nigra]
                   >gi_1199774_dbj_BAA11855_ (D83227) extensin like protein
                   [Populus nigra]
Seq. No.
                   237547
Seq. ID
                   uC-gsronu33B144b02b1
Method
                   BLASTX
NCBI GI
                   g3075397
BLAST score
                   324
E value
                   3.0e-30
Match length
                   112
% identity
                   57
NCBI Description
                  (AC004484) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   237548
Seq. ID
                   uC-gsronu33B144b06b1
Method
                   BLASTX
NCBI GI
                   g1572819
BLAST score
                   208
E value
                   1.0e-16
Match length
                   113
% identity
                   41
NCBI Description
                  (U70855) similar to the RAS gene family [Caenorhabditis
                  elegans]
Seq. No.
                  237549
Seq. ID
                  uC-gsronu33B144e10b1
Method
                  BLASTX
NCBI GI .
                  g2351378
```

E value

Match length

% identity

3.0e-28 91

60

```
Match length
                  129
% identity
                  50
NCBI Description
                  (U54558) translation initiation factor eIF3 p66 subunit
                  [Homo sapiens] >gi 4200328 emb CAA18440 (AL022313)
                  EIF3-P66 [Homo sapiens]
                  >gi 4503523 ref NP 003744.1 pEIF3S7 UNKNOWN
                  237550
Seq. No.
                  uC-gsronu33B144f09b1
Seq. ID
Method
                  BLASTX
                  g2980777
NCBI GI
BLAST score
                  217
E value
                  1.0e-17
Match length
                  110
                  41
% identity
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
Seq. No.
                  237551
                  uC-gsronu33B144h03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2970051
BLAST score
                  243
E value
                  1.0e-20
Match length
                  75
% identity
                  63
NCBI Description (AB012110) ARG10 [Vigna radiata]
                  237552
Seq. No.
Seq. ID
                  uC-gsronu33B145c08b1
                  BLASTX
Method
NCBI GI
                  g3687223
BLAST score
                  160
                  8.0e-11
E value
                  38
Match length
                  82
% identity
NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]
Seg. No.
                  237553
Seq. ID
                  uC-gsronu33B145d10b1
Method
                  BLASTX
NCBI GI
                  q548770
BLAST score
                  213
E value
                  1.0e-28
Match length
                  81
% identity
                  83
NCBI Description
                 60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal
                  protein L3 - rice >gi 303853 dbj BAA02155 (D12630)
                  ribosomal protein L3 [Oryza sativa]
                  237554
Seq. No.
Seq. ID
                  uC-gsronu33B145f08b1
Method
                  BLASTX
NCBI GI
                  g3046693
BLAST score
                  308
```

```
NCBI Description
                 (AL022140) receptor like protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                  237555
Seq. ID
                  uC-gsronu33B145g01b1
                  BLASTX
Method
NCBI GI
                  q3953458
BLAST score
                  362
E value
                  9.0e-46
Match length
                  127
% identity
                  72
NCBI Description (AC002328) F20N2.3 [Arabidopsis thaliana]
Seq. No.
                  237556
                  uC-gsronu33B145g08b1
```

Seq. ID uC-gsronu33B145g08b1
Method BLASTX
NCBI GI g2347188
BLAST score 277
E value 1.0e-24

E value 1.0e-Match length 122 % identity 42

NCBI Description (AC002338) laccase isolog [Arabidopsis thaliana] >gi\_3150401 (AC004165) putative laccase [Arabidopsis

thaliana]

Seq. No. 237557

Seq. ID uC-gsronu33B145h10b1

Method BLASTX
NCBI GI g2647949
BLAST score 422
E value 1.0e-41
Match length 87

Match length 87 % identity 83

NCBI Description (AJ001369) cytochrome b5 [Olea europaea]

Seq. No. 237558

Seq. ID uC-gsronu33B145h12b1

Method BLASTX
NCBI GI g2244780
BLAST score 556
E value 2.0e-61
Match length 152
% identity 87

NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237559

Seq. ID uC-gsronu33B146b07b1

Method BLASTX
NCBI GI g1173055
BLAST score 217
E value 4.0e-18
Match length 47
% identity 96

NCBI Description 60S RIBOSOMAL PROTEIN L11 (L5) >gi\_541961\_pir\_\_\$42497

ribosomal protein L11.e - alfalfa >gi 1076504 pir S51819 RL5 ribosomal protein - alfalfa >gi 463252 emb CAA55090

(X78284) RL5 ribosomal protein [Medicago sativa]

Seq. ID

Method

```
237560
Seq. No.
Seq. ID
                  uC-gsronu33B146d04b1
Method
                  BLASTX
NCBI GI
                  q2894612
BLAST score
                  372
E value
                  1.0e-35
                  106
Match length
% identity
                  64
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
                  237561
Seq. No.
Seq. ID
                  uC-gsronu33B146d12b1
Method
                  BLASTX
NCBI GI
                  g3935150
BLAST score
                  337
E value
                  1.0e-31
Match length
                  117
% identity
                  40
NCBI Description
                  (AC005106) T25N20.14 [Arabidopsis thaliana]
Seq. No.
                  237562
Seq. ID
                  uC-gsronu33B146e04b1
Method
                  BLASTX
NCBI GI
                  g4580461
BLAST score
                  354
E value
                  1.0e-33
                  81
Match length
                  83
% identity
NCBI Description
                  (AC006081) unknown protein [Arabidopsis thaliana]
                  237563
Seq. No.
Seq. ID
                  uC-gsronu33B146e06b1
Method
                  BLASTX
NCBI GI
                  g1871192
BLAST score
                  183
E value
                  1.0e-13
Match length
                  114
% identity
                  45
NCBI Description
                  (U90439) Cys3His zinc finger protein isolog [Arabidopsis
                  thaliana]
Seq. No.
                  237564
Seq. ID
                  uC-gsronu33B146f11b1
Method
                  BLASTX
NCBI GI
                  q113624
BLAST score
                  515
E value
                  2.0e-52
Match length
                  115
                  87
% identity
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
                  >gi_22620_emb_CAA46649_ (X65742) fructose-bisphosphate
                  aldolase [Spinacia oleracea]
                  237565
Seq. No.
```

34494

uC-gsronu33B146g03b1

BLASTX



```
NCBI GI
                  q2827528
BLAST score
                  155
E value
                  2.0e-10
Match length
                  43
                  89
% identity
NCBI Description (AL021633) predicted protein [Arabidopsis thaliana]
                  237566
Seq. No.
Seq. ID
                  uC-gsronu33B146g07b1
Method
                  BLASTX
NCBI GI
                  q4220462
BLAST score
                  356
E value
                  7.0e - 34
                  124
Match length
                  54
% identity
NCBI Description
                  (AC006216) Strong similarity to gb Z50851 HD-zip (athb-8)
                  gene from Arabidopsis thaliana containing Homeobox PF 00046
                  and bZIP PF_00170 domains. [Arabidopsis thaliana]
                  237567
                  uC-gsronu33B146h01b1
                  BLASTX
                  q4539305
                  223
```

Seq. No. Seq. ID Method NCBI GI BLAST score 2.0e-18 E value Match length 42 % identity 88

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

237568 Seq. No. Seq. ID uC-gsronu33B147a01b1 Method BLASTX NCBI GI g2351374 BLAST score 326 E value 6.0e-31 70

Match length 91 % identity

NCBI Description (U54560) putative 26S proteasome subunit athMOV34

[Arabidopsis thaliana]

Seq. No. 237569

uC-gsronu33B147b02b1 Seq. ID

Method BLASTX NCBI GI q3879754 BLAST score 214 E value 5.0e-17 Match length 108 % identity 41

NCBI Description (Z72514) Similarity to Rabbit glycogenin (SW:GLYG RABIT)

[Caenorhabditis elegans]

Seq. No. 237570

Seq. ID uC-gsronu33B147c05b1

Method BLASTX NCBI GI g4185819 BLAST score 180 3.0e-13 E value

NCBI Description

thaliana]



```
Match length
% identity
NCBI Description
                  (AF116845) metallothionein-like type 1 protein [Ipomoea
                  batatas]
                  237571
Seq. No.
Seq. ID
                  uC-gsronu33B147c07b1
Method
                  BLASTX
                  g2218141
NCBI GI
BLAST score
                  168
E value
                  4.0e-12
Match length
                  49
                  61
% identity
NCBI Description (AF004914) E8 protein homolog [Lycopersicon esculentum]
Seq. No.
                  237572
Seq. ID
                  uC-gsronu33B147c12b1
Method
                  BLASTX
NCBI GI
                  g4455188
BLAST score
                  263
                  6.0e-23
E value
                  105
Match length
                  57
% identity
NCBI Description (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                  237573
                  uC-gsronu33B147d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4091117
BLAST score
                  462
E value
                  4.0e-46
Match length
                  124
% identity
                  69
NCBI Description (AF047428) nucleic acid binding protein [Oryza sativa]
Seq. No.
                  237574
Seq. ID
                  uC-gsronu33B147d11b1
Method
                  BLASTX
NCBI GI
                  g2145356
BLAST score
                  534
E value
                  9.0e-55
Match length
                  128
% identity
                  77
NCBI Description
                  (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi 3132474
                  (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]
Seq. No.
                  237575
Seq. ID
                  uC-gsronu33B147e12b1
Method
                  BLASTX
NCBI GI
                  q3892055
BLAST score
                  461
E value
                  5.0e-46
Match length
                  133
% identity
                  69
```

(AC002330) putative transport protein [Arabidopsis

E value

Match length

% identity

1.0e-18

96



```
Seq. No.
                  237576
Seq. ID
                  uC-gsronu33B147h11b1
Method
                  BLASTX
NCBI GI
                  q134976
BLAST score
                  166
E value
                  4.0e-12
Match length
                  48
% identity
                  71
NCBI Description
                 GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi 81619 pir S12042
                  glucose transport protein STP1 - Arabidopsis thaliana
                  >gi_16520_emb_CAA39037 (X55350) glucose transporter
                  [Arabidopsis thaliana]
Seq. No.
                  237577
                  uC-gsronu33B148a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2181186
BLAST score
                  378
                  1.0e-36
E value
Match length
                  91
% identity
                  45
NCBI Description
                  (X97323) outward rectifying potassium channel KCO1
                  [Arabidopsis thaliana] >gi 2230761 emb CAA69158 (Y07825)
                  kcol [Arabidopsis thaliana]
Seq. No.
                  237578
Seq. ID
                  uC-gsronu33B148e04b1
Method
                  BLASTX
                  g3600053
NCBI GI
BLAST score
                  453
E value
                  3.0e-45
Match length
                  123
% identity
NCBI Description
                  (AF080120) contains similarity to HMG (high mobility group)
                  box (Pfam: HMG box.hmm, scores: 70.67, 53.09 and 80.15)
                  [Arabidopsis thaliana]
Seq. No.
                  237579
Seq. ID
                  uC-gsronu33B148f02b1
Method
                  BLASTX
NCBI GI
                  q3822225
BLAST score
                  165
E value
                  2.0e-11
Match length
                  106
% identity
                  37
NCBI Description
                  (AF079183) RING-H2 finger protein RHG1a [Arabidopsis
                  thaliana]
Seq. No.
                  237580
Seq. ID
                  uC-gsronu33B148f06b1
Method
                  BLASTX
NCBI GI
                  q4249380
BLAST score
                  228
```

34497

NCBI Description (AC005966) ESTs gb Z37637, gb AA042498 and gb AA042269 come



## from this gene. [Arabidopsis thaliana]

```
Seq. No. -
                   237581
Seq. ID
                   uC-gsronu33B149a05b1
Method
                   BLASTX
NCBI GI
                   g4185819
BLAST score
                   192
E value
                   1.0e-14
                   47
Match length
% identity
                   68
NCBI Description
                  (AF116845) metallothionein-like type 1 protein [Ipomoea
                  batatas]
                   237582
Seq. No.
Seq. ID
                  uC-gsronu33B149a06b1
Method
                   BLASTX
NCBI GI
                  q3927835
BLAST score
                   559
E value
                   1.0e-57
Match length
                   132
% identity
                   80
NCBI Description
                  (AC005727) similar to Streptomyces PapA [Arabidopsis
                  thaliana]
Seq. No.
                  237583
                  uC-gsronu33B149c12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g218157
BLAST score
                  191
E value
                  1.0e-14
Match length
                  43
% identity
                  86
NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]
Seq. No.
                  237584
Seq. ID
                  uC-gsronu33B149e05b1
Method
                  BLASTX
NCBI GI
                  q1703446
BLAST score
                  449
E value
                  9.0e-45
Match length
                  122
% identity
                  70
NCBI Description L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE)
                  >gi 1076292_pir S53127 asparaginase - Arabidopsis thaliana
                  >gi_735918 emb CAA84367 (Z34884) asparaginase [Arabidopsis
                  thaliana]
                  237585
Seq. No.
Seq. ID
                  uC-gsronu33B149f10b1
Method
                  BLASTX
NCBI GI
                  g2541876
BLAST score
                  279
E value
                  1.0e-24
Match length
                  150
% identity
                  39
                  (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
```



```
237586
Seq. No.
                  uC-gsronu33B149g08b1
Seq. ID
Method
                  BLASTX
                  g4056496
NCBI GI
                  516
BLAST score
                  1.0e-52
E value
                  119
Match length
% identity
                  (AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
                  237587
Seq. No.
                  uC-gsronu33B149g11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2827141
                  340
BLAST score
                   3.0e-32
E value
                   65
Match length
                   91
% identity
                   (AF027173) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   237588
                   uC-gsronu33B149h01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4512705
                   476
BLAST score
                   4.0e-48
E value
                   105
Match length
                   89
% identity
                   (AC006569) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   237589
Seq. No.
                   uC-gsronu33B149h07b1
Seq. ID
Method
                   BLASTX
                   q4432855
NCBI GI
                   234
BLAST score
                   1.0e-19
E value
                   116
Match length
% identity
                   53
                  (AC006300) unknown protein [Arabidopsis thaliana]
NCBI Description
                   237590
Seq. No.
                   uC-gsronu33B150a11b1
Seq. ID
                   BLASTX
Method
                   g2129770
NCBI GI
                   183
BLAST score
                   1.0e-13
E value
                   48
Match length
% identity
                   xyloglucan endotransglycosylase-related protein XTR-2 -
NCBI Description
                   Arabidopsis thaliana >gi 1244756 (U43487) xyloglucan
                   endotransglycosylase-related protein [Arabidopsis thaliana]
```

>gi\_2154611\_dbj\_BAA20290\_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]



```
Seq. No.
                  237591
Seq. ID
                  uC-qsronu33B150d06b1
Method
                  BLASTX
NCBI GI
                  g1174867
BLAST score
                  153
E value
                  3.0e-10
                  35
Match length
% identity
                  83
NCBI Description
                  UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING
                  PROTEIN QP-C (UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.2
                  KD PROTEIN) >gi_633687_emb_CAA55862_ (X79275)
                  ubiquinol--cytochrome c reductase [Solanum tuberosum]
                  >qi 1094912 prf 2107179A cytochrome c
                  oxidase:SUBUNIT=8.2kD [Solanum tuberosum]
                  237592
Seq. No.
Seq. ID
                  uC-gsronu33B150d10b1
Method
                  BLASTX
NCBI GI
                  q3335366
BLAST score
                  218
E value
                  2.0e-17
Match length
                  76
% identity
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                  237593
Seq. ID
                  uC-gsronu33B150d12b1
                  BLASTX
Method
NCBI GI
                  g3643082
BLAST score
                  149
E value
                  1.0e-09
Match length
                  67
% identity
                  51
                  (AF075579) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                  237594
Seq. ID
                  uC-gsronu33B150e01b1
Method
                  BLASTX
NCBI GI
                  g3582434
BLAST score
                  255
E value
                  4.0e-22
Match length
                  97
% identity
                  58
NCBI Description
                  (AB017273) low-molecular-weight heat shock protein [Cuscuta
                  japonica]
                  237595
Seq. No.
Seq. ID
                  uC-gsronu33B150g10b1
Method
                  BLASTX
NCBI GI
                  g4455293
BLAST score
                  253
```

E value 1.0e-21

Match length 58 % identity

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

NCBI Description



```
237596
Seq. No.
Seq. ID
                  uC-gsronu33B150g12b1
                  BLASTX
Method
NCBI GI
                  g3152585
                  321
BLAST score
                  1.0e-29
E value
                  134
Match length
% identity
                  (AC002986) Contains similarity to auxin-induced protein
NCBI Description
                  TM018A10.6 from A. thaliana BAC gb AF013294. [Arabidopsis
                  thaliana]
                  237597
Seq. No.
                  uC-gsronu33B150h07b1
Seq. ID
Method
                  BLASTX
                  g3264830
NCBI GI
                  276
BLAST score
                  2.0e-24
E value
                  128
Match length
                  53
% identity
NCBI Description
                  (AF072405) cotton fiber expressed protein 2 [Gossypium
                  hirsutum]
Seq. No.
                  237598
                  uC-gsronu33B150h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4115371
BLAST score
                  206
E value
                  4.0e-16
Match length
                  81
% identity
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  237599
Seq. ID
                  uC-gsronu33B153b03b2
Method
                  BLASTX
NCBI GI
                  g123178
BLAST score
                  480
E value
                  1.0e-48
                  106 %
Match length
% identity
                  89
NCBI Description
                  HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH)
                  >gi 99844 pir A39358 histidinol dehydrogenase (EC
                  1.1.1.23) precursor, chloroplast - cabbage >gi 167142
                  (M60466) histidinol dehydrogenase [Brassica oleracea]
                  237600
Seq. No.
                  uC-gsronu33B153c01b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g461753
BLAST score
                  586
                  6.0e-61
E value
Match length
                  118
                  98
% identity
```

- 1900 1900

ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG

proteinase regulatory chain homolog precursor, chloroplast

PRECURSOR >gi\_419773\_pir\_\_S31164 ATP-dependent ClpB



- garden pea >gi\_169128 (L09547) nuclear encoded precursor to chloroplast protein [Pisum sativum]

```
Seq. No.
 Seq. ID
                   uC-gsronu33B153c02b2
 Method
                   BLASTX
 NCBI GI
                   q1903357
 BLAST score
                   384
                   4.0e-37
 E value
 Match length
                   116
                   59
 % identity
 NCBI Description (AC000104) Strong similarity to Arabidopsis 2A6
                    (gb_X83096). [Arabidopsis thaliana]
                   237602
 Seq. No.
                   uC-gsronu33B153c09b2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   q2924520
 BLAST score
                   470
 E value
                   2.0e-47
                   99
 Match length
                   90
% identity
 NCBI Description (AL022023) plasma membrane intrinsic protein (SIMIP)
                    [Arabidopsis thaliana]
 Seq. No.
                   237603
 Seq. ID
                   uC-gsronu33B153e02b2
 Method
                   BLASTX
 NCBI GI
                   g3603456
 BLAST score
                   493
                   4.0e-50
 E value
 Match length
                   98
 % identity
 NCBI Description (AF088848) polyubiquitin [Capsicum chinense]
 Seq. No.
                   237604
 Seq. ID
                   uC-gsronu33B153e08b2
 Method
                   BLASTX
 NCBI GI
                   g2213600
 BLAST score
                   160
 E value
                   5.0e-11
 Match length
                   68
                   50
 % identity
 NCBI Description (ACO00348) T7N9.20 [Arabidopsis thaliana]
 Seq. No.
                   237605
                 - uC-gsronu33B153g01b2
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q3915826
 BLAST score
                   191
 E value
                   1.0e-14
                   50
 Match length
                   76
 % identity
 NCBI Description 60S RIBOSOMAL PROTEIN L5
                   237606
 Seq. No.
 Seq. ID
                   uC-gsronu33B153g07b2
```

```
BLASTX
Method
                   q4490708
NCBI GI
                   223
BLAST score
                   2.0e-18
E value
                   56
Match length
                   79
% identity
                   (AL035680) putative protein [Arabidopsis thaliana]
NCBI Description
                   237607
Seq. No.
                   uC-gsronu33B153h06b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3935145
                   253
BLAST score
                   9.0e-22
E value
                   94
Match length
                   52
% identity
                   (AC005106) T25N20.9 [Arabidopsis thaliana]
NCBI Description
                   237608
Seq. No.
                   uC-gsronu33B153h11b2
Seq. ID
                   BLASTX
Method
                   g2244827
NCBI GI
                   231
BLAST score
                   3.0e-19
E value
                   97
Match length
 % identity
                   60
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                   237609
 Seq. No.
                   uC-gsronu33B154a10b2
 Seq. ID
                   BLASTX
 Method
                   q3832528
 NCBI GI
                    166
 BLAST score
                    4.0e-12
 E value
 Match length
                    59
                    59
 % identity
                   (AF100167) unknown [Glycine max]
 NCBI Description
                    237610
 Seq. No.
                    uC-gsronu33B154b08b2
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g1420887
                    154
 BLAST score
                    3.0e-10
 E value
                    55
 Match length
                    49
 % identity
                    (U34334) non-specific lipid transfer-like protein
NCBI Description
                    [Phaseolus vulgaris]
                    237611
 Seq. No.
                    uC-gsronu33B154c10b2
 Seq. ID
                    BLASTX
 Method
                    g2384696
 NCBI GI
```

34503

164

66

48

2.0e-11

BLAST score

Match length % identity

E value



```
(AF013216) acyl-CoA oxidase [Myxococcus xanthus]
NCBI Description
                   237612
Seq. No.
Seq. ID
                   uC-gsronu33B154d02b2
Method
                   BLASTX
                   g3426039
NCBI GI
                   196
BLAST score
                   2.0e-15
E value
                   53
Match length
                   66
 % identity
                  (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   237613
 Seq. No.
                   uC-gsronu33B154d03b2
 Seq. ID
                   BLASTX
Method
                   g2244975
NCBI GI
                   140
 BLAST score
                   1.0e-08
E value
                   57
Match length
                   53
 % identity
 NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]
                   237614
 Seq. No.
                   uC-gsronu33B154d08b2
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g2245131
BLAST score
                   325
                   3.0e - 30
E value
                   112
 Match length
                   64
 % identity
 NCBI Description (Z97344) hypothetical protein [Arabidopsis thaliana]
                   237615
 Seq. No.
                   uC-gsronu33B154e03b2
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                    q3892056
 BLAST score
                    208
∘ E value
                    2.0e-16
 Match length
                    48
 % identity
 NCBI Description (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
                    237616
 Seq. No.
                    uC-gsronu33B154e06b2
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g1172004
 BLAST score
                    726
 E value
                    3.0e-77
 Match length
                    154
                    93
 % identity
 NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 1345583 emb CAA53581
                    (X75967) phenylalanine ammonium lyase [Vitis vinifera]
 Seq. No.
                    237617
                    uC-gsronu33B154e08b2
 Seq. ID
```

BLASTX

g3395432

Method NCBI GI

```
299
BLAST score
                   3.0e-27
E value
                   105
Match length
                   59
% identity
                  (AC004683) unknown protein [Arabidopsis thaliana]
NCBI Description
                   237618
Seq. No.
                   uC-gsronu33B154f04b2
Seq. ID
                   BLASTX
Method
                   g2245094
NCBI GI
                   304
BLAST score
                   1.0e-27
E value
                   148
Match length
% identity
                   45
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   237619
Seq. No.
                   uC-gsronu33B154f09b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1657948
BLAST score
                   293
                   1.0e-26
E value
                   59
Match length
                   92
% identity
                  (U73466) MipC [Mesembryanthemum crystallinum]
NCBI Description
Seq. No.
                   237620
                   uC-gsronu33B154g06b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1332579
BLAST score
                   594
E value
                   9.0e-62
                   120
Match length
                   10
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
Seq. No.
                   237621
                   uC-gsronu33B155a06b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q115492
BLAST score
                   438
E value
                   1.0e-43
Match length
                   85
                   50
 % identity
NCBI Description CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
                   calmodulin-related protein [Petunia hybrida]
Seq. No.
                   237622
```

Seq. ID uC-gsronu33B155a09b2

Method BLASTX NCBI GI g2252856 BLAST score 292 2.0e-26 E value 130 Match length 52 % identity

NCBI Description (AF013294) No definition line found [Arabidopsis thaliana]



Seq. No. 237623

Seq. ID uC-gsronu33B155a11b2

Method BLASTX
NCBI GI g2252839
BLAST score 465
E value 8.0e-47
Match length 97
% identity 88

NCBI Description (AF013293) Similar to receptor-like protein kinase precusor

[Arabidopsis thaliana]

Seq. No. 237624

Seq. ID uC-gsronu33B155b05b2

Method BLASTX
NCBI GI g2924258
BLAST score 621
E value 6.0e-65
Match length 131
% identity 90

NCBI Description (Z00044) RNA polymerase beta'' subunit [Nicotiana tabacum]

Seq. No. 237625

Seq. ID uC-gsronu33B155b12b2

Method BLASTX
NCBI GI g4164159
BLAST score 666
E value 5.0e-70
Match length 169
% identity 82

NCBI Description (AB015496) ethylene receptor [Passiflora edulis]

Seq. No. 237626

Seq. ID uC-gsronu33B155c11b2

Method BLASTX
NCBI GI g1755166
BLAST score 309
E value 2.0e-28
Match length 83
% identity 71

NCBI Description (U75194) germin-like protein [Arabidopsis thaliana]

Seq. No. 237627

Seq. ID uC-gsronu33B155f01b2

Method BLASTX
NCBI GI g4220512
BLAST score 467
E value 4.0e-47
Match length 99
% identity 83

NCBI Description (AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No. 237628

Seq. ID uC-gsronu33B155f07b2

Method BLASTX
NCBI GI g3641868
BLAST score 292
E value 3.0e-26

```
86
Match length
                   69
% identity
NCBI Description
                   (AJ011012) hypothetical protein [Cicer arietinum]
Seq. No.
                   237629
                   uC-gsronu33B155g07b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q484656
BLAST score
                   186
                   5.0e-14
E value
                   51
Match length
                   69
% identity
                   monodehydroascorbate reductase (NADH) (EC 1.6.5.4) -
NCBI Description
                   cucumber >gi 452165_dbj_BAA05408_ (D26392)
                   monodehydroascorbate reductase [Cucumis sativus]
                   237630
Seq. No.
                   uC-gsronu33B155g09b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3551247
BLAST score
                   160
                   9.0e-11
E value
                   32
Match length
                   94
% identity
NCBI Description
                  (AB012703) 181 [Daucus carota]
Seq. No.
                   237631
                   uC-gsronu33B155h10b2
Seq. ID
Method
                   BLASTX
                   g2765837
NCBI GI
BLAST score
                   176
E value
                   1.0e-12
Match length
                   42
                   79
% identity
NCBI Description (Z96936) NAP16kDa protein [Arabidopsis thaliana]
Seq. No.
                   237632
                   uC-gsronu33B156b08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2130080
BLAST score
                   264
E value
                    2.0e-27
Match length
                   130
% identity
                   Nramp1 protein - rice >gi 1470320 bbs_177441 (S81897)
NCBI Description
                    OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa,
                   indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi_2231132 (L41217) integral membrane
                    protein [Oryza sativa]
Seq. No.
                    237633
```

Seq. IĐ uC-gsronu33B156c05b1

Method BLASTX
NCBI GI g3493172
BLAST score 149
E value 4.0e-10
Match length 27

```
100
% identity
                  (U89609) fiber annexin [Gossypium hirsutum]
NCBI Description
                  237634
Seq. No.
                  uC-gsronu33B156d11b1
Seq. ID
                  BLASTX
Method
                  g1279588
NCBI GI
                   468
BLAST score
                   7.0e-47
E value
Match length
                  146
                   62
% identity
                  (Z71749) glutathione S-transferase [Nicotiana
NCBI Description
                  plumbaginifolia]
                   237635
Seq. No.
                  uC-gsronu33B156d12b1
Seq. ID
                  BLASTX
Method
                  g2213586
NCBI GI
                   200
BLAST score
                   1.0e-15
E value
Match length
                  83
                   49
% identity
                  (AC000348) T7N9.6 [Arabidopsis thaliana]
NCBI Description
                   237636
Seq. No.
                   uC-gsronu33B156e01b1
Seq. ID
Method
                   BLASTX
                   g3135274
NCBI GI
BLAST score
                   263
                   6.0e-23
E value
Match length
                   123
% identity
                   46
                  (AC003058) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   237637
Seq. ID
                   uC-gsronu33B156f11b1
Method
                   BLASTX
NCBI GI
                   a465820
BLAST score
                   473
E value
                   1.0e-47
Match length
                   124
                   67
% identity
                   HYPOTHETICAL 18.5 KD PROTEIN C40H1.6 IN CHROMOSOME III
NCBI Description
                   >gi_280536_pir__S28301 hypothetical protein C40H1.6 -
                   Caenorhabditis elegans >gi_3874819_emb_CAA79557_ (Z19154)
                   C40H1.6 [Caenorhabditis elegans]
Seq. No.
                   237638
                   uC-gsronu33B157a03b1
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g1370174
BLAST score 282
E value 4.0e-25
Match length 60
% identity 88

NCBI Description (Z73936) RAB1Y [Lotus japonicus]

Seq. ID

```
237639
Seq. No.
                  uC-gsrenu33B157d09b1
Seq. ID
Method
                  BLASTX
                  g3786008
NCBI GI
BLAST score
                  282
                  3.0e-25
E value
                  111
Match length
                  50
% identity
NCBI Description
                  (AC005499) unknown protein [Arabidopsis thaliana]
                  237640
Seq. No.
                  uC-gsronu33B157f11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4006870
BLAST score
                  439
E value
                  2.0e-43
                  175
Match length
                  49
% identity
                  (Z99707) patatin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  237641
                  uC-gsronu33B158a12b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1684855
                  323
BLAST score
E value
                  5.0e-30
                  69
Match length
                  20
% identity
                  (U77939) ubiquitin-like protein [Phaseolus vulgaris]
NCBI Description
Seq. No.
                  237642
                  uC-gsronu33B158b03b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q398966
BLAST score
                  607
E value
                   3.0e-63
Match length
                  135
% identity
                  85
                  4-COUMARATE--COA LIGASE 2 (4CL) (CLONE 4CL16)
NCBI Description
                  >gi_541937_pir__PQ0772 4-coumarate--CoA ligase (EC
                   6.2.1.12) (clone GM4CL1B) - soybean (fragment)
                  >gi 18520 emb CAA49576 (X69955) 4-coumarate--CoA ligase
                   [Glycine max]
Seq. No.
                  237643
Seq. ID
                  uC-gsronu33B158b04b2
Method
                  BLASTX
NCBI GI
                  g4138583
BLAST score
                  165
E value
                  2.0e-11
Match length
                  87
% identity
                   56
NCBI Description
                  (Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
Seq. No.
                  237644
```

34509

uC-gsronu33B158b06b2



Method BLASTX
NCBI GI g3024148
BLAST score 411
E value 1.0e-40
Match length 86
% identity 90

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)

>gi\_1655580\_emb\_CAA95858\_ (Z71273) S-adenosyl-L-methionine

synthetase 3 [Catharanthus roseus]

Seq. No. 237645

Seq. ID uC-gsronu33B158b08b2

Method BLASTX
NCBI GI g4204277
BLAST score 138
E value 8.0e-09
Match length 56
% identity 54

NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 237646

Seq. ID uC-gsronu33B158c03b2

Method BLASTX
NCBI GI g294668
BLAST score 403
E value 1.0e-39
Match length 100
% identity 79

NCBI Description (L13242) beta-ketoacyl-ACP synthase [Ricinus communis]

Seq. No. 237647

Seq. ID uC-gsronu33B158d01b2

Method BLASTX
NCBI GI g4191788
BLAST score 418
E value 4.0e-41
Match length 99
% identity 76

NCBI Description (AC005917) putative 1-aminocyclopropane-1-carboxylate

oxidase [Arabidopsis thaliana]

Seq. No. 237648

Seq. ID uC-gsronu33B158d09b2

Method BLASTX
NCBI GI g2894379
BLAST score 205
E value 5.0e-16
Match length 90
% identity 47

NCBI Description (Y14573) ring finger protein [Hordeum vulgare]

Seq. No. 237649

Seq. ID uC-gsronu33B158d10b2

Method BLASTX NCBI GI g2388689 BLAST score 456

% identity

NCBI Description

56

```
2.0e-45
E value
Match length
                   123
                   73
% identity
NCBI Description (AF016633) GH1 protein [Glycine max]
                   237650
Seq. No.
                   uC-gsronu33B158e11b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3123349
                   179
BLAST score
E value
                   2.0e-13
Match length
                   57
                   63
% identity
NCBI Description (AJ005788) hypothetical protein [Cicer arietinum]
                   237651
Seq. No.
                   uC-gsronu33B158f01b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2582800
BLAST score
                   516
E value
                   1.0e-52
Match length
                   119
                   82
 % identity
NCBI Description (Y11607) protein phosphatase 2C [Medicago sativa]
                   237652
Seq. No.
Seq. ID
                   uC-gsronu33B158g02b2
                   BLASTX
Method
NCBI GI
                   g3193332
                   277
BLAST score
E value
                   3.0e-25
Match length
                   60
                   90
 % identity
NCBI Description (AF069299) similar to Arabidopsis AT-hook protein 1
                   (GB:AJ222585) [Arabidopsis thaliana]
                   237653
 Seq. No.
Seq. ID
                   uC-gsronu33B158g08b2
Method
                   BLASTX
NCBI GI
                   g2281090
                   190
BLAST score
                   6.0e-15
 E value
Match length
                   51
 % identity
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]
                   237654
 Seq. No.
 Seq. ID
                   uC-gsronu33B158h08b2
Method
                   BLASTX
 NCBI GI
                   g1929056
 BLAST score
                   183
 E value
                   7.0e-14
Match length
                   63
```

[Lycopersicon esculentum]

(Y12090) putative 3,4-dihydroxy-2-butanone kinase



```
237655
Seq. No.
Seq. ID
                  uC-gsronu33B158h12b2
Method
                  BLASTX
NCBI GI
                  g2160756
BLAST score
                  455
E value
                  2.0e-45
Match length
                  139
% identity
                  11
NCBI Description (U96879) CLV1 receptor kinase [Arabidopsis thaliana]
                  237656
Seq. No.
                  uC-gsronu33B159a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2673915
BLAST score
                  298
E value
                  2.0e-36
Match length
                  111
% identity
                  65
NCBI Description (AC002561) putative cytochrome P-450 [Arabidopsis thaliana]
Seq. No.
                  237657
Seq. ID
                  uC-gsronu33B159b07b1
Method
                  BLASTX
NCBI GI
                  q4510428
BLAST score
                  349
E value
                  1.0e-36
Match length
                  122
% identity
                  60
NCBI Description (AC006929) putative argonaute protein [Arabidopsis
                  thaliana]
                  237658
Seq. No.
Seq. ID
                  uC-gsronu33B159b10b1
Method
                  BLASTX
NCBI GI
                  q2341039
BLAST score
                  486
E value
                  5.0e-49
Match length
                  141
% identity
                  67
NCBI Description
                  (AC000104) Similar to Nicotiana lesion-inducing ORF
                  (gb U66269). [Arabidopsis thaliana]
Seq. No.
                  237659
Seq. ID
                  uC-gsronu33B159d11b1
Method
                  BLASTX
NCBI GI
                  q3043432
BLAST score
                  284
E value
                  2.0e-25
Match length
                  54
% identity
                  100
```

NCBI Description (AJ005348) Ubiquitin conjugating enzyme [Cicer arietinum]

Seq. No.

237660

Seq. ID

uC-gsronu33B159e01b1

Method BLASTX NCBI GI g2129770 BLAST score 285



E value 2.0e-25 Match length 87

Match length 87 % identity 61

NCBI Description xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi 1244756 (U43487) xyloglucan

endotransglycosylase-related protein [Arabidopsis thaliana]

>gi\_2154611\_dbj\_BAA20290\_ (D63510) endoxyloglucan
transferase related protein [Arabidopsis thaliana]

Seq. No. 237661

% identity

Seq. ID uC-gsronu33B159f04b1

88

Method BLASTX
NCBI GI g1363492
BLAST score 817
E value 9.0e-88
Match length 173

NCBI Description outer envelope membrane protein OEP75 precursor - garden

pea >gi\_576507 (L36858) outer membrane protein [Pisum sativum] >gi\_633607\_emb\_CAA58720\_ (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]

Seq. No. 237662

Seq. ID uC-gsronu33B159g08b1

Method BLASTX
NCBI GI g4234953
BLAST score 191
E value 2.0e-14
Match length 97
% identity 24

NCBI Description (AF098970) NBS-LRR-like protein cD7 [Phaseolus vulgaris]

Seq. No. 237663

Seq. ID uC-gsronu33B159g10b1

Method BLASTX
NCBI GI g4206789
BLAST score 206
E value 4.0e-16
Match length 67
% identity 60

NCBI Description (AF112864) syntaxin-related protein At-SYR1 [Arabidopsis

thaliana]

Seq. No. 237664

Seq. ID uC-gsronu33B159h09b1

Method BLASTX
NCBI GI g4539314
BLAST score 158
E value 1.0e-17
Match length 82
% identity 62

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 237665

Seq. ID uC-gsronu33B160a03b1

Method BLASTX NCBI GI g1762945

Match length

% identity

151

57

```
BLAST score
                  300
E value
                  4.0e-27
                  92
Match length
                  58
% identity
                  (U66269) ORF; able to induce HR-like lesions [Nicotiana
NCBI Description
                  tabacum]
                  237666
Seq. No.
Seq. ID
                  uC-gsronu33B160a04b1
Method
                  BLASTX
NCBI GI
                  g4530126
BLAST score
                  504
E value
                  4.0e-51
Match length
                  162
                  57
% identity
NCBI Description (AF078082) receptor-like protein kinase homolog RK20-1
                  [Phaseolus vulgaris]
Seq. No.
                  237667
Seq. ID
                  uC-gsronu33B160b04b1
Method
                  BLASTX
NCBI GI
                  g4510402
BLAST score
                  601
E value
                  1.0e-62
Match length
                  139
                  51
% identity
NCBI Description (AC006587) putative AP2 domain [Arabidopsis thaliana]
                  237668
Seq. No.
Seq. ID
                  uC-gsronu33B160b05b1
Method
                  BLASTX
NCBI GI
                  g4335763
BLAST score
                  286
E value
                  1.0e-25
Match length
                  106
% identity
                  52
NCBI Description (AC006284) unknown protein [Arabidopsis thaliana]
Seq. No.
                  237669
Seq. ID
                  uC-gsronu33B160c04b1
Method
                  BLASTX
NCBI GI
                  g3687251
BLAST score
                  361
E value
                  3.0e - 34
Match length
                  95
% identity
                  75
NCBI Description (AC005169) unknown protein [Arabidopsis thaliana]
                  237670
Seq. No.
                  uC-gsronu33B160d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1708073
BLAST score
                  416
E value
                  8.0e-41
```

34514

NCBI Description GMP SYNTHASE (GLUTAMINE-HYDROLYSING) (GLUTAMINE



AMIDOTRANSFERASE) (GMP SYNTHETASE) >gi 1077145 pir S55099 GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) - yeast (Saccharomyces cerevisiae) >gi\_854469\_emb\_CAA89932\_ (Z49809) Gualp [Saccharomyces cerevisiae]

237671 Seq. No.

Seq. ID uC-gsronu33B160d11b1

Method BLASTX NCBI GI g114171 BLAST score 240 E value 3.0e-20Match length 48

90 % identity

NCBI Description .3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE PRECURSOR

(3-ENOLPYRUVYLSHIKIMATE-5-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) >gi 99781 pir S12744 3-phosphoshikimate

1-carboxyvinyltransferase (EC 2.5.1.19) precursor - rape

>gi 17815 emb CAA35839 (X51475)

5-enolpyruvylshikimate-3-phosphate synthase [Brassica

napus]

Seq. No. 237672

uC-gsronu33B160e01b1 Seq. ID

BLASTX Method NCBI GI q2462746 BLAST score 217 E value 1.0e-17 Match length 47 85 % identity

NCBI Description (AC002292) Similar to ATP-citrate-lyase [Arabidopsis

thaliana]

Seq. No. 237673

uC-gsronu33B160e11b1 Seq. ID

Method BLASTX NCBI GI g3114901 BLAST score 410 E value 5.0e-40 Match length 101 78 % identity

(AJ005804) pcbere [Populus balsamifera subsp. trichocarpa] NCBI Description

>gi\_3114905\_emb\_CAA06709\_ (AJ005806) pceberh [Populus

balsamifera subsp. trichocarpa]

237674 Seq. No.

uC-gsronu33B160f03b1 Seq. ID

Method BLASTX NCBI GI q3157924 BLAST score 164 2.0e-11 E value 57 Match length % identity

(AC002131) Contains homology to extensin-like protein NCBI Description qb D83227 from Populus nigra. ESTs qb H76425, gb T13883,

gb T45348, gb H37743, gb AA042634, gb Z26960 and gb\_Z25951 come from this gene. There is a similar ORF on the

opposite strand. [... >gi\_4063707 (AF104327) extensin-like

Seq. ID



## protein [Arabidopsis thaliana]

```
237675
Seq. No.
                  uC-gsronu33B160f07b1
Seq. ID
                  BLASTX
Method
                  g1907076
NCBI GI
                  389
BLAST score
E value
                  9.0e-38
Match length
                  113
% identity
                  63
                  (Y07867) pirin [Homo sapiens] >gi_1907078_emb_CAA69195_
NCBI Description
                   (Y07868) pirin [Homo sapiens]
                  >gi 4505823 ref NP 003653.1_pPIR_ pirin
                  237676
Seq. No.
                  uC-gsronu33B162a03b2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4539348
BLAST score
                  297
                   2.0e-27
E value
                  76
Match length
                   72
% identity
NCBI Description (AL035539) putative pollen allergen [Arabidopsis thaliana]
                   237677
Seq. No.
                   uC-gsronu33B162a07b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q557472
                   172
BLAST score
E value
                   2.0e-12
                   84
Match length
                   42
% identity
NCBI Description (U15178) arabinosidase [Bacteroides ovatus]
Seq. No.
                   237678
                   uC-gsronu33B162b04b2
Seq. ID
                   BLASTX
Method
                   g4455323
NCBI GI
                   259
BLAST score
                   1.0e-22
E value
                   117
Match length
                   48
% identity
                  (AL035525) aminopeptidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   237679
Seq. No.
                   uC-gsronu33B162d02b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4006878
BLAST score
                   317
                   3.0e-29
E value
Match length
                   120
% identity
                  (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
NCBI Description
                   237680
Seq. No.
```

uC-gsronu33B162e05b2



```
BLASTX
Method
                  °q2226436
NCBI GI
                  225
BLAST score
E value
                  2.0e-18
                  122
Match length
                  43
% identity
                  (L39907) LA-MSC [Oxytricha fallax]
NCBI Description
                  237681
Seq. No.
                  uC-gsronu33B162e07b2
Seq. ID
Method
                  BLASTX
                  g439493
NCBI GI
                  257
BLAST score
                   3.0e-22
E value
Match length
                  138
% identity
                   36
                  (D26086) zinc-finger protein [Petunia x hybrida]
NCBI Description
                   237682
Seq. No.
                  uC-gsronu33B162e11b2
Seq. ID
                  BLASTX
Method
                   q3063449
NCBI GI
BLAST score
                   558
E value
                   2.0e-57
                   159
Match length
                   70
% identity
NCBI Description (AC003981) F22013.11 [Arabidopsis thaliana]
                   237683
Seq. No.
                   uC-gsronu33B162f08b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4371296
BLAST score
                   152
                   6.0e-10
E value
Match length
                   125
% identity
                   34
                  (AC006260) putative receptor protein kinase [Arabidopsis,
NCBI Description
                   thalianal
                   237684
Seq. No.
                   uC-gsronu33B162f09b2
Seq. ID
                   BLASTX
Method
                   g2832619
NCBI GI
                   279
BLAST score
E value
                   9.0e-25
Match length
                   80
% identity
                   69
                  (AL021711) major intrinsic protein (MIP) - like [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. ID uC-gsronu33B162f12b2

BLASTX Method NCBI GI g4140371 BLAST score 403 E value 3.0e - 39Match length 95

```
% identity
                   (U43711) 3-hydroxy-3-methylglutaryl-coenzyme A reductase
NCBI Description
                   [Morus alba]
                   237686
Seq. No.
Seq. ID
                   uC-gsronu33B162h08b2
Method
                   BLASTX
NCBI GI
                   g4049399
BLAST score
                   167
                   3.0e-22
E value
Match length
                   117
                   55
% identity
                   (Y09581) FRO2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   237687
                   uC-gsronu33B163a11b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120669
BLAST score
                   390
E value
                    3.0e-38
Match length
                   80
                    93
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                    >qi 19566 emb CAA42905 (X60347) glyceraldehyde
                    3-phosphate dehydrogenase [Magnolia liliiflora]
                    237688
Seq. No.
                    uC-gsronu33B163b11b2
Seq. ID
                    BLASTX
Method
                    g2315153
NCBI GI
BLAST score
                    288
                    3.0e-26
E value
Match length
                    88
                    58
% identity
NCBI Description (Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
                    237689
Seq. No.
                    uC-gsronu33B163c05b2
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2829911
                    505
BLAST score
E value
                    2.0e-51
Match length
                    121
% identity
NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]
```

Seq. ID uC-gsronu33B163c06b2

Method BLASTX
NCBI GI g3786005
BLAST score 545
E value 5.0e-56
Match length 126
% identity 44

NCBI Description (AC005499) putative phosphoethanolamine



## cytidylyltransferase [Arabidopsis thaliana]

```
237691
Seq. No.
                  uC-gsronu33B163c09b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2642158
BLAST score
                  441
                  6.0e-44
E value
Match length
                  118
                   70
% identity
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  237692
Seq. No.
Seq. ID
                  uC-gsronu33B163d01b2
Method
                  BLASTX
NCBI GI
                  g1840425
BLAST score
                   322
E value
                   6.0e - 30
Match length
                  79
% identity
                   72
NCBI Description (U36586) alcohol dehydrogenase [Vitis vinifera]
Seq. No.
                   237693
Seq. ID
                  uC-qsronu33B163d03b2
Method
                  BLASTX
NCBI GI
                  g3005576
BLAST score
                   347
E value
                   6.0e - 33
Match length
                  86
% identity
                   76
                   (AF047718) putative high affinity nitrate transporter;
NCBI Description
                   GmNRT2 [Glycine max]
Seq. No.
                   237694
Seq. ID
                   uC-gsronu33B163d08b2
Method
                   BLASTX
NCBI GI
                   g4557078
BLAST score
                   283
E value
                   1.0e-27
Match length
                   166
% identity
                   42
                  (AC007045) putative Tall-1 pol polyprotein, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   237695
Seq. ID
                   uC-gsronu33B163e11b2
                   BLASTX
Method
NCBI GI
                   g3152618
BLAST score
                   406
E value
                   8.0e-40
Match length
                   115
% identity
                  (AC004482) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                   >gi 3242724 (AC003040) putative pectinesterase [Arabidopsis
                   thaliana]
```

Seq. No. 237696



```
uC-gsronu33B163f02b2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1644291
BLAST score
                   158
E value
                   1.0e-10
Match length
                   116
% identity
                   32
NCBI Description (Z73295) receptor-like protein kinase [Catharanthus roseus]
                  237697
Seq. No.
Seq. ID
                  uC-qsronu33B163f04b2
Method
                  BLASTX
NCBI GI
                   g2245108
BLAST score
                   540
E value
                   2.0e-55
Match length
                  136
% identity
                   73
NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
Seq. No.
                   237698
Seq. ID
                   uC-gsronu33B163g11b2
Method
                   BLASTX
NCBI GI
                   g99737
BLAST score
                   225
E value
                   2.0e-18
Match length
                   76
% identity
                   59
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) -
NCBI Description
                   Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017)
                   NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]
                   237699
Seq. No.
Seq. ID
                   uC-gsronu33B163h03b2
                   BLASTX
Method
NCBI GI
                   q4512673
BLAST score
                   782
E value
                   1.0e-83
                   157
Match length
% identity
                   92
                  (AC006931) putative phosphoprotein phosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   237700
Seq. No.
Seq. ID
                   uC-gsronu33B164a01b2
Method
                  {\tt BLASTX}
NCBI GI
                   g3283912
BLAST score
                   226
E value
                   1.0e-18
                  112
Match length
% identity
                   38
NCBI Description (AF070639) unknown [Homo sapiens]
                   237701
Seq. No.
Seq. ID
                   uC-gsronu33B164c10b2
```

Method BLASTX
NCBI GI g3335359
BLAST score 416



```
6.0e-41
E value
                  124
Match length
%.identity
                   64
                  (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                  237702
Seq. No.
                  uC-gsronu33B164c11b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3152618
BLAST score
                  409
E value
                   5.0e-40
Match length
                  123
                   56
% identity
                   (AC004482) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                   >gi 3242724 (AC003040) putative pectinesterase [Arabidopsis
                   thaliana]
                   237703
Seq. No.
Seq. ID
                   uC-gsronu33B164e06b2
Method
                   BLASTX
NCBI GI
                   q4455223
BLAST score
                   409
E value
                   5.0e-40
Match length
                   115
                   27
% identity
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   237704
Seq. No.
                   uC-gsronu33B164e11b2
Seq. ID
                   BLASTX
Method
                   g1234787
NCBI GI
                   142
BLAST score
E value
                   1.0e-08
Match length
                   145
                   32
% identity
NCBI Description (U37373) up-regulated by thyroid hormone in tadpoles;
                   expressed specifically in the tail and only at
                metamorphosis; membrane bound or extracellular protein;
                   C-terminal basic region [Xenopus laevis]
                   237705
Seq. No.
                   uC-gsronu33B164f07b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2598599
                   288
BLAST score
E value
                   6.0e - 26
                   82
Match length
                   66
% identity
NCBI Description (Y15372) MtN4 [Medicago truncatula]
```

Seq. ID uC-gsronu33B164g01b2

Method BLASTX
NCBI GI g2464905
BLAST score 279
E value 6.0e-25



```
80
Match length
                   68
% identity
                   (Z99708) minor allergen [Arabidopsis thaliana]
NCBI Description
                   237707
Seq. No.
                   uC-gsronu33B164g10b2
Seq. ID
                   BLASTX
Method
                   g2980788
NCBI GI
BLAST score
                   225
                   2.0e-18
E value
Match length
                   129
                   43
% identity
                  (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   237708
Seq. No.
                   uC-gsronu33B166a01b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4567278
                   224
BLAST score
E value
                   2.0e-18
                   117
Match length
                   55
% identity.
                  (AC006841) putative anthracycline associated resistance ARX
NCBI Description
                   protein [Arabidopsis thaliana]
                   237709
Seq. No.
                   uC-gsronu33B166a06b2
Seq. ID
                   BLASTX
Method
                   g3757514
NCBI GI
                   567
BLAST score
E value
                   1.0e-58
Match length
                   123
                   90
% identity
                   (AC005167) putative plasma membrane intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
                   237710
Seq. No.
                   uC-gsronu33B166b02b2
Seq. ID
                   BLASTX
Method
                   g2194118
NCBI GI
                   207
BLAST score
                   2.0e-16
E value
                   71
Match length
% identity
NCBI Description (AC002062) F20P5.4 gene product [Arabidopsis thaliana]
Seq. No.
                   237711
                   uC-gsronu33B166d04b2
Seq. ID
                   BLASTX
Method
                   g2982283
NCBI GI
                   357
BLAST score
                   7.0e - 34
E value
                   135
Match length
                   47
```

% identity

NCBI Description

(AF051226) PREG-like protein [Picea mariana]



```
uC-gsronu33B166d08b2
Seq. ID
                  BLASTX
Method
                  a4262151
NCBI GI
BLAST score
                  544
                  6.0e-56
E value
                  130
Match length
                  78
% identity
                  (AC005275) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                  237713
Seq. No.
                  uC-gsronu33B166d11b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  a4220482
BLAST score
                  442
E value
                  8.0e-44
Match length
                  121
                  45
% identity
                  (AC006069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  237714
Seq. No.
                  uC-gsronu33B166f11b2
Seq. ID
Method
                  BLASTX
                  g466044
NCBI GI
BLAST score
                  166
E value
                  2.0e-11
                  50
Match length
% identity
                   58
                  HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III
NCBI Description
                  >gi_630780_pir__S44909 ZK686.4 protein - Caenorhabditis
                  elegans >gi 304346 (L17337) coded for by C. elegans cDNAs
                  GenBank: M88869 and T01933; putative [Caenorhabditis
                  elegans]
                   237715
Seq. No.
Seq. ID
                  uC-gsronu33B167a04b1
Method
                  BLASTX
NCBI GI
                   g2129854
BLAST score
                   454
E value
                   2.0e-45
Match length
                   130
% identity
                   65
                  early nodulin 8 precursor - alfalfa >gi 304037 (L18899)
NCBI Description
                   early nodulin [Medicago sativa]
Seq. No.
                   2,37716
                  uC-gsronu33B167a07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2497743
                   178
BLAST score
E value
                   4.0e-13
Match length
                   35
```

% identity 94

NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (GH3) NCBI Description >gi 999315\_bbs\_166991 (S78173) LTP=lipid transfer protein

[Gossypium hirsutum=cotton, fiber, Peptide, 120 aa]

[Gossypium hirsutum]



```
237717
Seq. No.
Seq. ID
                   uC-gsronu33B167c01b1
Method
                  BLASTX
NCBI GI
                   g497896
                   330
BLAST score
E value
                   1.0e-30
                   151
Match length
% identity
                   54
NCBI Description
                  (D12921) transcription factor HBP-1b(c1) [Triticum
                   aestivum]
                   237718
Seq. No.
Seq. ID
                  uC-gsronu33B167c08b1
Method
                   BLASTX
NCBI GI
                   g3600054
BLAST score
                   144
E value
                   5.0e-09
                   83
Match length
% identity
                   37
NCBI Description (AF080120) No definition line found [Arabidopsis thaliana]
Seq. No.
                   237719
Seq. ID
                   uC-gsronu33B167c12b1
                  BLASTX
Method
NCBI GI
                   g4262222
BLAST score
                   517
E value
                   1.0e-52
Match length
                   125
                   76
% identity
NCBI Description
                  (AC006200) putative RNA helicase A, 3' partial [Arabidopsis
                   thaliana]
Seq. No.
                   237720
Seq. ID
                   uC-gsronu33B167d04b1
Method
                   BLASTX
NCBI GI
                   g2317906
BLAST score
                   292
E value
                   2.0e-26
                   62
Match length
% identity
                   97
NCBI Description (U89959) ARA-5 [Arabidopsis thaliana]
                   237721
Seq. No.
                   uC-gsronu33B167e03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885340
BLAST score
                   224
E value
                   6.0e-19
Match length
                   68
% identity
NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]
```

Seq. ID uC-gsronu33B167f05b1

Method BLASTX
NCBI GI g3548810
BLAST score 373



9.0e-36 E value Match length 144 % identity 57 (AC005313) putative chloroplast nucleoid DNA binding NCBI Description protein [Arabidopsis thaliana] 237723 Seq. No. uC-gsronu33B167h04b1 Seq. ID Method BLASTX NCBI GI q629561 BLAST score 328 2.0e-30 E value Match length 138 54 % identity SRG1 protein - Arabidopsis thaliana NCBI Description >gi\_479047\_emb\_CAA55654\_ (X79052) SRG1 [Arabidopsis thaliana] 237724 Seq. No. Seq. ID uC-gsronu33B168a05b1 Method BLASTX g3157950 NCBI GI BLAST score 413 E value 2.0e-40 Match length 147 % identity (AC002131) Contains similarity to hypothetical protein NCBI Description C18b11.05 qb Z50728 from S. pombe. EST gb H76601 comes from this gene. [Arabidopsis thaliana] Seq. No. 237725 uC-gsronu33B168a07b1 Seq. ID Method BLASTX NCBI GI g2570338 BLAST score 401 E value 4.0e-39 125 Match length % identity 60 NCBI Description (U90927) glyoxalase II isozyme [Arabidopsis thaliana] Seq. No. 237726 uC-gsronu33B168a09b1 Seq. ID BLASTX Method NCBI GI g81857 BLAST score 170

E value 3.0e-1233 Match length 91 % identity

IgE-dependent histamine-releasing factor homolog - alfalfa NCBI Description

(fragment) >gi\_19658\_emb\_CAA45349\_ (X63872) translationally

controlled tumor protein [Medicago sativa]

237727 Seq. No.

Seq. ID uC-gsronu33B168a12b1

BLASTX Method NCBI GI g3142293 BLAST score 142



```
1.0e-08
E value
Match length
                   43
% identity
                   60
NCBI Description
                   (AC002411) Contains similarity to myosin IB heavy chain
                   gb X70400 from Gallus gallus. [Arabidopsis thaliana]
                   237728
Seq. No.
                   uC-gsronu33B168c01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3402673
BLAST score
                   389
E value
                   9.0e-38
                   123
Match length
                   62
 % identity
NCBI Description
                  (AC004697) unknown protein [Arabidopsis thaliana]
                   237729
Seq. No.
                   uC-gsronu33B168c03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q417060
BLAST score
                   618
E value
                   2.0e-64
Match length
                   119
                   94
 % identity
                   GLUTAMINE SYNTHETASE NODULE ISOZYME (GLUTAMATE--AMMONIA
NCBI Description
                   LIGASE) (GS) >gi_170637 (M94765) glutamine synthetase
                   [Vigna aconitifolia] >gi_1094850_prf__2106409A Gln
                   synthetase [Vigna aconitifolia]
                   237730
 Seq. No.
                   uC-gsronu33B168d04b1
 Seq. ID
                   BLASTX
Method
 NCBI GI
                   q4335745
 BLAST score
                   191
 E value
                   2.0e-14
 Match length
                   84
 % identity
                   49
                   (AC006284) putative hydrolase (contains an
 NCBI Description
                   esterase/lipase/thioesterase active site serine domain
                    (prosite: PS50187) [Arabidopsis thaliana]
 Seq. No.
                   237731
                   uC-gsronu33B168d05b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3281861
 BLAST score
                   541
· E value
                   1.0e-55
                   132
 Match length
 % identity
 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
```

Seq. ID uC-gsronu33B168e09b1

Method BLASTX NCBI GI g548702 BLAST score 387 E value 2.0e-37



```
Match length
                    59
% identity
                    DNA-DIRECTED RNA POLYMERASE II 14.5 KD POLYPEPTIDE (RPB9)
NCBI Description
                    (RPB14.5) >gi_543001_pir__S41621 DNA-directed RNA polymerase (EC 2.7.7.6) II 14.5K chain - human
                    >gi 397150_emb_CAA80649_ (Z23102) RNA Polymerase II subunit
14.5 kD [Homo sapiens] >gi 1905901 (AD001527) HUMAN
                    DNA-DIRECTED RNA POLYMERASE II 14.5 KD SUBUNIT [Homo
                    sapiens]
                    237733
Seq. No.
                    uC-gsronu33B168f02b1
Seq. ID
Method
                    BLASTX
                    g2281090
NCBI GI
BLAST score
                    221
                    5.0e-18
E value
                    141
Match length
                    37
% identity
NCBI Description (AC002333) hypothetical protein [Arabidopsis thaliana]
                    237734
Seq. No.
                    uC-gsronu33B168f03b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4204793
                    606
BLAST score
E value
                    4.0e-63
                    136
Match length
% identity
NCBI Description (U52079) P-glycoprotein [Solanum tuberosum]
Seq. No.
                    237735
                    uC-gsronu33B168f12b1
Seq. ID
                    BLASTX
Method
NCBI GI
                    g4200165
BLAST score
                    612
E value
                    8.0e-64
Match length
                    139
                    76
% identity
NCBI Description (Y16262) neutral invertase [Daucus carota]
Seq. No.
                    237736
                    uC-gsronu33B168g07b1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3914685
                    294
BLAST score
E value
                    8.0e-27
Match length
                    91
% identity
                    64
NCBI Description 60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal
                    protein L17 [Zea mays]
```

Method BLASTX NCBI GI g2832617

BLAST score 164 E value 3.0e-11



92 Match length % identity 43

(AL021711) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

237738

Seq. ID

uC-gsronu33B168g09b1

Method NCBI GI BLAST score BLASTX g3309243 597 4.0e-62

E value Match length % identity

125 91

NCBI Description

(AF073507) aconitase-iron regulated protein 1 [Citrus

limon]

Seq. No.

237739 uC-gsronu33B168g12b1 Seq. ID

Method BLASTX g3122914 NCBI GI BLAST score 175 E value . 1.0e-12

63 Match length 52 % identity

VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) NCBI Description

>gi 1890130 (U89986) valyl tRNA synthetase [Arabidopsis

thaliana]

Seq. No.

237740 Seq. ID

uC-gsronu33B168h10b1

Method BLASTX NCBI GI g541848 BLAST score 444 E value 4.0e-44 Match length 146 % identity 52

amino acid transport protein I - Arabidopsis thaliana NCBI Description

>gi\_22641\_emb\_CAA47603\_ (X67124) amino acid permease I [Arabidopsis thaliana] >gi\_404019 (L16240) amino acid

transporter [Arabidopsis thaliana]

Seq. No. 237741

Seq. ID uC-gsronu33B169a07b1

Method BLASTX NCBI GI g2341024 BLAST score 384 E value 6.0e-37 Match length 127 % identity

NCBI Description (AC000104) F19P19.1 [Arabidopsis thaliana]

Seq. No.

237742

Seq. ID

uC-gsronu33B169a10b1

Method BLASTX NCBI GI g282848 BLAST score 586 E value 9.0e-61 Match length 143



% identity 82

NCBI Description malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)

(EC 1.1.1.40) (clone 064) - western balsam poplar x

cottonwood

Seq. No. 237743

Seq. ID uC-gsronu33B169b03b1

Method BLASTX
NCBI GI g4115381
BLAST score 217
E value 2.0e-17
Match length 86
% identity 52

NCBI Description (AC005967) putative limonene cyclase [Arabidopsis thaliana]

Seq. No. 237744

Seq. ID uC-gsronu33B169b08b1

Method BLASTX
NCBI GI g218157
BLAST score 378
E value 2.0e-36
Match length 85
% identity 88

NCBI Description (D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No. 237745

Seq. ID uC-gsronu33B169b09b1

Method BLASTX
NCBI GI g4220481
BLAST score 506
E value 2.0e-51
Match length 134
% identity 71

NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]

Seq. No. 237746

Seq. ID uC-gsronu33B169c04b1

Method BLASTX
NCBI GI g1345644
BLAST score 314
E value 5.0e-29
Match length 83
% identity 69

NCBI Description CYTOCHROME P450 86A1 (CYPLXXXVI) >gi\_940446\_emb\_CAA62082

(X90458) cytochrome p450 [Arabidopsis thaliana]

Seq. No. 237747

Seq. ID uC-gsronu33B169c11b1

Method BLASTX
NCBI GI g4006888
BLAST score 668
E value 3.0e-70
Match length 172
% identity 71

NCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 237748



```
Seq. ID
                   uC-gsronu33B169d04b1
                   BLASTX
Method
NCBI GI
                   g1173187
BLAST score
                   412
E value
                   2.0e-40
Match length
                   81
% identity
                   100
NCBI Description
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
                   ribosomal protein S23.e, cytosolic (clone RJ3) - garden
                   strawberry >gi 643074 (U19940) putative 40S ribosomal
                   protein s12 [Fragaria x ananassa]
                   237749
Seq. No.
Seq. ID
                   uC-gsronu33B169d08b1
Method
                  BLASTX
NCBI GI
                   g2232354
BLAST score
                   247
E value
                   6.0e-21
Match length
                  155
% identity
                   41
NCBI Description (AF006081) UDPG glucosyltransferase [Solanum berthaultii]
Seq. No.
                   237750
Seq. ID
                   uC-gsronu33B169d10b1
Method
                  BLASTX
NCBI GI
                   q3790569
BLAST score
                   340
E value
                   7.0e-32
Match length
                  130
% identity
                   54
NCBI Description
                  (AF078822) RING-H2 finger protein RHA2a [Arabidopsis
                  thaliana]
                   237751
Seq. No.
Seq. ID
                  uC-gsronu33B169e08b1
Method
                  BLASTX
NCBI GI
                  q1184123
BLAST score
                  234
E value
                  2.0e-19
                  79
Match length
                  56
% identity
NCBI Description (U20809) auxin-induced protein [Vigna radiata]
Seq. No.
                  237752
Seq. ID
                  uC-gsronu33B169f07b1
Method
                  BLASTX
NCBI GI
                  q4006818
BLAST score
                  165
E value
                  2.0e-11
Match length
                  70
% identity
                  47
NCBI Description
                  (AC005970) putative translation initiation factor eIF-2B,
                  alpha subunit [Arabidopsis thaliana]
```

Seq. ID uC-gsronu33B169h11b1

Method BLASTX

```
NCBI GI
                  a1669599
BLAST score
                  327
E value
                  2.0e-30
Match length
                  130
                  53
% identity
NCBI Description (D88746) AR791 [Arabidopsis thaliana]
Seq. No.
                  237754
Seq. ID
                  uC-gsronu33B170a12b1
Method
                  BLASTX
NCBI GI
                  g1616628
BLAST score
                  220
E value
                  6.0e-18
Match length
                  106
% identity
                  51
NCBI Description (X80472) sts15 [Solanum tuberosum]
Seq. No.
                  237755
Seq. ID
                  uC-gsronu33B170b08b1
Method
                  BLASTX
NCBI GI
                  g3927829
BLAST score
                  298
E value
                  7.0e-27
Match length
                  164
% identity
                  43
                  (AC005727) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  237756
Seq. No.
Seq. ID
                  uC-gsronu33B170c01b1
Method
                  BLASTX
NCBI GI
                  g2911076
BLAST score
                  388
E value
                  1.0e-37
Match length
                  99
                  74
% identity
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]
                  237757
Seq. No.
Seq. ID
                  uC-gsronu33B170c03b1
Method
                  BLASTX
NCBI GI
                  g4567313
BLAST score
                  151
```

E value 1.0e-09 Match length 34 74 % identity

NCBI Description (AC005956) putative SUPERMAN transcription factor

[Arabidopsis thaliana]

Seq. No. 237758

Seq. ID uC-gsronu33B170f01b1

BLASTX Method NCBI GI g3269283 BLAST score 148 E value 2.0e-09 135 Match length % identity 30

34531

```
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
                  237759
Seq. No.
                  uC-gsronu33B170f09b1
Seq. ID
                  BLASTX
Method
                  g1703478
NCBI GI
BLAST score
                  708
E value
                  5.0e-75
Match length
                  157
% identity
                  47
NCBI Description (U40566) ubiquitin activating enzyme 2 [Arabidopsis
                  thaliana]
                  237760
Seq. No.
Seq. ID
                  uC-gsronu33B170h02b1
                  BLASTX
                  g4580392
                  177
```

Method NCBI GI BLAST score E value 1.0e-15 Match length 130 % identity 41

NCBI Description (AC007171) hypothetical protein [Arabidopsis thaliana]

237761 Seq. No. Seq. ID uC-gsronu33B171a01b1 BLASTX Method NCBI GI g4539389 BLAST score 183 E value 4.0e-14

49 Match length 76 % identity

NCBI Description (AL035526) putative protein kinase [Arabidopsis thaliana]

237762 Seq. No.

Seq. ID uC-gsronu33B171c05b1

Method BLASTX NCBI GI g266972 BLAST score 143 E value 4.0e-09 35 Match length 71 % identity

NCBI Description 40S RIBOSOMAL PROTEIN S29 >gi\_631884\_pir\_\_S30298 ribosomal protein S29 - rat >gi 1362934 pir S55919 ribosomal protein

S29 - human >gi 57133 emb CAA41778 (X59051) ribosomal protein S29 [Rattus norvegicus] >gi 550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi 1220361 (L31610)

homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi 1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi 1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi 1096945 prf 2113200H ribosomal protein S29 [Homo sapiens] >gi\_4506717\_ref\_NP\_001023.1\_pRPS29\_

ribosomal protein S29

Seq. No. 237763

Seq. ID uC-gsronu33B171d12b1

Method BLASTX NCBI GI q4544464

34532

```
BLAST score
                   423
E value
                   7.0e-42
Match length
                  94
                  70
% identity
NCBI Description
                  (AC006580) putative chloroplast nucleoid DNA binding
                  protein [Arabidopsis thaliana]
Seq. No.
                  237764
Seq. ID
                  uC-gsronu33B171e09b1
Method
                  BLASTX
NCBI GI
                  q1076511
BLAST score
                  576
E value
                  1.0e-59
Match length
                  123
% identity
                  95
                  H+-transporting ATPase (EC 3.6.1.35) - kidney bean
NCBI Description
                  >gi 758250_emb_CAA59799_ (X85804) H(+)-transporting ATPase
                  [Phaseolus vulgaris]
                  237765
Seq. No.
Seq. ID
                  uC-gsronu33B172a08b1
Method
                  BLASTX
NCBI GI
                  g2252836
BLAST score
                  167
                  9.0e-12
E value
Match length
                  109
% identity
                  38
NCBI Description
                  (AF013293) contains weak similarity to S. cerevisiae BOB1
                  protein (PIR:S45444) [Arabidopsis thaliana]
Seq. No.
                  237766
Seq. ID
                  uC-gsronu33B172b05b1
Method
                  BLASTX
NCBI GI
                  g547683
BLAST score
                  144
E value
                  3.0e-09
                  37
Match length
                  89
% identity
NCBI Description HEAT SHOCK COGNATE PROTEIN 80 >gi 170456 (M96549) heat
                  shock cognate protein 80 [Solanum lycopersicum]
                  >gi_445601_prf__1909348A heat shock protein hsp80
                  [Lycopersicon esculentum]
Seq. No.
                  237767
Seq. ID
                  uC-gsronu33B172b06b1
Method
                  BLASTX
NCBI GI
                  g2129651
BLAST score
                  166
E value
                  7.0e-12
Match length
                  48
```

% identity 69

NCBI Description myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) >gi\_499045\_emb CAA84065 (Z34292) myosin [Arabidopsis

thaliana]

237768 Seq. No.

uC-gsronu33B172b07b1 Seq. ID



Method BLASTX NCBI GI g232278 BLAST score 307 E value 4.0e-28 Match length 115 % identity 63

NCBI Description CHLOROPLAST SMALL HEAT SHOCK PROTEIN PRECURSOR

>gi\_100397\_pir\_\_S16004 heat shock protein 21 - garden petunia >gi\_14158\_emb\_CAA38037\_ (X54103) heat shock protein

[Petunia x hybrida]

237769 Seq. No.

Seq. ID uC-gsronu33B172c03b1

Method BLASTX NCBI GI g3763921 BLAST score 322 E value 8.0e-30 Match length 84 % identity 74

NCBI Description (AC004450) putative pirin protein [Arabidopsis thaliana]

Seq. No. 237770

Seq. ID uC-gsronu33B172d09b1

Method BLASTX NCBI GI q4559384 BLAST score 156 E value 2.0e-10 Match length 43 70 % identity

NCBI Description (AC006526) unknown protein [Arabidopsis thaliana]

Seq. No. 237771

Seq. ID uC-gsronu33B172e04b1

Method BLASTX NCBI GI g3785989 BLAST score 188 E value 3.0e-14Match length 41 % identity

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

237772 Seq. No.

Seq. ID uC-gsronu33B172f06b1

Method BLASTX NCBI GI q4098129 BLAST score 370 E value 2.0e-35 Match length 70 % identity 100

NCBI Description (U73588) sucrose synthase [Gossypium hirsutum]

Seq. No. 237773

Seq. ID uC-gsronu33B178a01b1

Method BLASTX NCBI GI q3242708 BLAST score 471 E value 3.0e-47

```
Match length
% identity
NCBI Description
                   (AC003040) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
                   237774
Seq. No.
Seq. ID
                   uC-gsronu33B178a02b1
Method
                   BLASTX
NCBI GI
                   g114682
BLAST score
                   301
E value
                   3.0e-27
Match length
                   73
% identity
                   79
NCBI Description ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR
                   (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP)
                   >gi_100471_pir__A35227 H+-transporting ATP synthase (EC
                   3.6.1.34) gamma chain precursor, mitochondrial - sweet
                   potato >gi 168270 (J05397) F-1-ATPase delta subunit
                   precursor (EC 3.6.1.3) [Ipomoea batatas]
Seq. No.
                   237775
Seq. ID
                   uC-gsronu33B178a10b1
Method
                   BLASTX
NCBI GI
                   q1084455
BLAST score
                   148
E value
                   9.0e-10
Match length
                   34
% identity
                   88
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                   >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   237776
Seq. ID
                   uC-gsronu33B178b09b1
Method
                   BLASTX
NCBI GI
                   g4263712
BLAST score
                   291
E value
                   3.0e-26
                   70
Match length
% identity
NCBI Description
                  (AC006223) putative ribosomal protein S12 [Arabidopsis
                   thaliana]
Seq. No.
                   237777
Seq. ID
                   uC-gsronu33B178c04b1
Method
                   BLASTX
NCBI GI
                   g445612
BLAST score
                   227
                   1.0e-18
E value
Match length
                   46
                   98
```

% identity

NCBI Description ribosomal protein S19 [Solanum tuberosum]

Seq. No.

237778

Seq. ID

uC-gsronu33B178c05b1

Method BLASTX NCBI GI q3882151 BLAST score 181



E value 3.0e-13 Match length 131 % identity 27

NCBI Description (AB018258) KIAA0715 protein [Homo sapiens]

Seq. No. 237779

Seq. ID uC-gsronu33B178e03b1

Method BLASTX
NCBI GI g2507281
BLAST score 885
E value 1.0e-95
Match length 162
% identity 99

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi\_1668706 emb CAA66048

(X97380) atran2 [Arabidopsis thaliana]

Seq. No. 237780

Seq. ID uC-gsronu33B178f04b1

Method BLASTX
NCBI GI g3006142
BLAST score 258
E value 3.0e-22
Match length 147
% identity 34

NCBI Description (AL022299) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 237781

Seq. ID uC-gsronu33B178f08b1

Method BLASTX
NCBI GI g4115731
BLAST score 192
E value 2.0e-14
Match length 98
% identity 43

NCBI Description (AB017507) Apg12 [Homo sapiens]

Seq. No. 237782

Seq. ID uC-gsronu33B178g05b1

Method BLASTX
NCBI GI g2062169
BLAST score 693
E value 3.0e-73
Match length 173
% identity 73

NCBI Description (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis

thaliana]

Seq. No. 237783

Seq. ID uC-gsronu33B178g10b1

Method BLASTX
NCBI GI g1518540
BLAST score 826
E value 8.0e-89
Match length 172
% identity 92

NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

```
237784
Seq. No.
Seq. ID
                   uC-gsronu33B178g11b1
Method
                   BLASTX
"NCBI GI
                   g1737492
BLAST score
                   411
E value
                   4.0e-40
                   99
Match length
% identity
                   82
NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]
Seq. No.
                   237785
Seq. ID
                   uC-gsronu33B178h10b1
Method
                  BLASTX
NCBI GI
                   g3757522
BLAST score
                   430
E value
                   2.0e-42
Match length
                   118
% identity
                   74
NCBI Description (AC005167) putative splicing factor [Arabidopsis thaliana]
Seq. No.
                   237786
Seq. ID
                   uC-gsronu33B179a01b1
Method
                  BLASTX
NCBI GI
                   g2655098
BLAST score
                   311
E value
                   2.0e-30
Match length
                  99
                   71
% identity
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]
Seq. No.
                   237787
Seq. ID
                  uC-gsronu33B179a09b1
Method
                  BLASTX
NCBI GI
                   g2967452
BLAST score
                   410
E value
                   4.0e-40
Match length
                  114
% identity
                   68
NCBI Description
                  (AB010882) hSNF2H [Homo sapiens]
                  >gi 4507075 ref NP 003592.1 pSMARCA5 SWI/SNF related,
                  matrix associated, actin dependent regulator of chromatin,
                  subfamily a, member
Seq. No.
                  237788
Seq. ID
                  uC-gsronu33B179a10b1
Method
                  BLASTX
NCBI GI
                  g2191130
BLAST score
                  139
```

E value 9.0e-09 Match length 78 % identity

NCBI Description (AF007269) A\_IG002N01.7 gene product [Arabidopsis thaliana]

Seq. No. 237789

Seq. ID uC-gsronu33B179b10b1

Method BLASTX NCBI GI g3341694

```
BLAST score
                   346
E value
                   1.0e-32
Match length
                  107
% identity
                   62
NCBI Description (AC003672) PREG-like protein [Arabidopsis thaliana]
Seq. No.
                  237790
Seq. ID
                  uC-gsronu33B179c01b1
Method
                  BLASTX
NCBI GI
                  q134944
BLAST score
                  537
E value
                  6.0e-55
Match length
                  115
% identity
                  87
NCBI Description ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
                  (STEAROYL-ACP DESATURASE) >gi_100502_pir__A39173
                  acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6)
                  precursor - safflower >gi 167197 (M61109)
                  stearoyl-acyl-carrier protein desaturase [Carthamus
                  tinctorius]
Seq. No.
                  237791
Seq. ID
                  uC-gsronu33B179c08b1
Method
                  BLASTX
NCBI GI
                  g4544403
BLAST score
                  288
E value
                  9.0e-26
Match length
                  78
% identity
                  60
NCBI Description
                  (AC007047) putative glucan endo-1,3-beta-D-glucosidase
                  precursor [Arabidopsis thaliana]
Seq. No.
                  237792
Seq. ID
                  uC-gsronu33B179d02b1
Method
                  BLASTX
NCBI GI
                  g4185819
BLAST score
                  170
E value
                  5.0e-12
Match length
                  43
% identity
NCBI Description
                 (AF116845) metallothionein-like type 1 protein [Ipomoea
                  batatas]
Seq. No.
                  237793
Seq. ID
                  uC-gsronu33B179d06b1
Method
                  BLASTX
NCBI GI
                  g3522945
```

BLAST score

132

E value

Match length

3.0e-11

% identity

91

NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.

237794

Seq. ID Method

uC-gsronu33B179e12b1

BLASTX

NCBI GI

g1350548

```
BLAST score
                   184
E value
                   2.0e-13
Match length
                   92
% identity
                   39
NCBI Description (L47609) heat shock-like protein [Picea glauca]
Seq. No.
                   237795
Seq. ID
                   uC-gsronu33B179g07b1
Method
                  BLASTX
NCBI GI
                  g2231312
BLAST score
                  213
E value
                   5.0e-17
                  47
Match length
                  81
% identity
NCBI Description (U75603) AtRab18 [Arabidopsis thaliana]
Seq. No.
                   237796
Seq. ID
                  uC-gsronu33B179h11b1
Method
                  BLASTX
NCBI GI
                  g2393767
BLAST score
                  137
E value
                  1.0e-08
Match length
                  35
% identity
                  74
NCBI Description (U70621) phosphate-binding protein precursor [Erwinia
                  carotovora subsp. carotovora]
Seq. No.
                  237797
Seq. ID
                  uC-gsronu33b023b01b1
Method
                  BLASTX
NCBI GI
                  g1737492
BLAST score
                  435
E value
                  4.0e-43
Match length
                  126
% identity
                  20
NCBI Description (U81318) poly(A)-binding protein [Triticum aestivum]
Seq. No.
                  237798
Seq. ID
                  uC-gsronu33b023b05b1
Method
                  BLASTX
NCBI GI
                  g3915961
BLAST score
                  284
E value
                  5.0e-26
Match length
                  66
% identity
                  85
NCBI Description HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
                  >gi_2924274_emb_CAA77427 (Z00044) Ycf2 protein [Nicotiana
                  tabacum] >gi_2924285_emb_CAA77438 (Z00044) hypothetical
                  protein [Nicotiana tabacum]
Seq. No.
                  237799
Seq. ID
                  uC-gsronu33b023d04b1
```

Seq. No. 237799

Seq. ID uC-gsronu33b023d04b

Method BLASTX

NCBI GI g3617770

BLAST score 379

E value 1.0e-36

Match length 92

% identity NCBI Description (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana] Seq. No. 237800 Seq. ID uC-gsronu33b023e02b1 BLASTX Method NCBI GI g4455184 BLAST score 161 E value 5.0e-11 Match length 75 % identity 56 NCBI Description (AL035521) extra-large G-protein-like [Arabidopsis thaliana Seq. No. 237801 Seq. ID uC-gsronu33b023f05b1 Method BLASTX NCBI GI g1076525 BLAST score 146 E value 2.0e-09 Match length 54 % identity 65 dehydrin-related protein - garden pea

NCBI Description

>gi\_18375\_emb\_CAA78515 (Z14145) dehydrin-cognate [Pisum

sativum]

Seq. No. 237802

Seq. ID uC-gsronu33b023g01b1

Method BLASTX NCBI GI g421843 BLAST score 371 E value 9.0e-36 Match length 101 % identity 69

NCBI Description protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana

>gi 217861 dbj BAA01715 (D10909) serine/threonine protein

kinase [Arabidopsis thaliana]

Seq. No. 237803

Seq. ID uC-gsronu33b023h07b1

Method BLASTX NCBI GI g1103318 BLAST score 242 E value 4.0e-23 Match length 69 % identity 80

NCBI Description (X78818) casein kinase I [Arabidopsis thaliana]

>gi\_2244791\_emb CAB10213.1 (Z97336) casein kinase I

[Arabidopsis thaliana]

Seq. No. 237804

Seq. ID uC-gsronu33b025c01b1

Method BLASTX NCBI GI g1666173 BLAST score 144 E value 3.0e-09Match length 32

```
% identity
NCBI Description
                  (Y09106) transcription factor [Nicotiana plumbaginifolia]
                   237805
Seq. No.
Seq. ID
                   uC-gsronu33b025d12b1
Method
                   BLASTX
NCBI GI
                   g1360088
BLAST score
                   316
E value
                   3.0e-29
                  78
Match length
                   71
% identity
NCBI Description (X97947) In finger protein [Nicotiana tabacum]
Seq. No.
                   237806
Seq. ID
                   uC-gsronu33b025e04b1
Method
                   BLASTX
NCBI GI
                   g2062168
BLAST score
                   331
E value
                   5.0e-31
Match length
                  83
                   76
% identity
NCBI Description (AC001645) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   237807
Seq. ID
                  uC-gsronu33b025e08b1
Method
                  BLASTX
NCBI GI
                   g4220479
BLAST score
                   319
E value
                  1.0e-29
                  97
Match length
% identity
                   70
NCBI Description (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                  237808
Seq. ID
                  uC-gsronu33b025e10b1
                  BLASTX
Method
NCBI GI
                  q2623295
BLAST score
                  394
E value
                  2.0e-38
Match length
                  119
% identity
NCBI Description
                  (AC002409) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  237809
Seq. ID
                  uC-gsronu33b025e11b1
Method
                  BLASTX
NCBI GI
                  g2495230
BLAST score
                  531
E value
                  2.0e-54
Match length
                  115
% identity
                  89
NCBI Description
                  IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (IGPD) >gi 1381086
                   (U49978) imidazoleglycerol-phosphate dehydratase [Pisum
```

Seq. ID uC-gsronu33b025f07b1

sativum]



Method BLASTX
NCBI GI g541951
BLAST score 445
E value 2.0e-44
Match length 113
% identity 79

NCBI Description SPCP2 protein - soybean >gi\_310578 (L12258) nodulin-26

[Glycine max]

Seq. No. 237811

Seq. ID uC-gsronu33b025f08b1

Method BLASTX
NCBI GI g129726
BLAST score 177
E value 8.0e-13
Match length 140
% identity 29

NCBI Description PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL

4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55) >gi\_68464\_pir\_\_ISBOSS protein disulfide-isomerase (EC 5.3.4.1) precursor - bovine >gi\_163497 (M17596) PDI (E.C.5.3.4.1) [Bos taurus]

Seq. No. 237812

Seq. ID uC-gsronu33b025f11b1

Method BLASTX
NCBI GI g541816
BLAST score 156
E value 8.0e-11
Match length 53
% identity 57

NCBI Description protein kinase - common ice plant >gi\_457689\_emb\_CAA82990\_

(Z30329) protein kinase [Mesembryanthemum crystallinum]

Seq. No. 237813

Seq. ID uC-gsronu33b025g06b1

Method BLASTX
NCBI GI g2208988
BLAST score 369
E value 2.0e-35
Match length 81
% identity 81

NCBI Description (Y10117) signal recognition particle subunit 9 [Zea mays]

Seq. No. 237814

Seq. ID uC-gsronu33b025h12b1

Method BLASTX
NCBI GI g3023832
BLAST score 355
E value 3.0e-34
Match length 78
% identity 82

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1

>gi\_1835161\_emb\_CAB06618\_ (Z84820) G protein beta subunit

[Nicotiana tabacum]

Seq. No. 237815

```
uC-gsronu33b112a02b1
Seq. ID
                   BLASTX
Method
                   g3831441
NCBI GI
BLAST score
                   183
```

Match length 79 % identity NCBI Description (AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No. 237816

E value

Seq. ID uC-gsronu33b112b02b1

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2.0e-13

BLASTX Method NCBI GI q3445207 172 BLAST score E value 3.0e-12 Match length 121 34 % identity

NCBI Description (AC004786) unknown protein [Arabidopsis thaliana]

Seq. No. 237817

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BLASTX Method NCBI GI q4467145 BLAST score 195 E value 4.0e-15 Match length 41 % identity 88

(AL035540) farnesylated protein (ATFP6) [Arabidopsis NCBI Description

thaliana]

Seq. No. 237818

Seq. ID uC-gsronu33b112e02b1

Method BLASTX NCBI GI g3024017 BLAST score 462 E value 3.0e-46Match length 100 91 % identity

EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) NCBI Description

(EIF-4C) >gi 2565421 (AF026804) eukaryotic translation

initiation factor eIF-1A [Onobrychis viciifolia]

Seq. No. 237819

Seq. ID uC-gsronu33b112e04b1

Method BLASTX NCBI GI g2829899 BLAST score 240 3.0e-20 E value Match length 87 % identity 51

(AC002311) similar to ripening-induced protein, NCBI Description

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gp\_X91961\_1107495 [Arabidopsis thaliana]

Seq. No. 237820

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Method BLASTX

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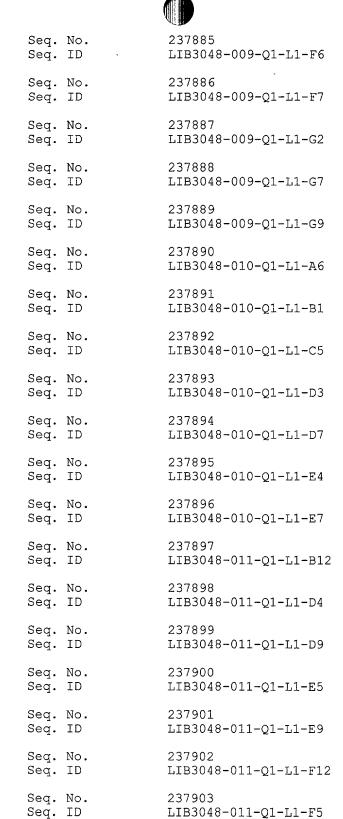
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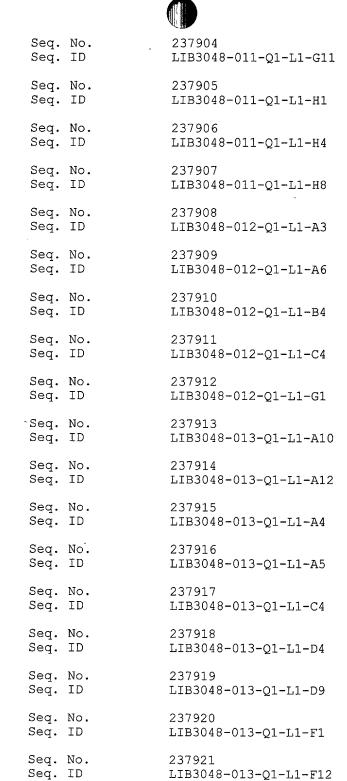
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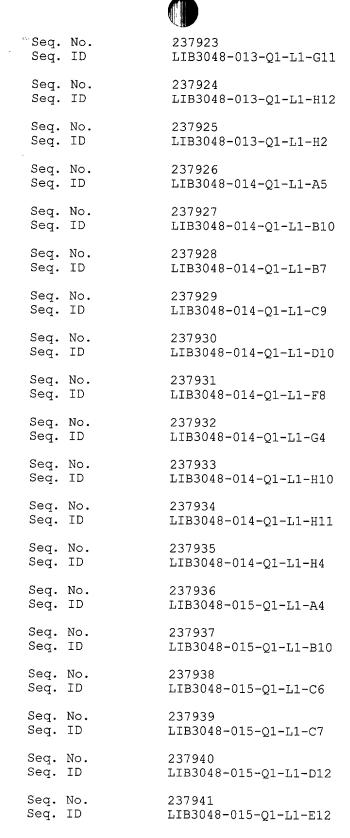


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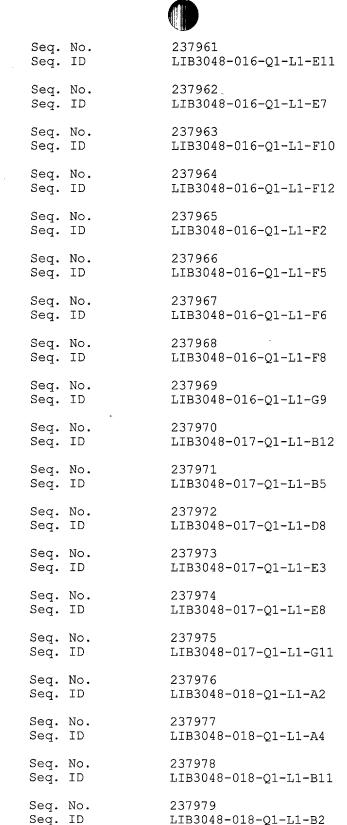


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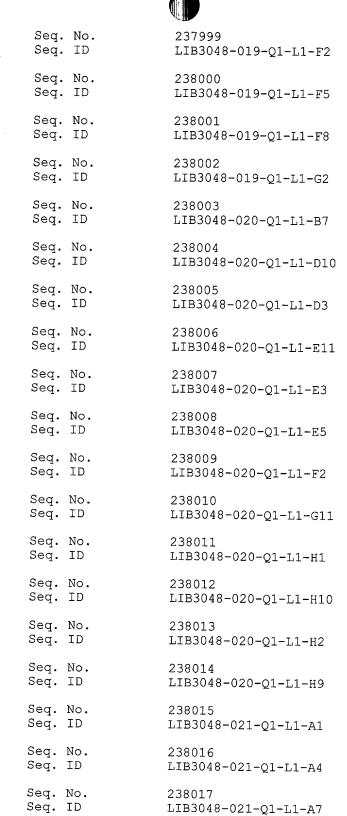
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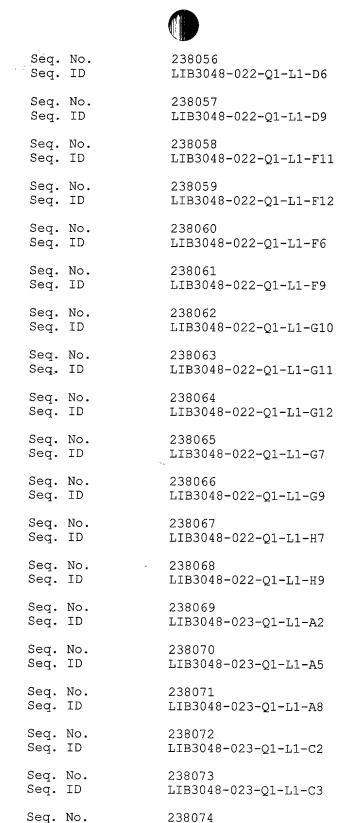
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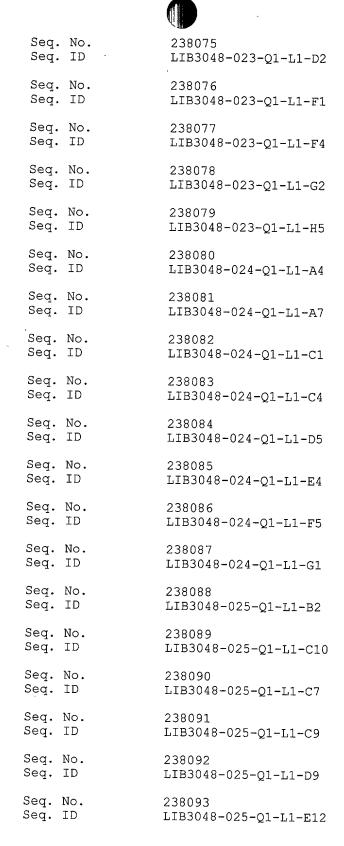
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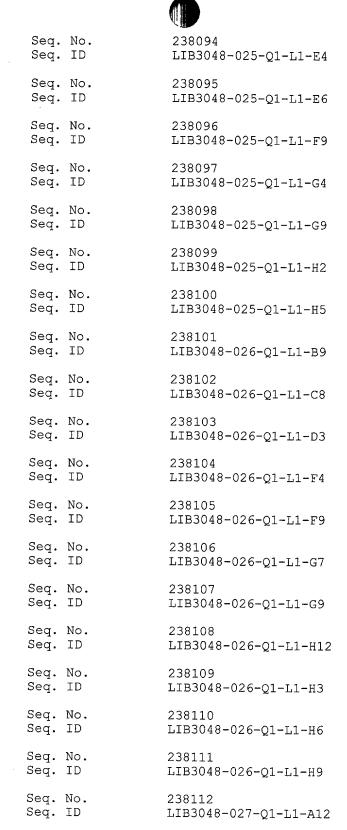
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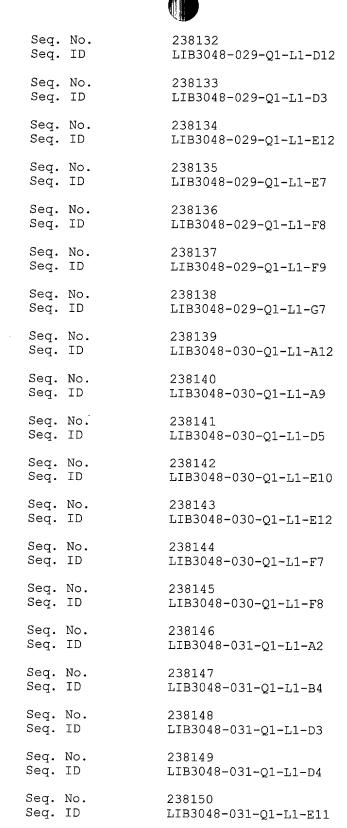
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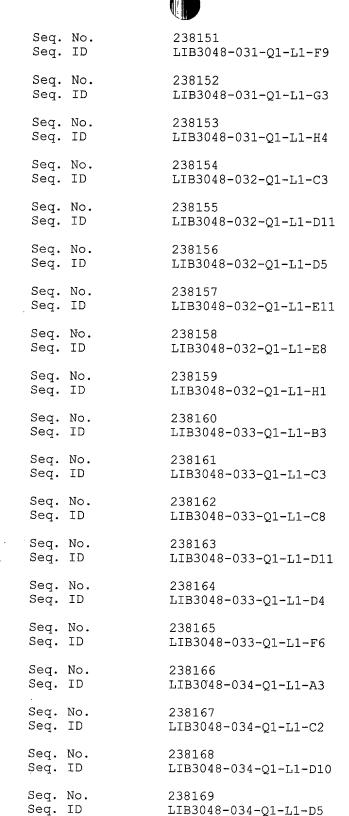
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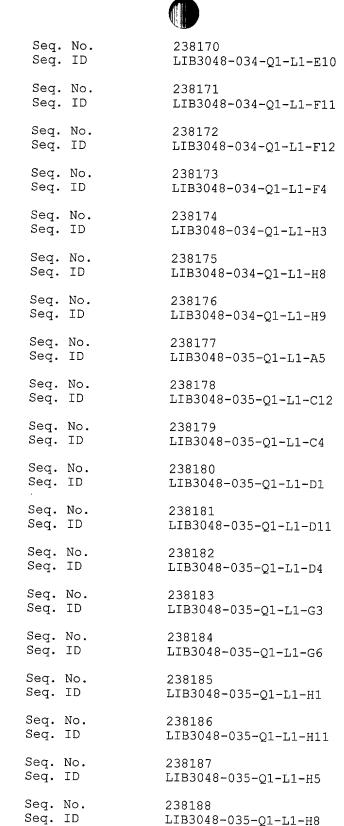




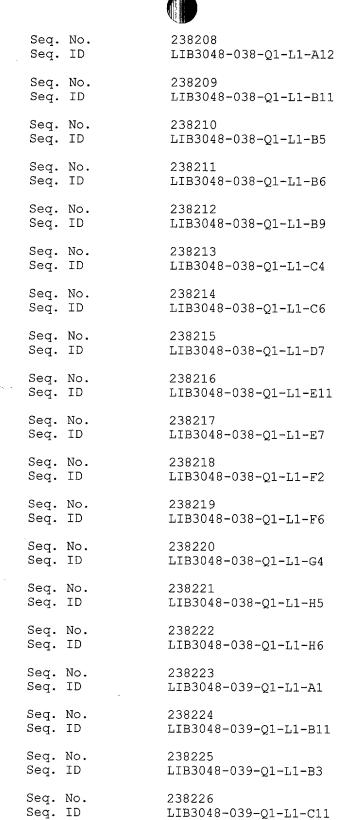
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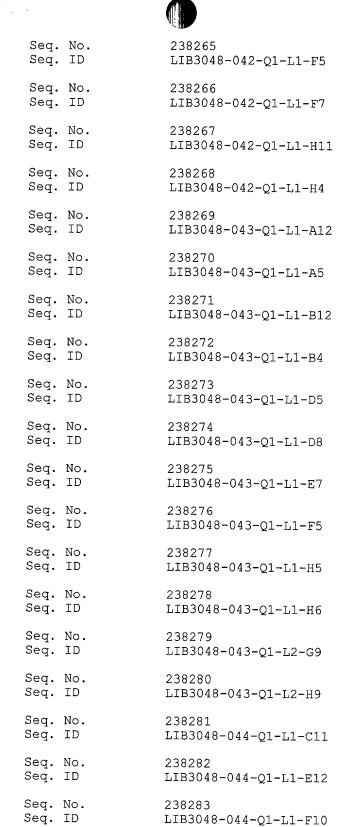


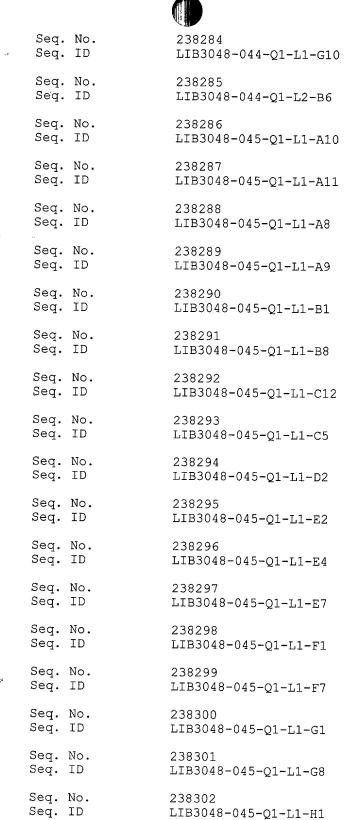
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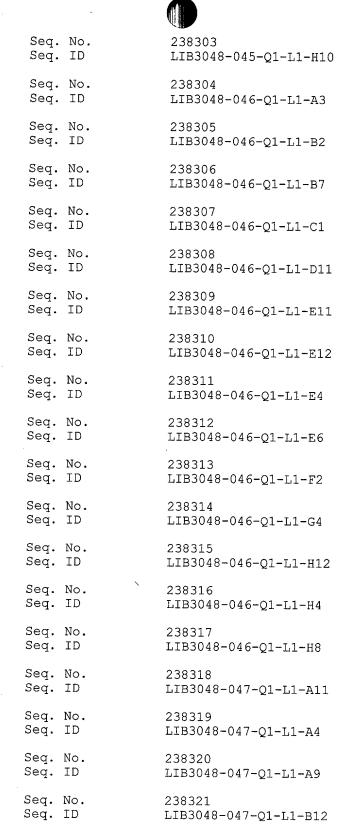


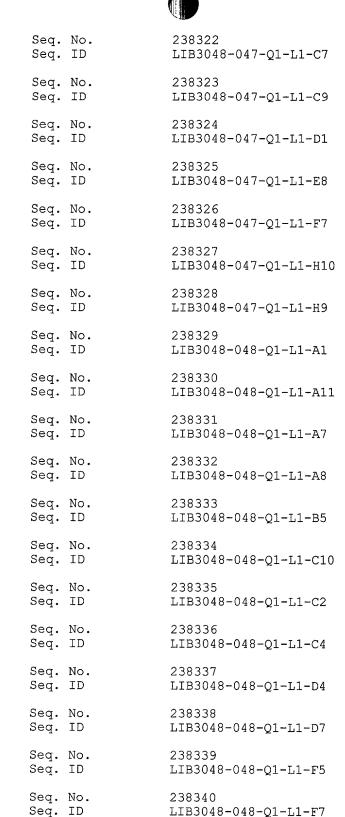
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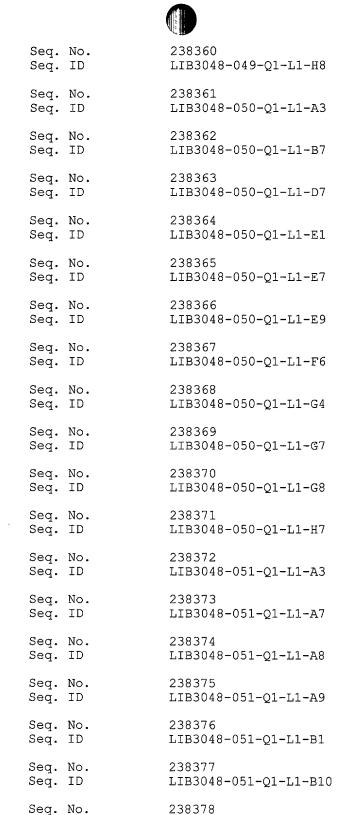






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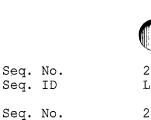
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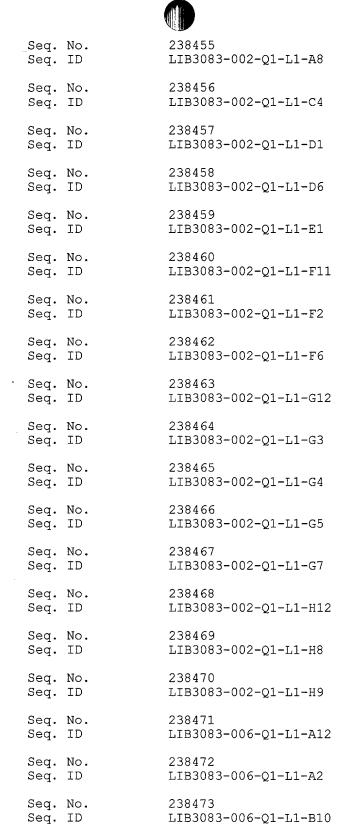
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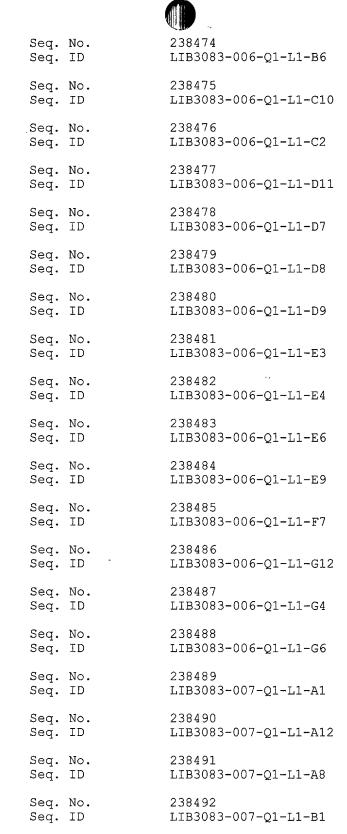
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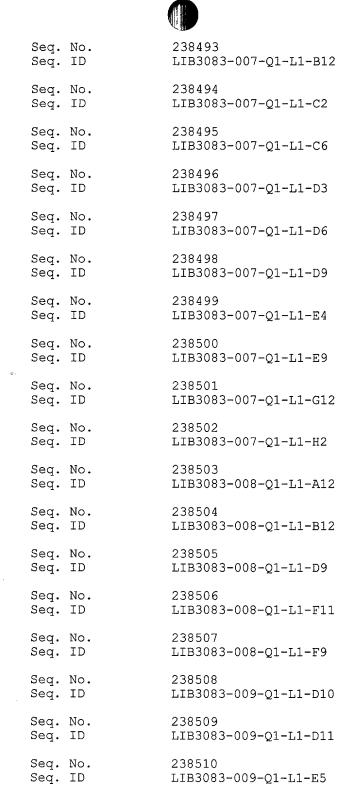
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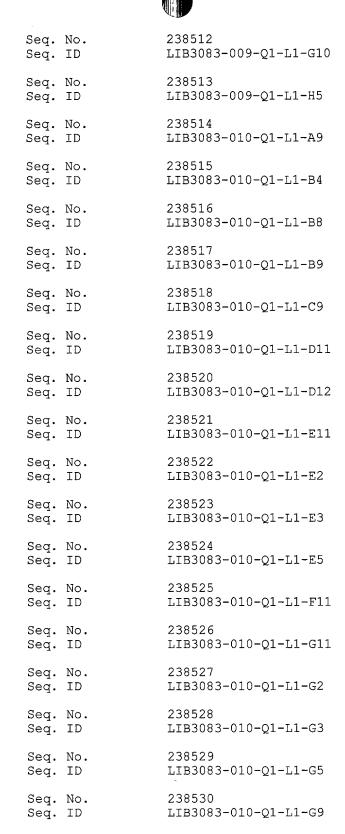
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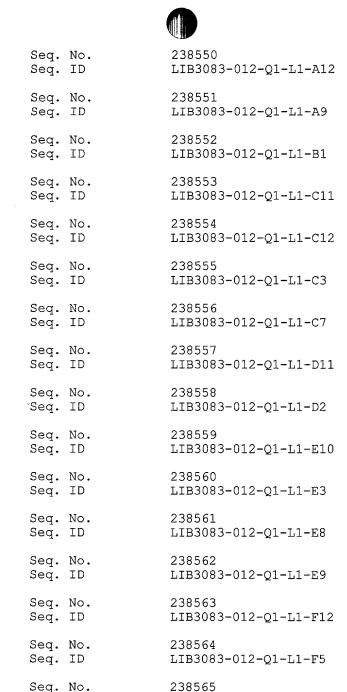
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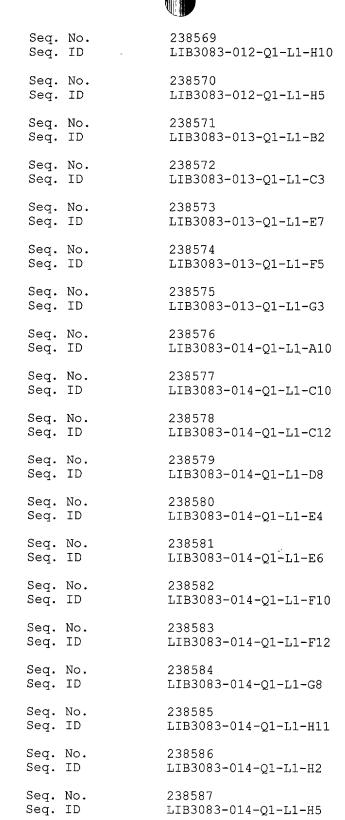
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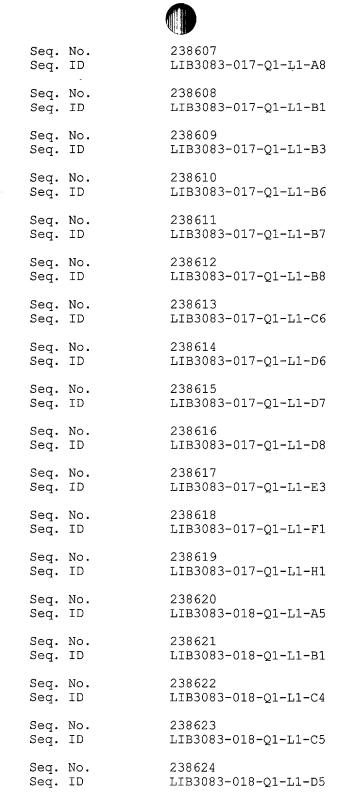
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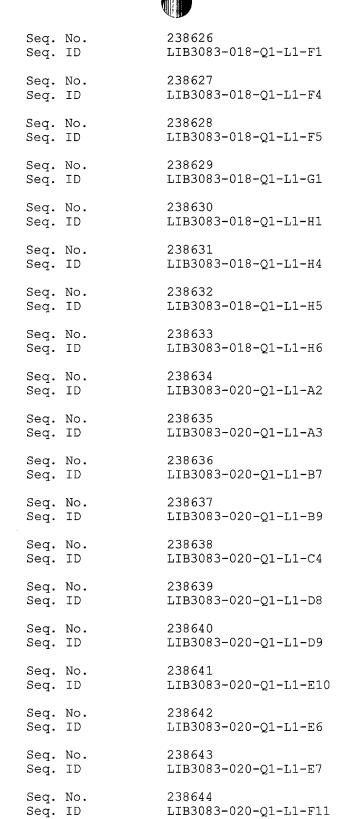
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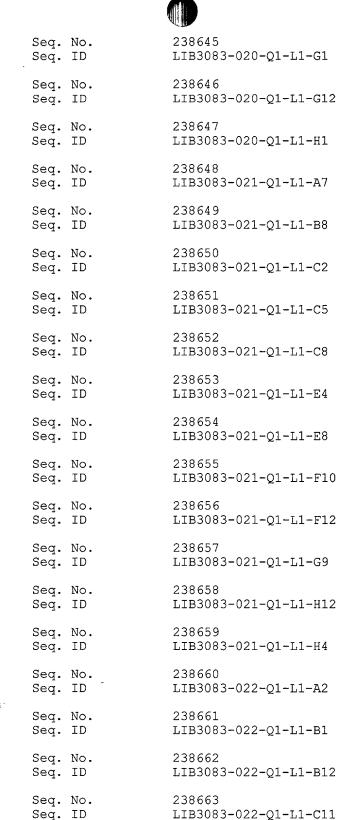
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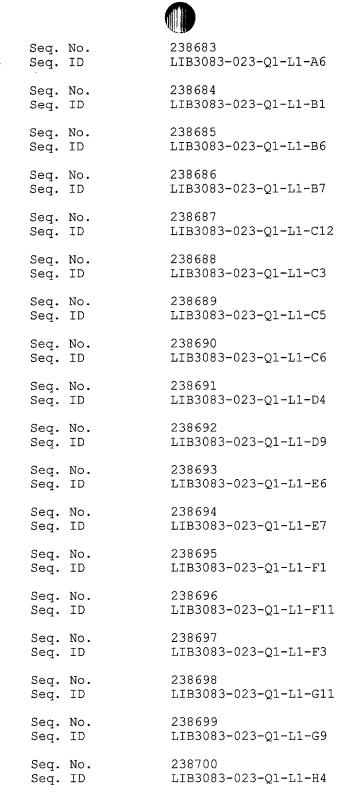






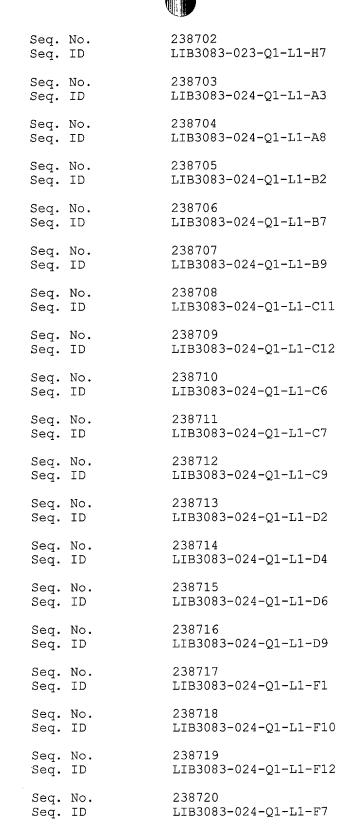
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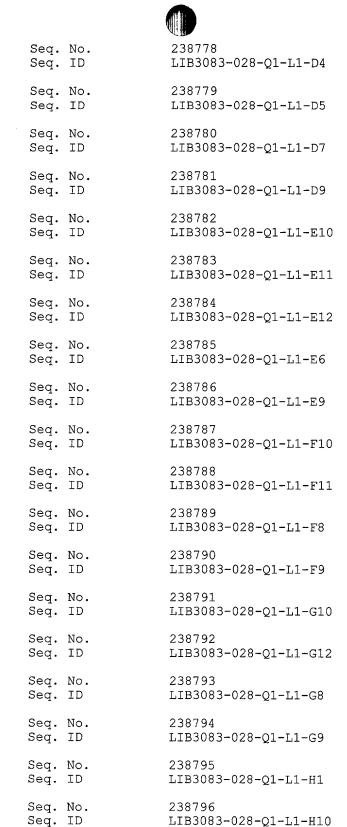
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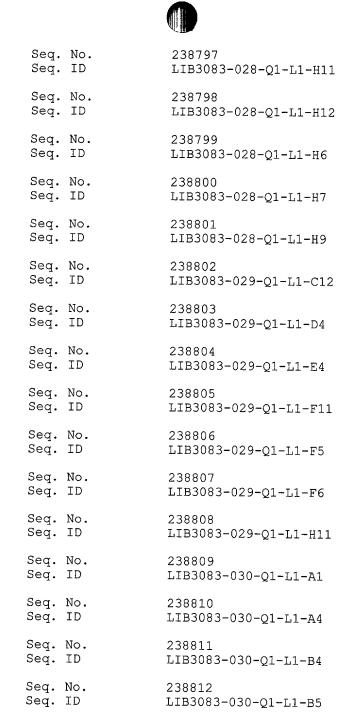


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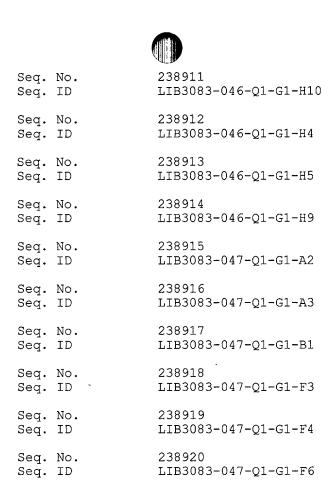
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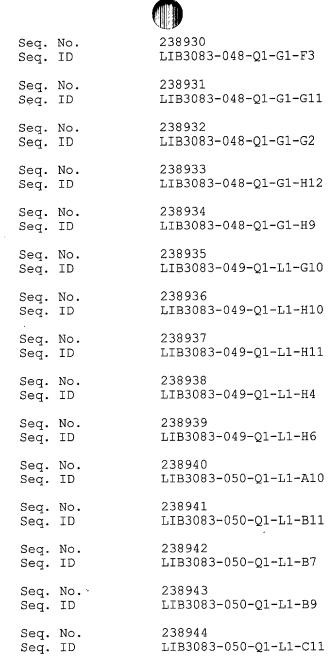
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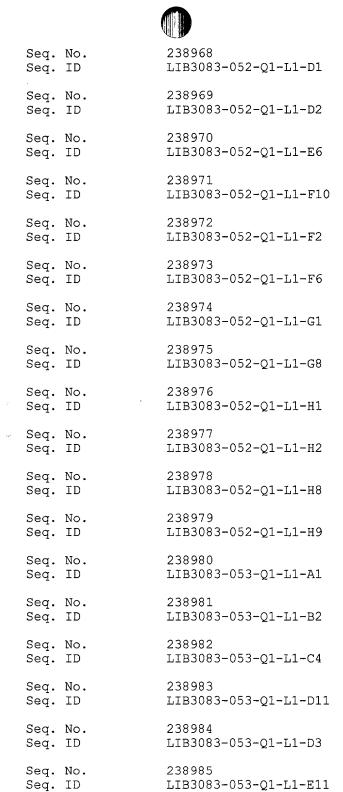
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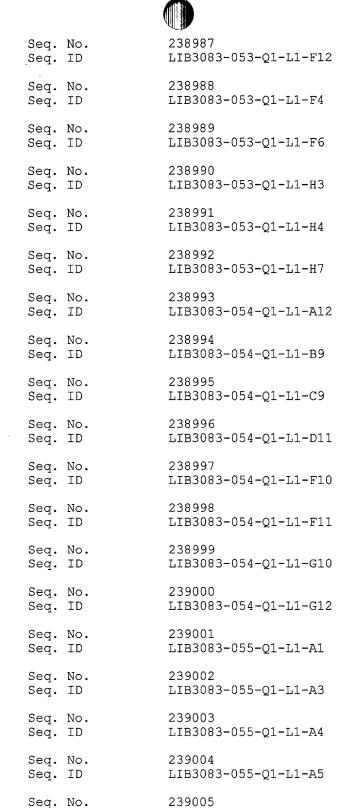


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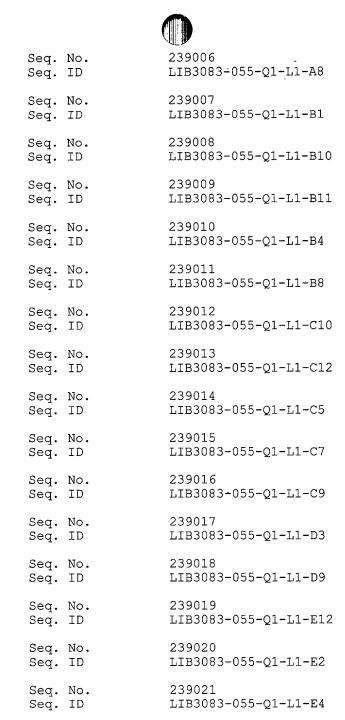
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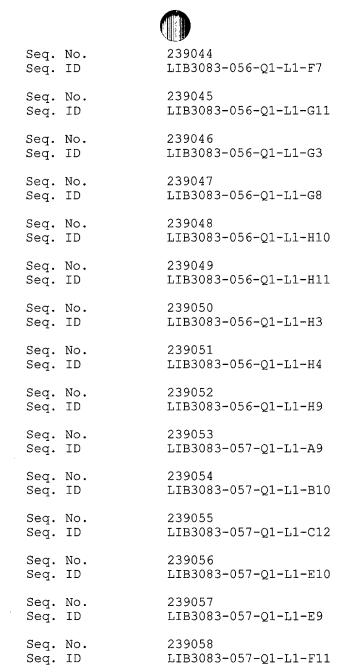
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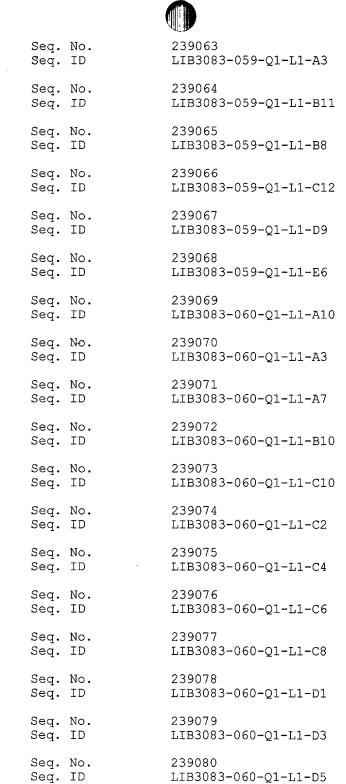
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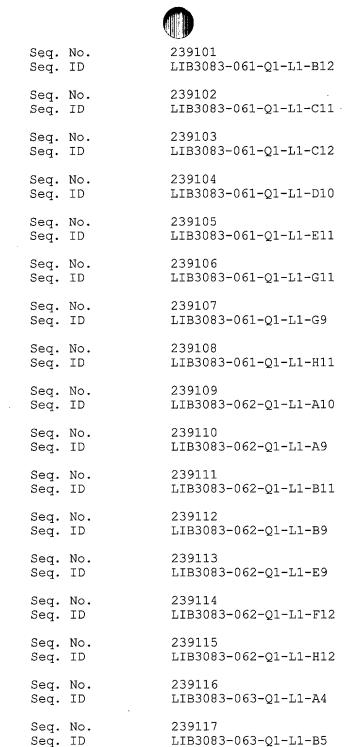


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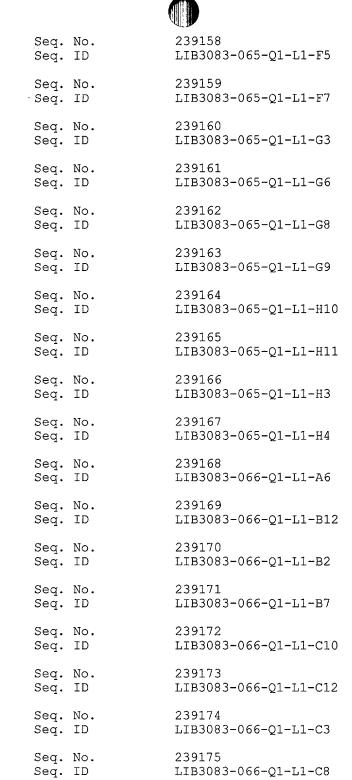


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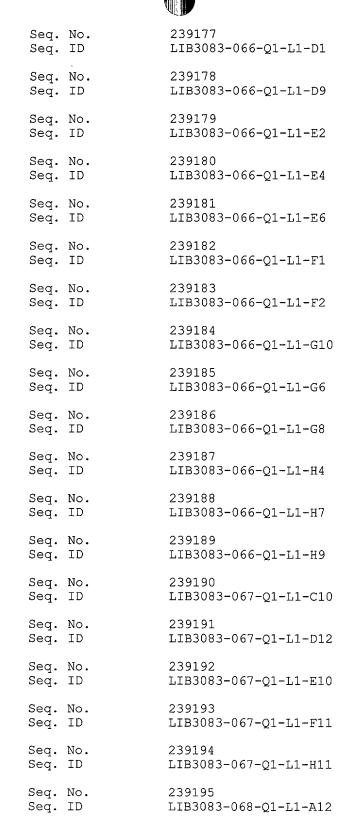
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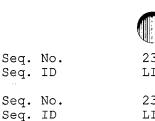
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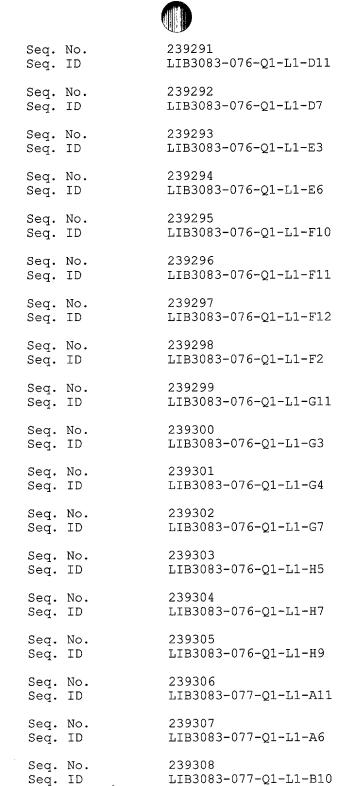
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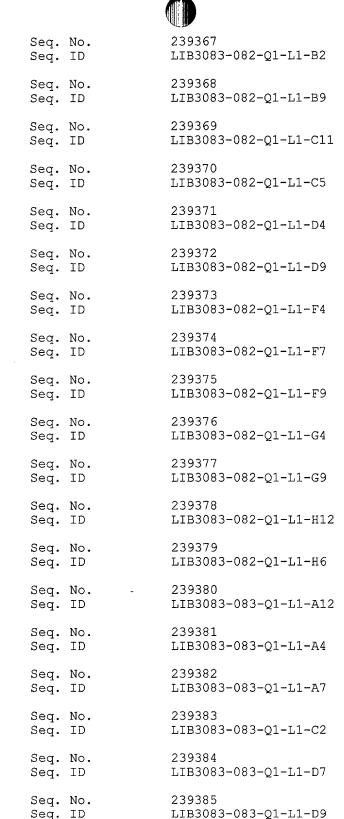
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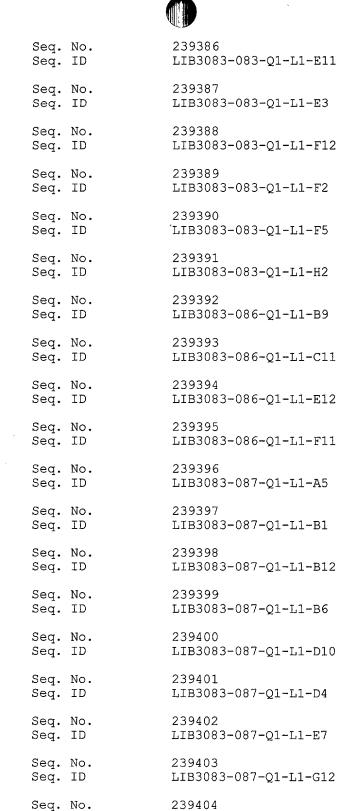


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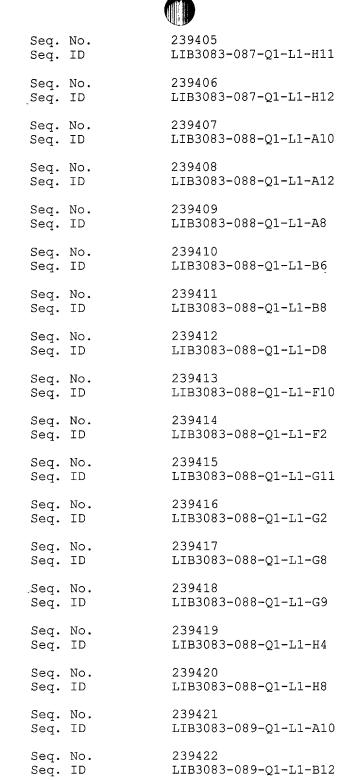


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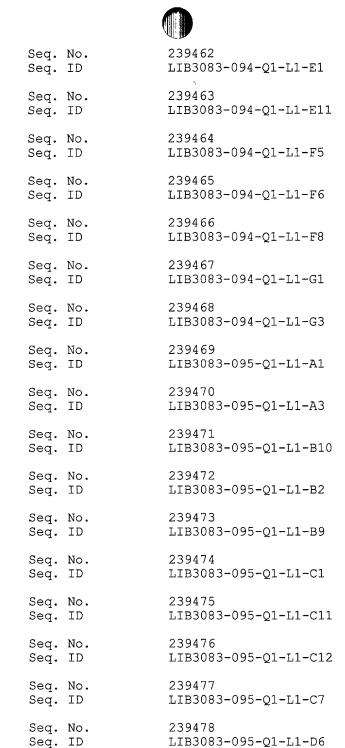
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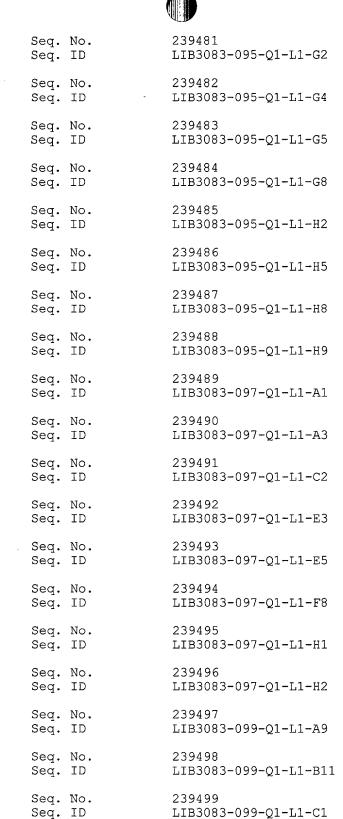


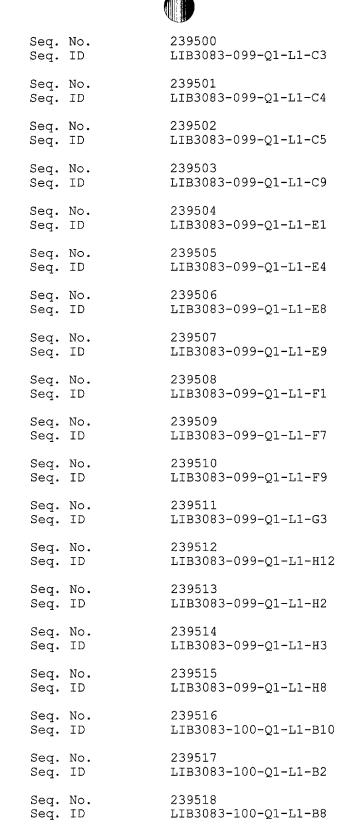
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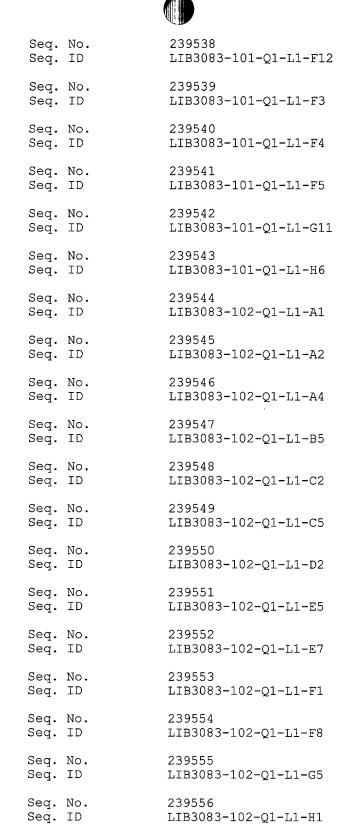
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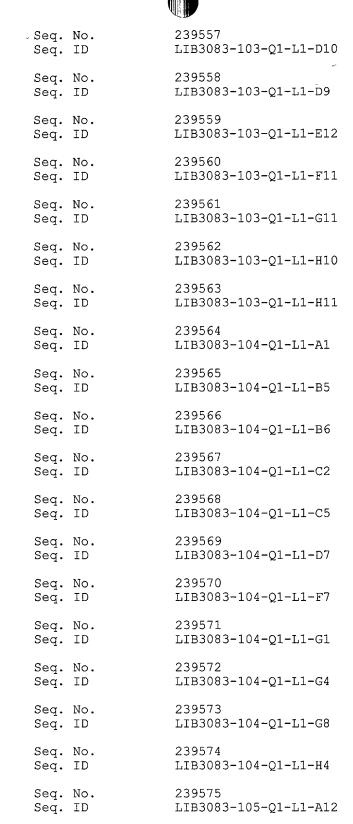
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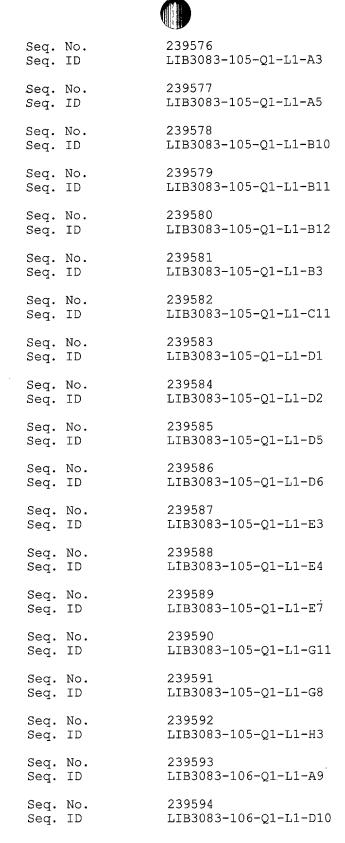




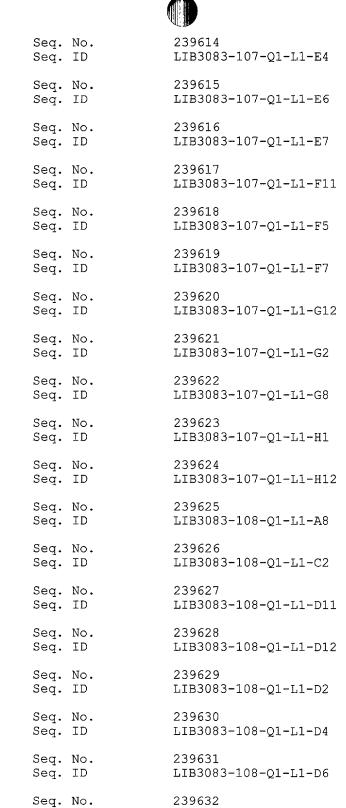
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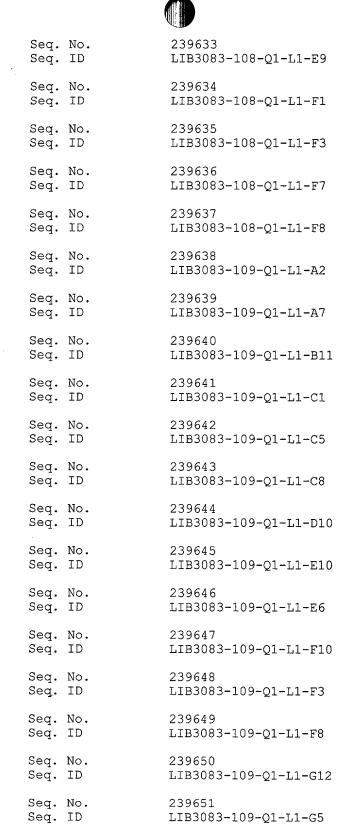


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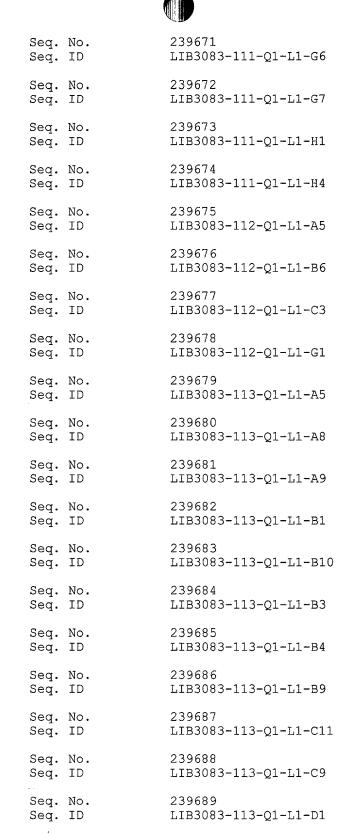


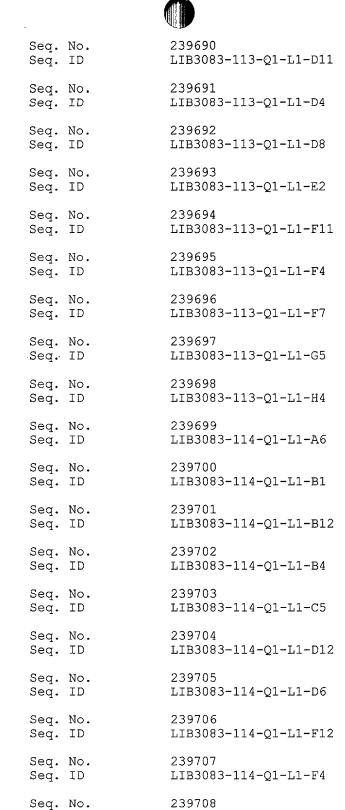
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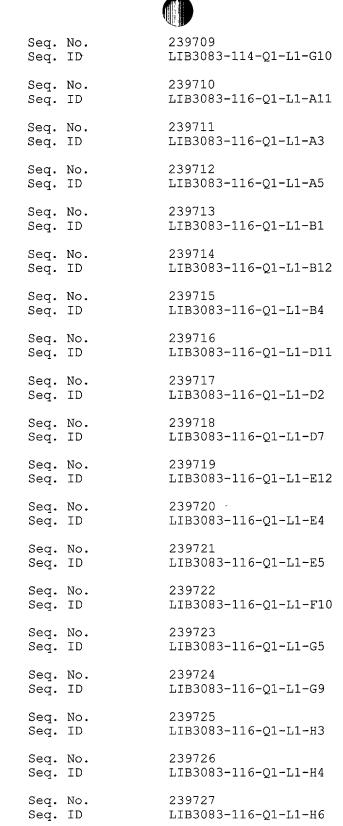
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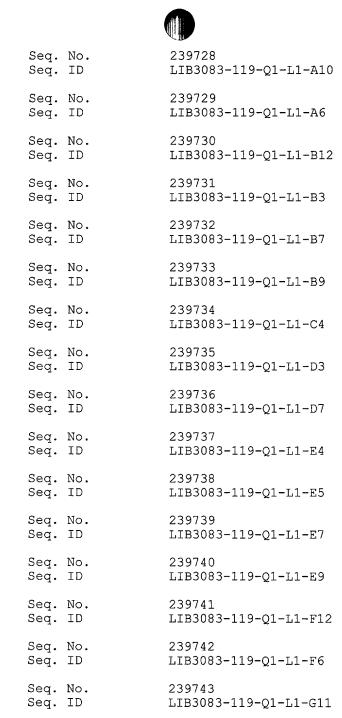




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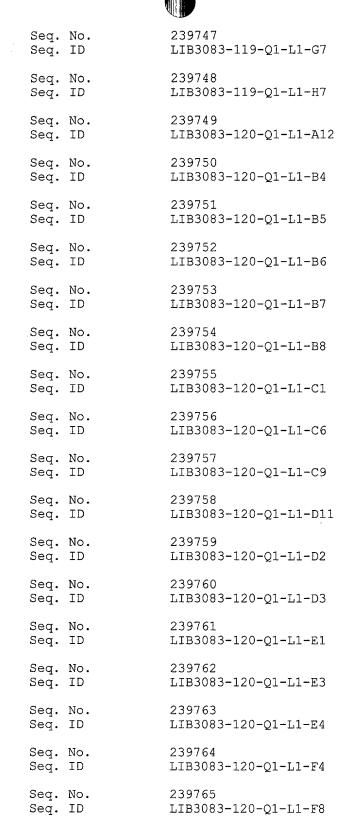
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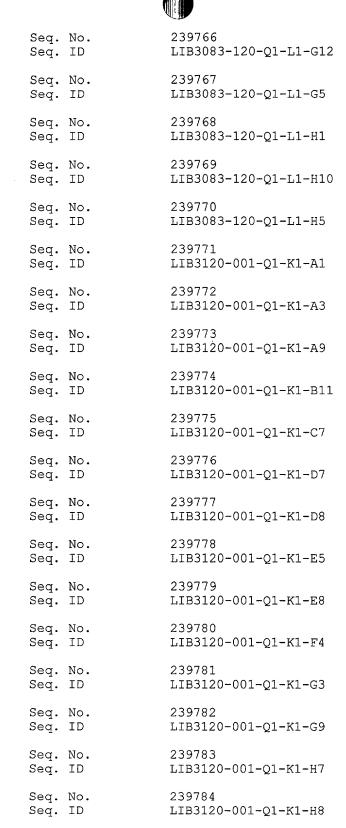
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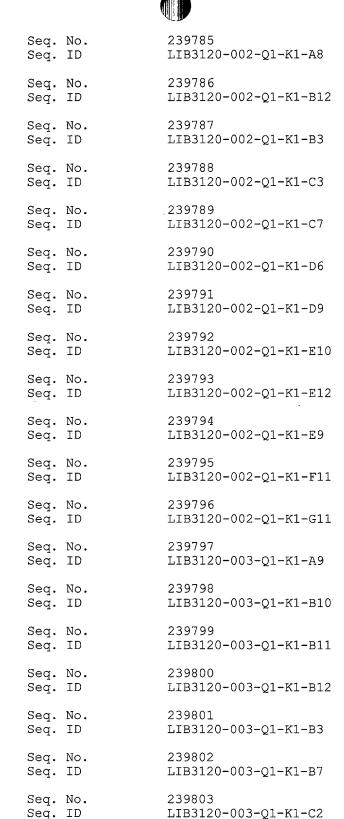
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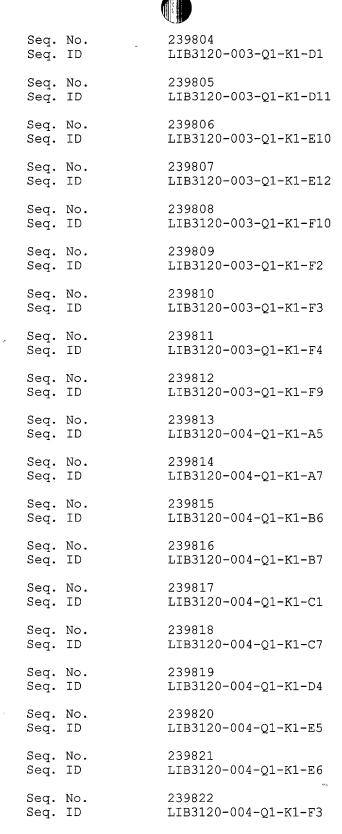
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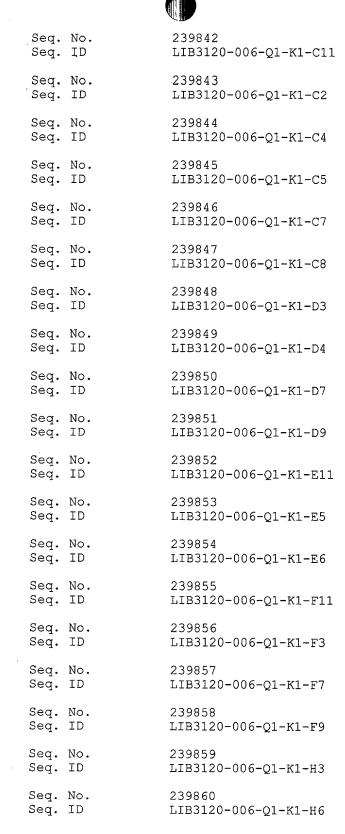


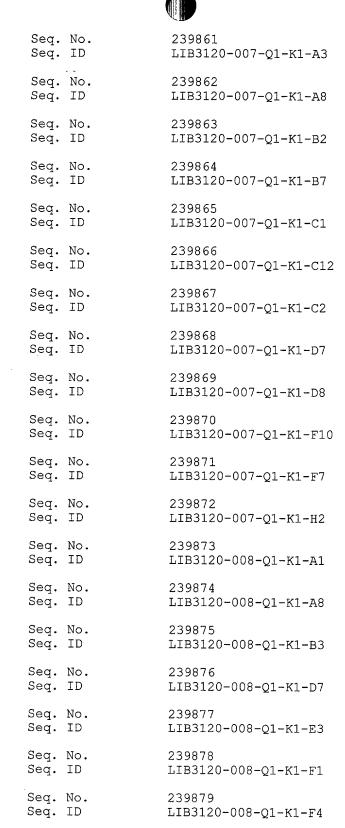


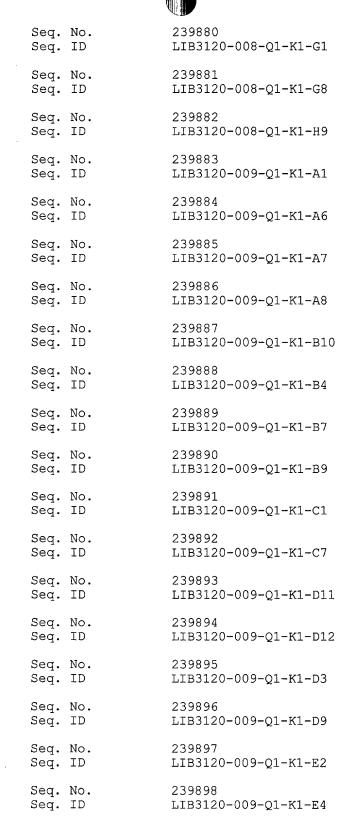


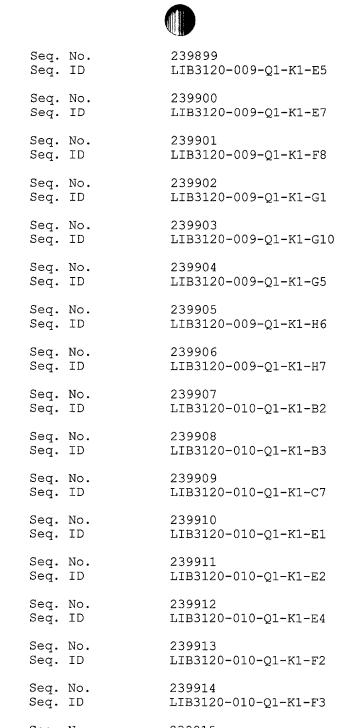


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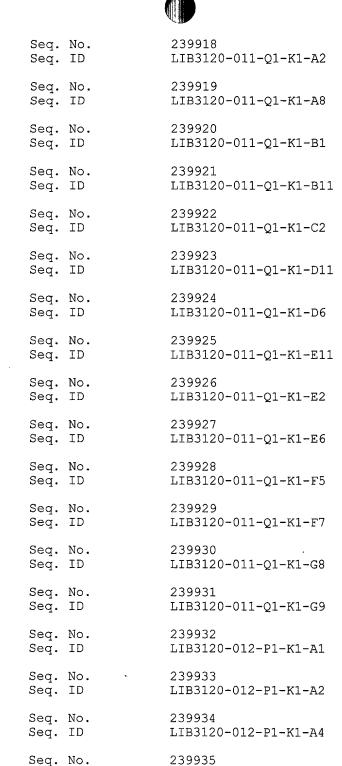
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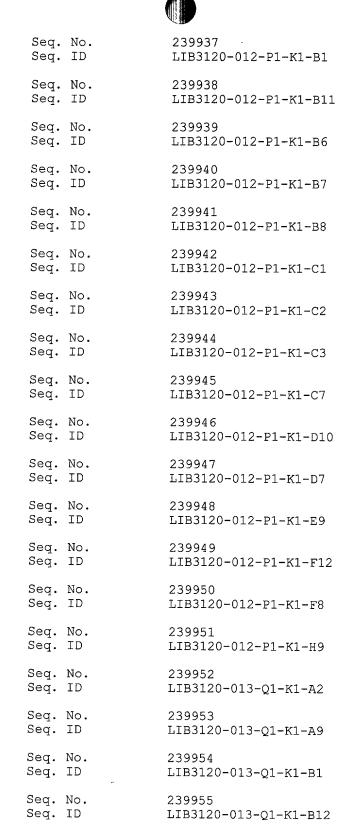
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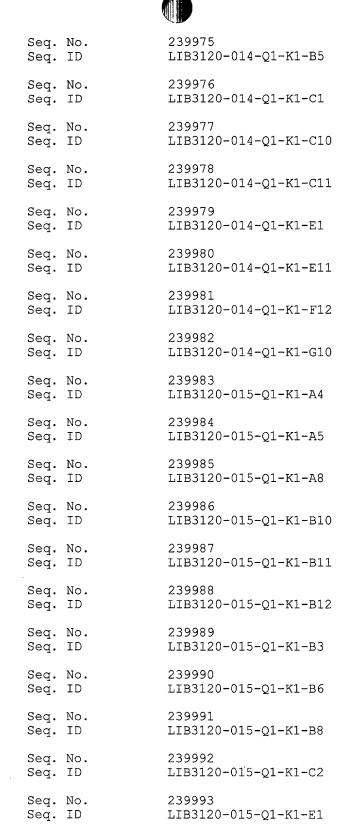
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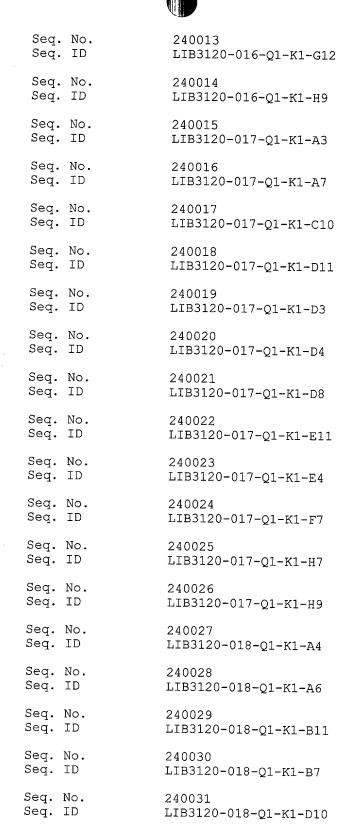
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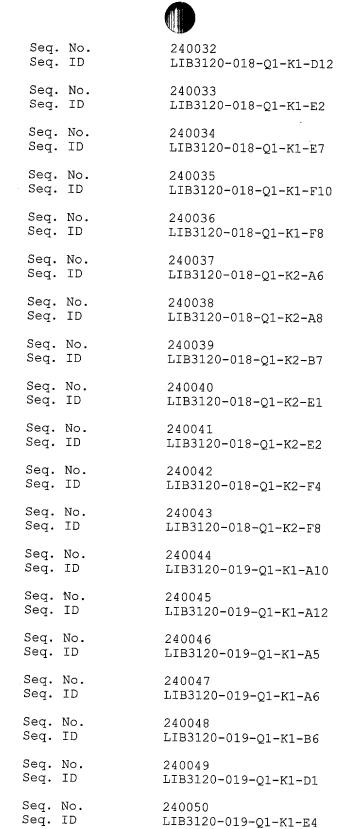


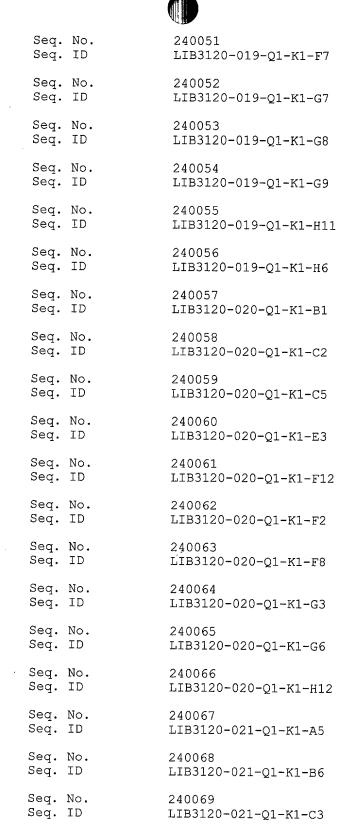
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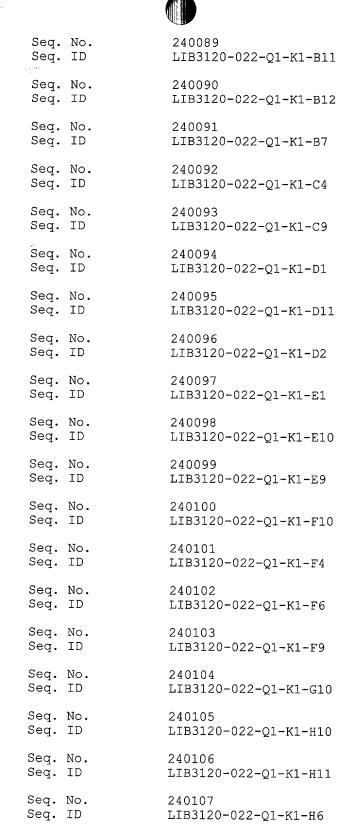
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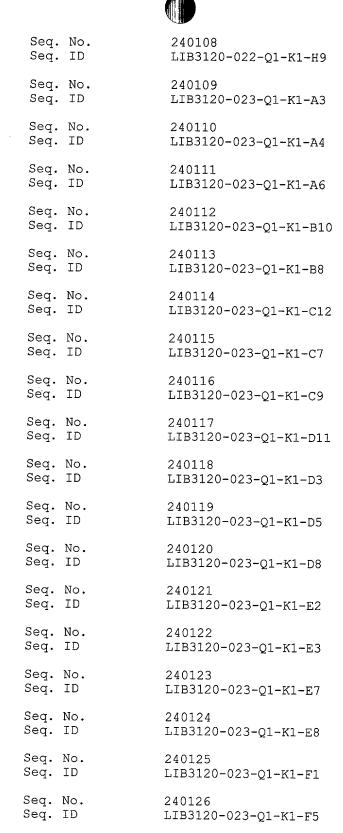


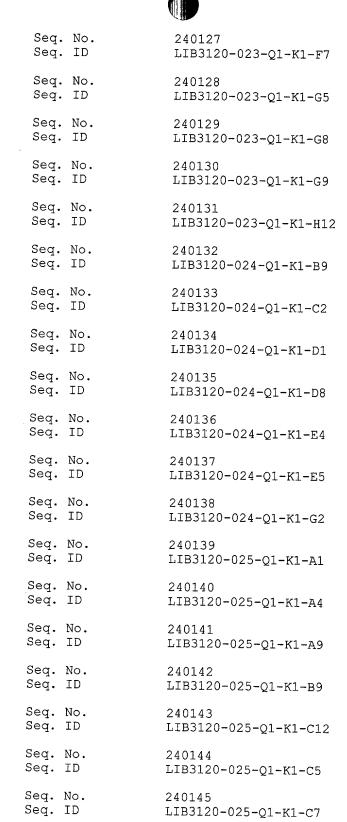


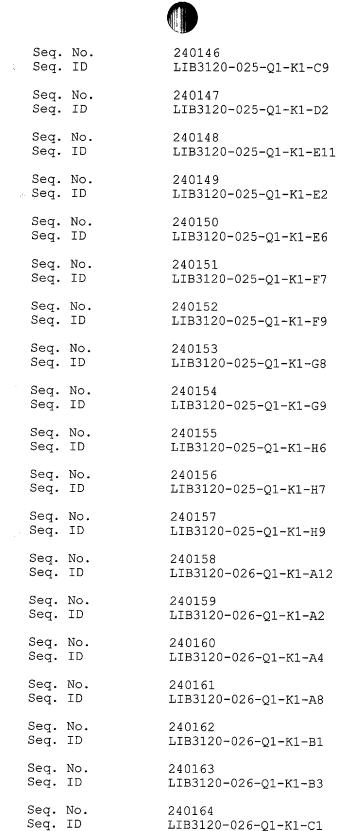


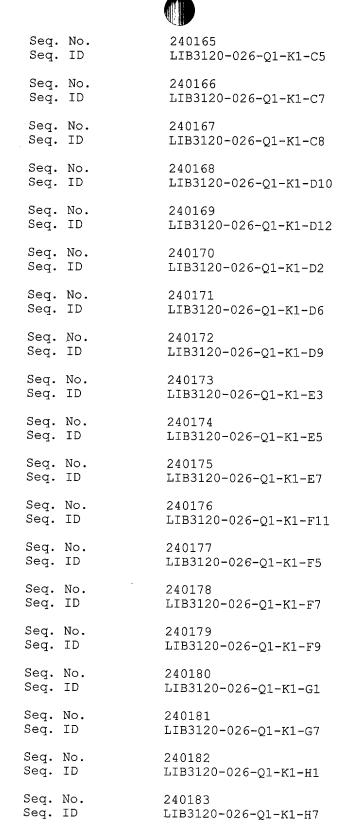
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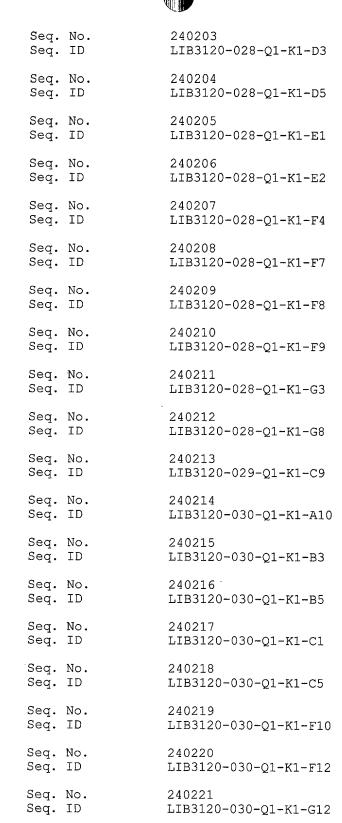




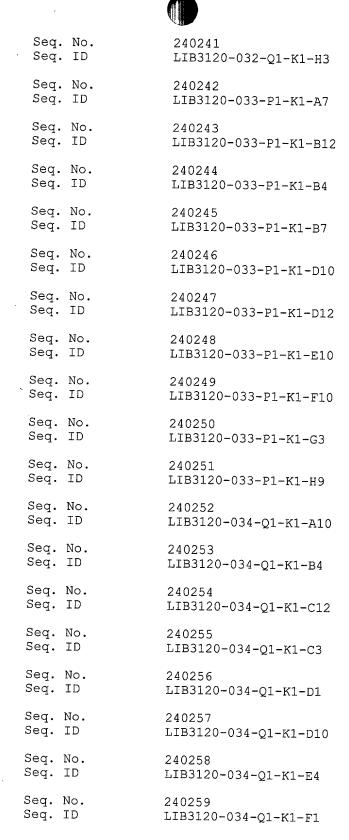




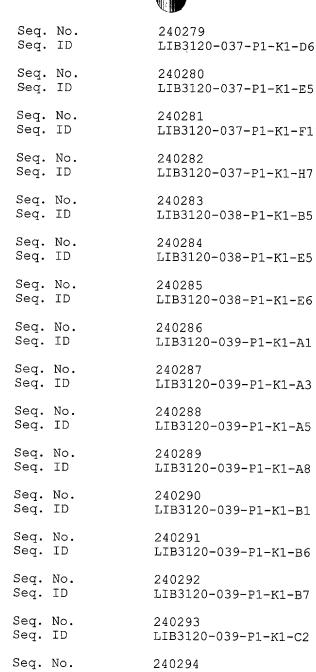
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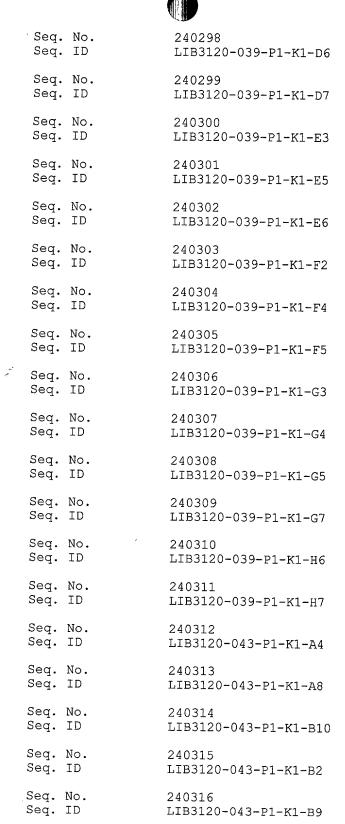
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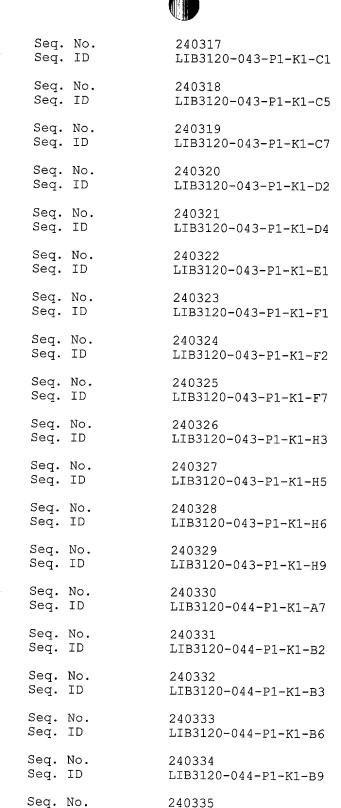
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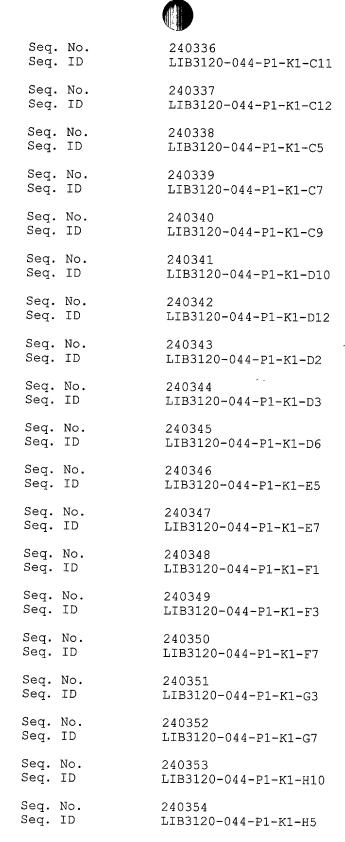


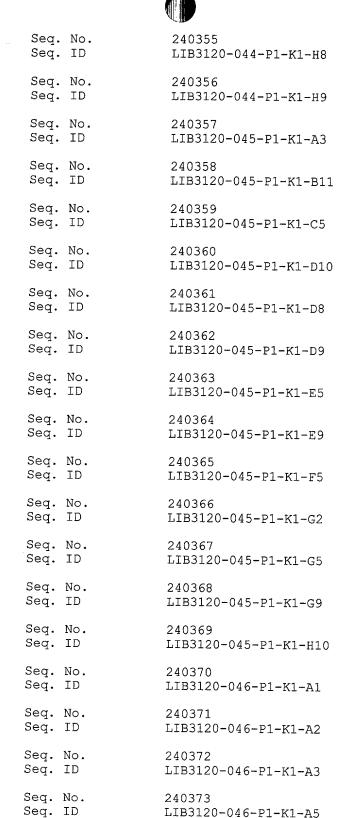
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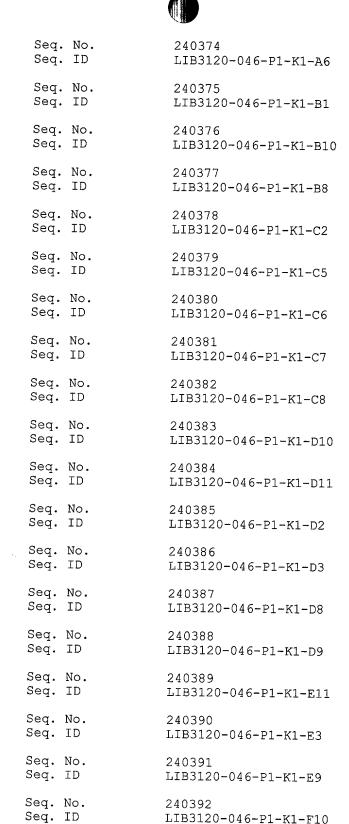


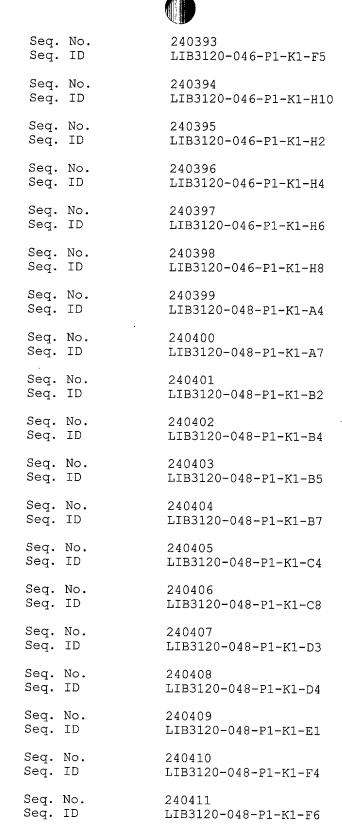
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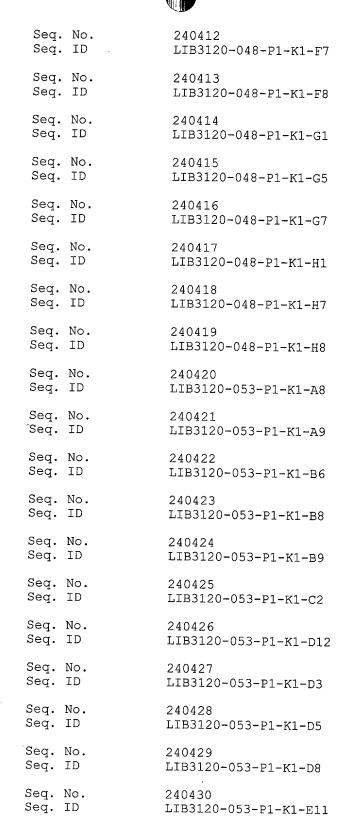
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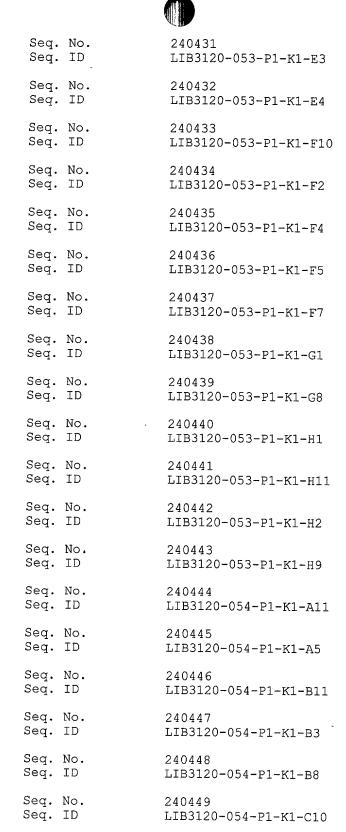




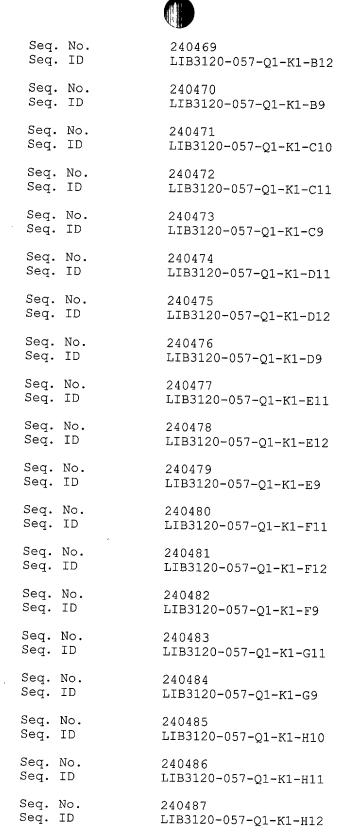


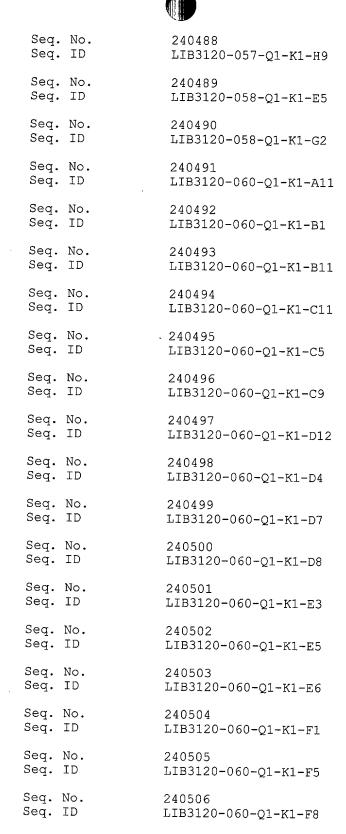


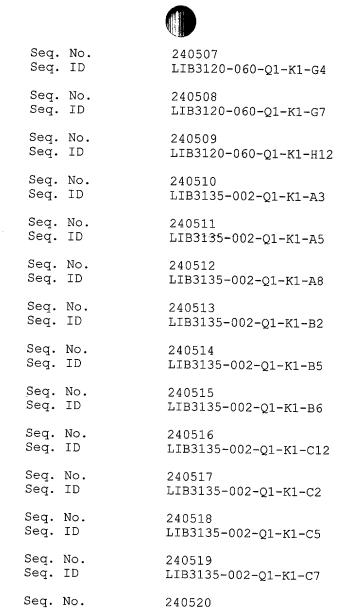




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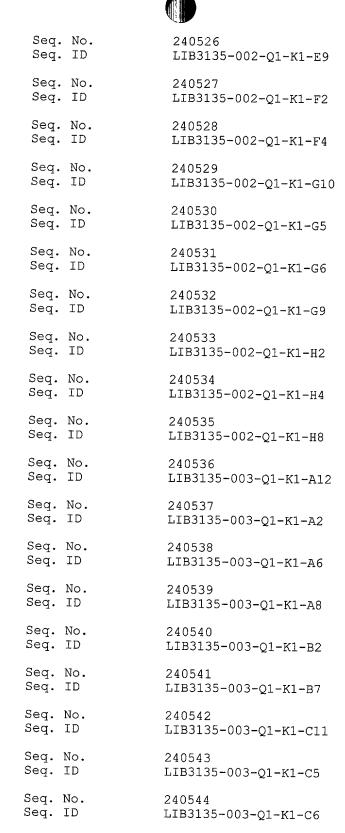
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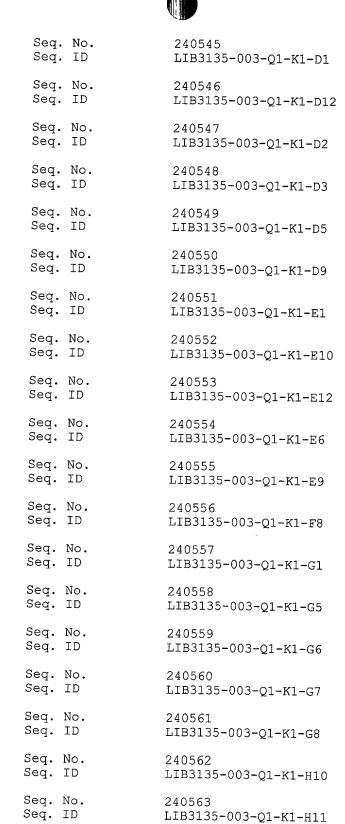
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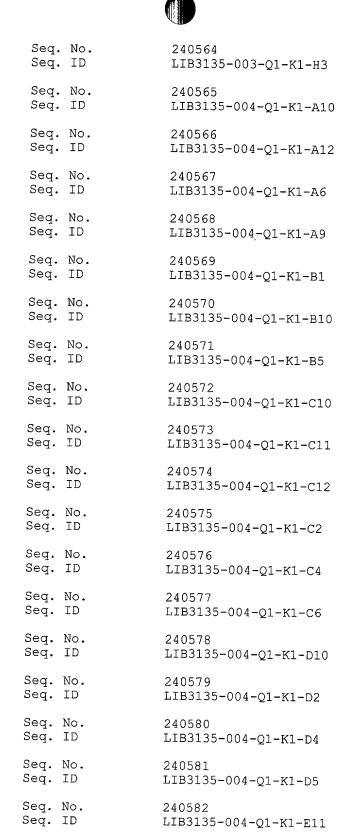
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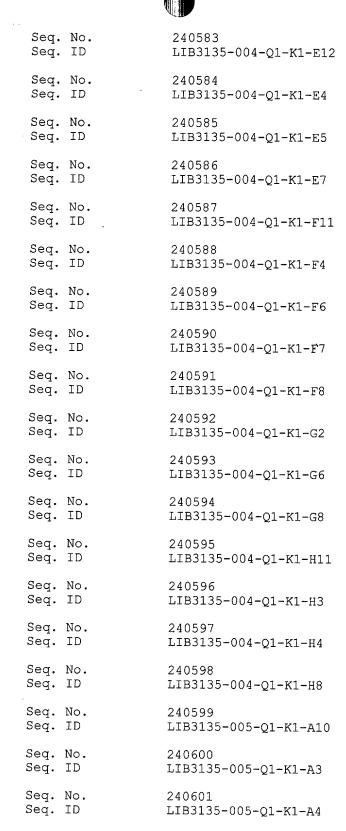
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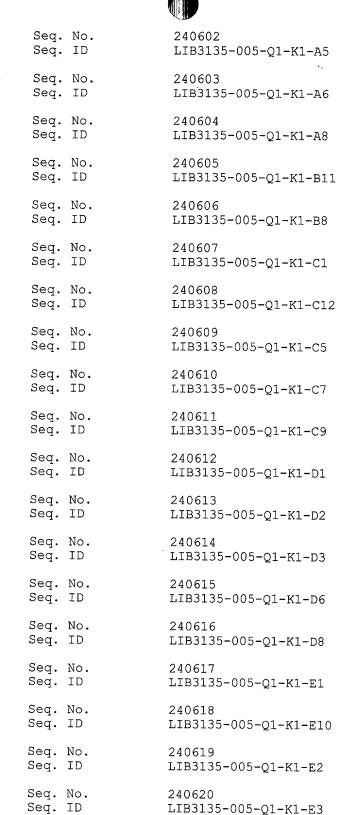
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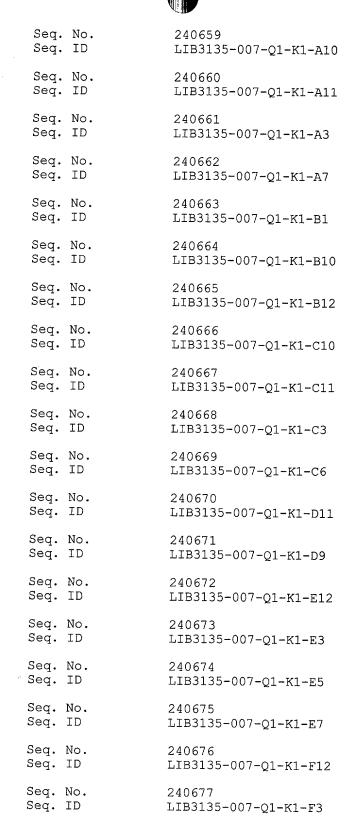


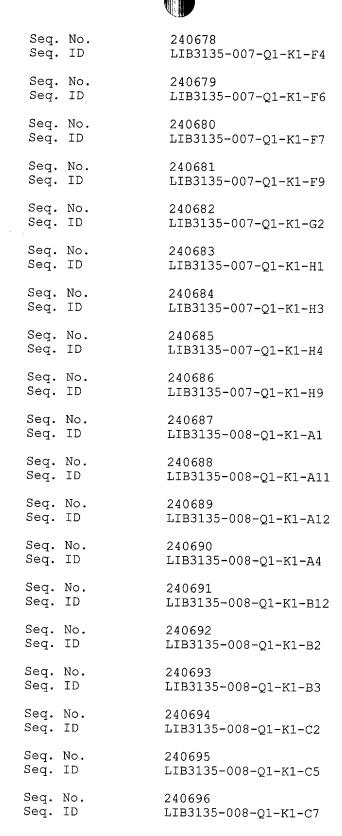


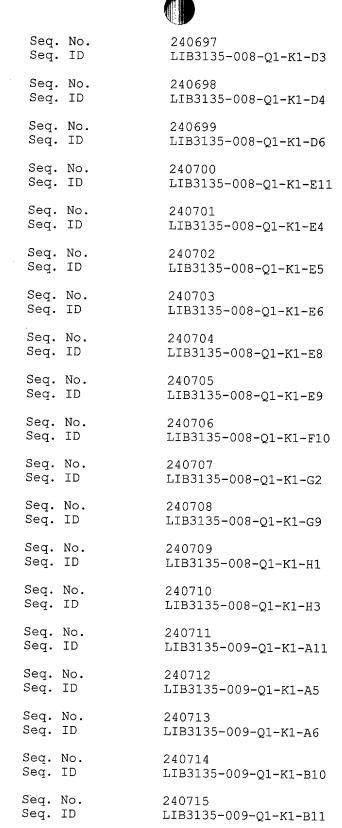
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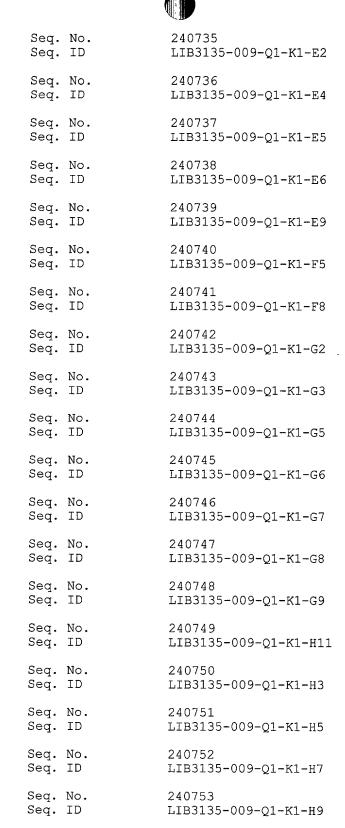
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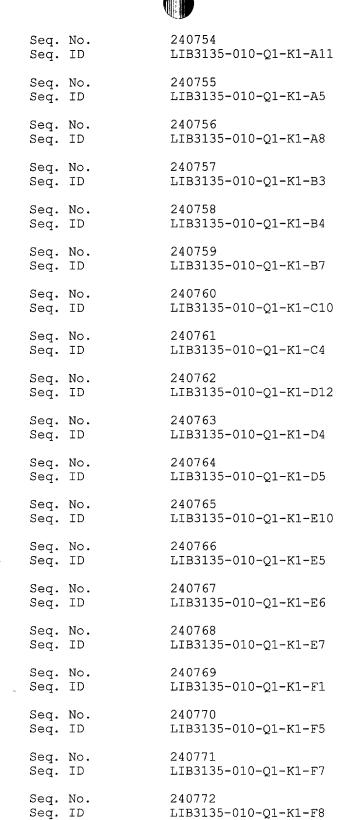




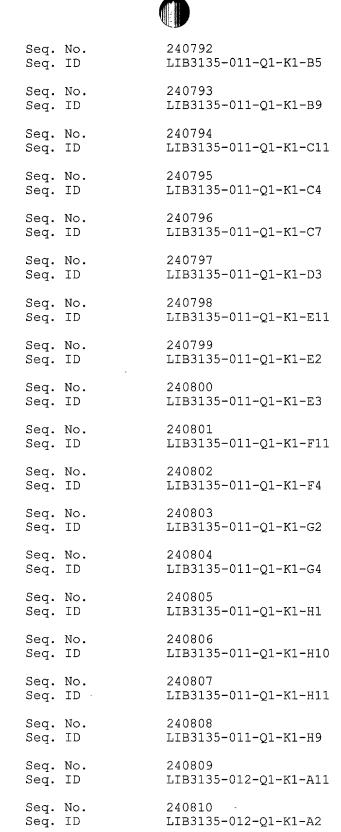


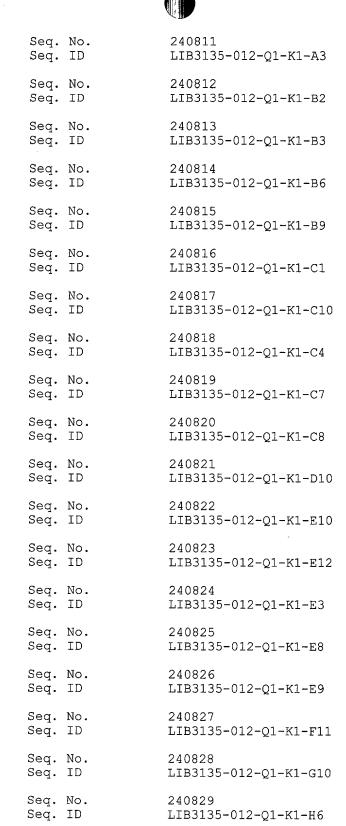
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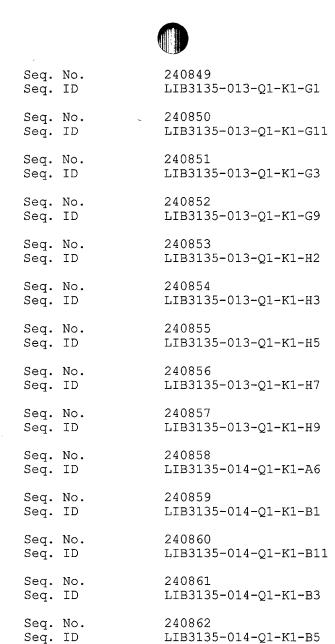
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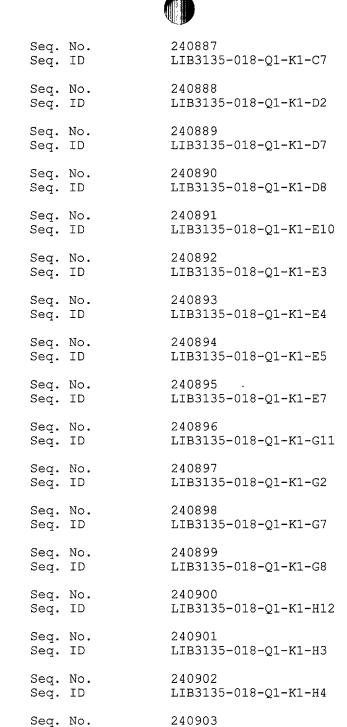
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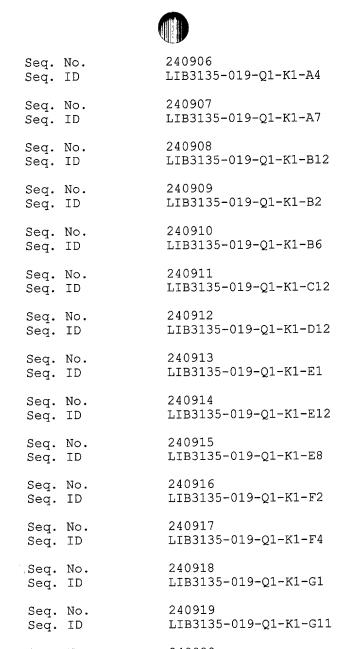
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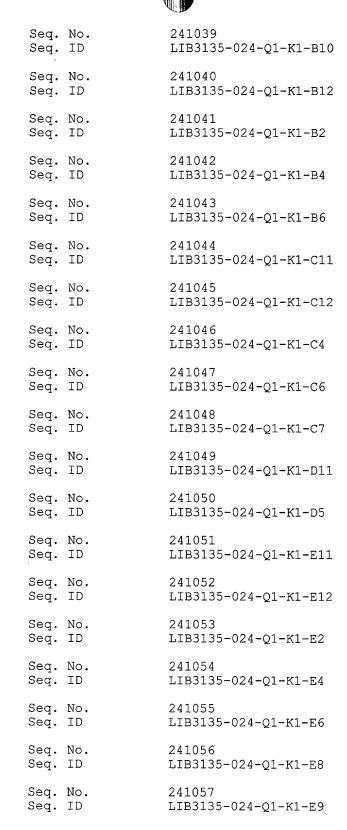


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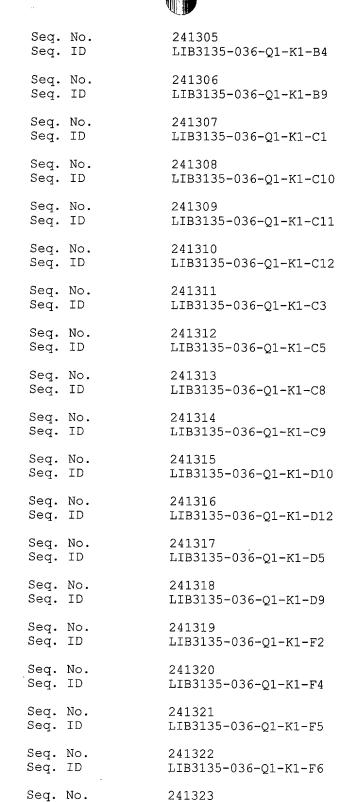


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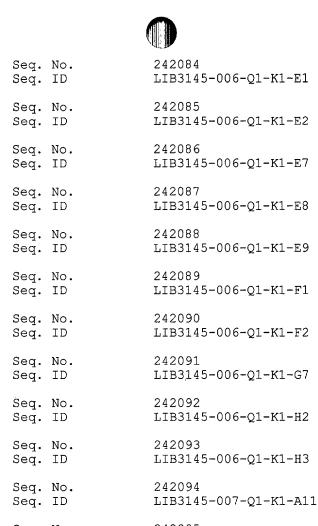
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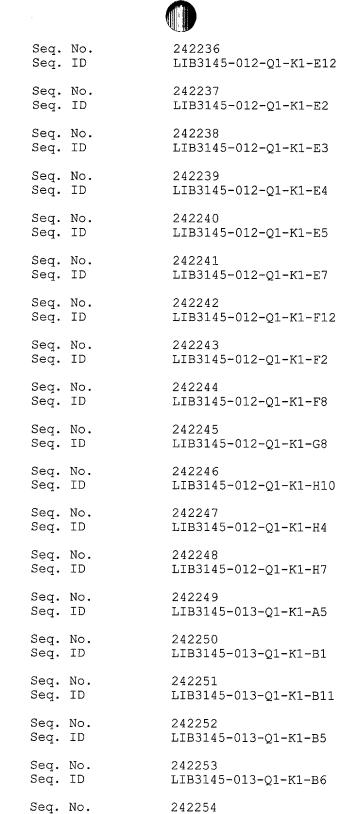


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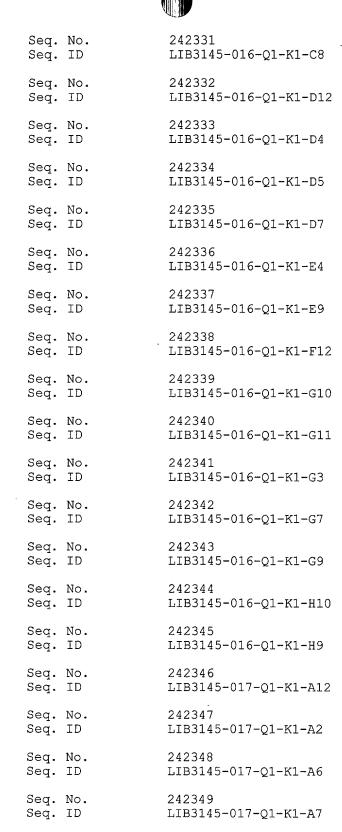
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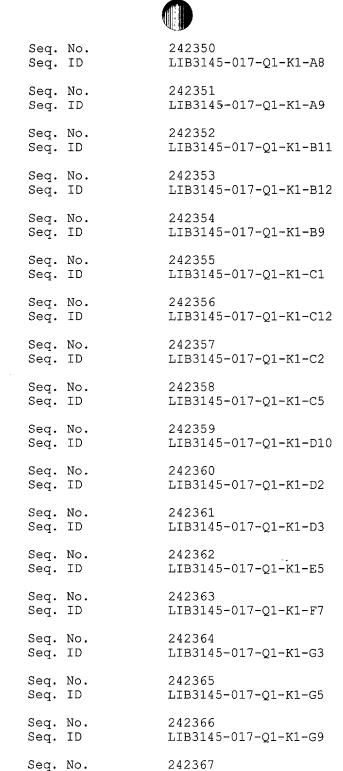
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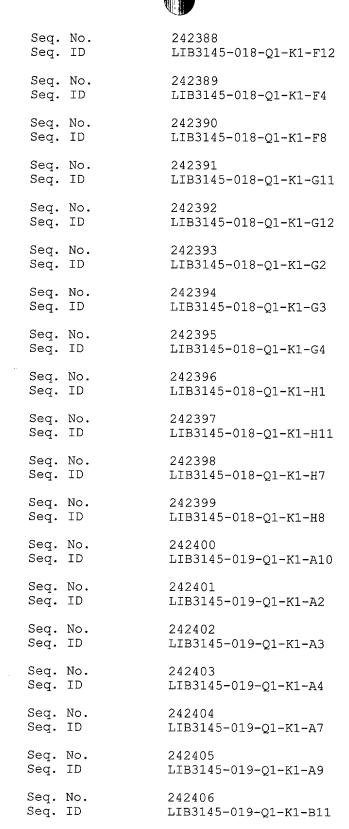


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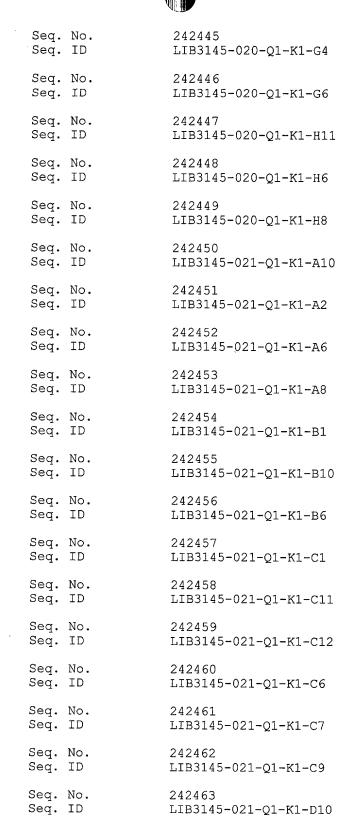
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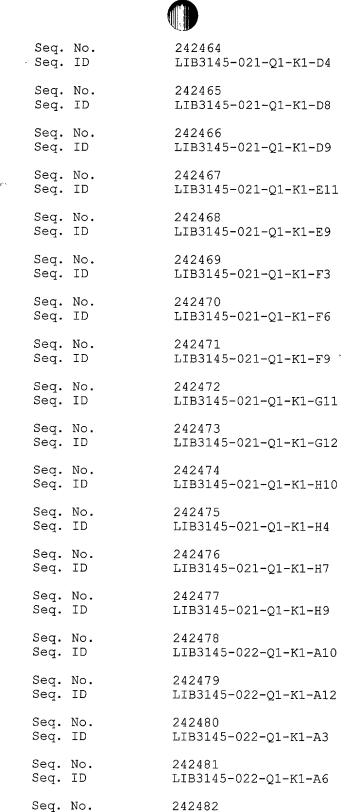


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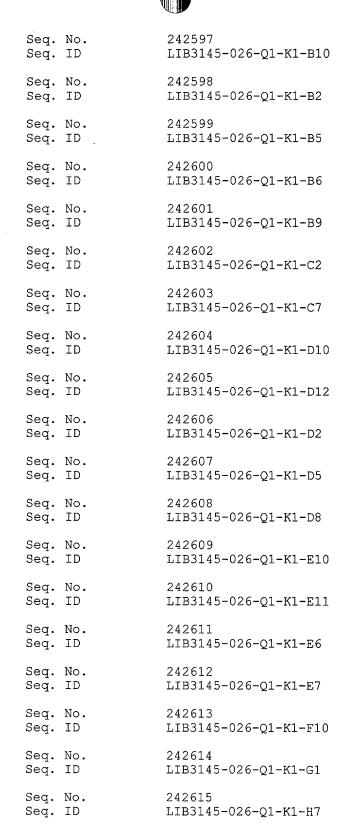
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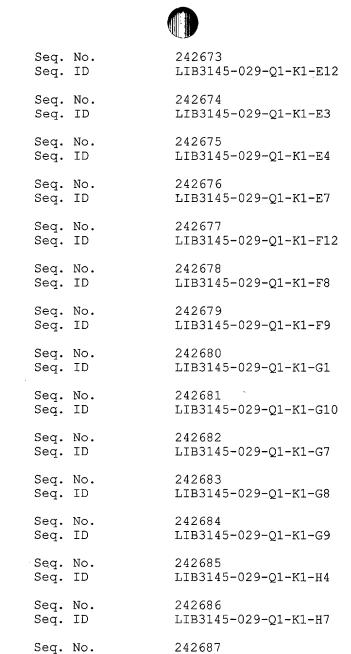


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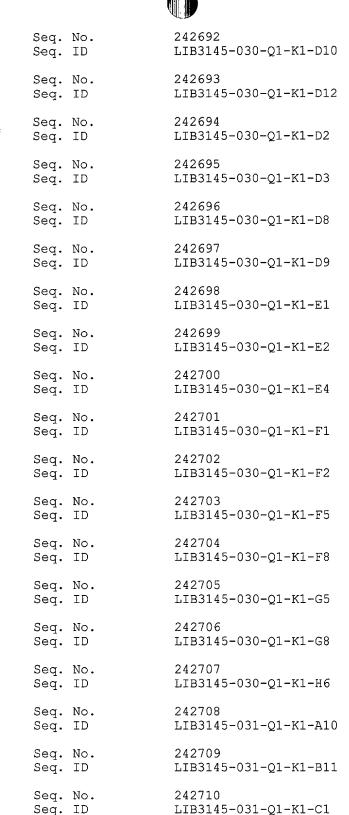
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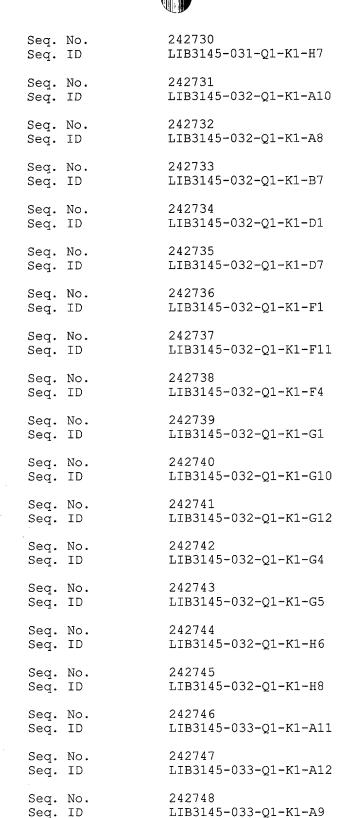
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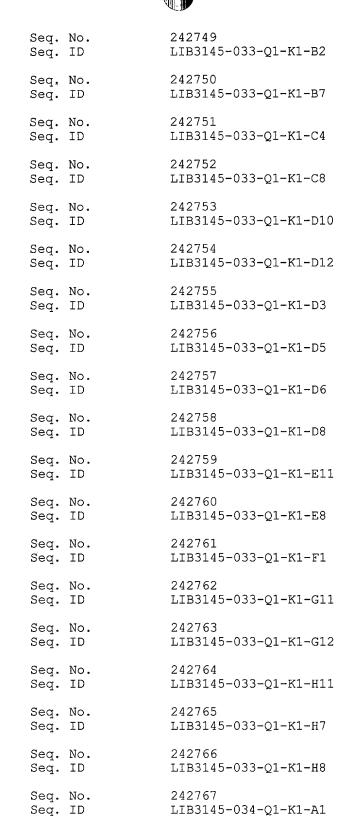
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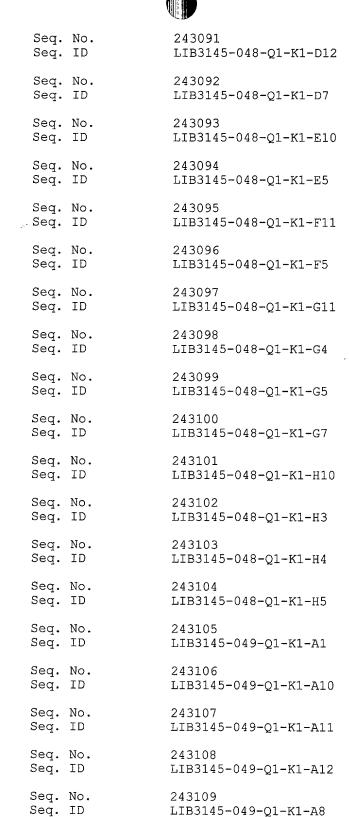
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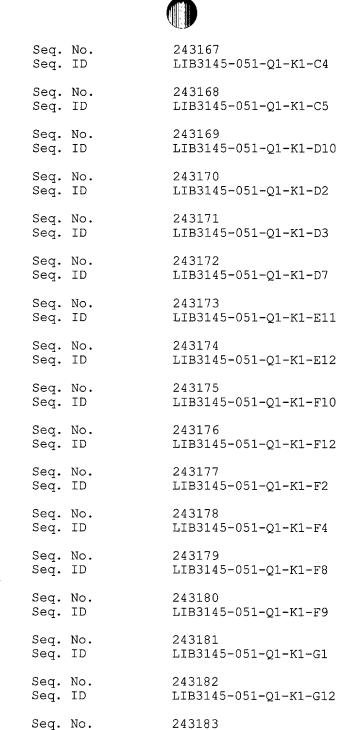
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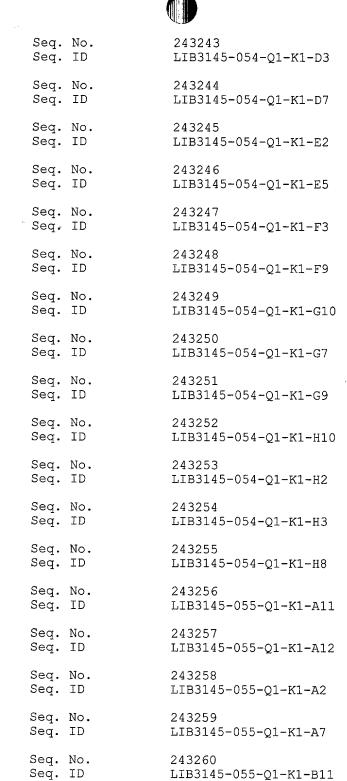


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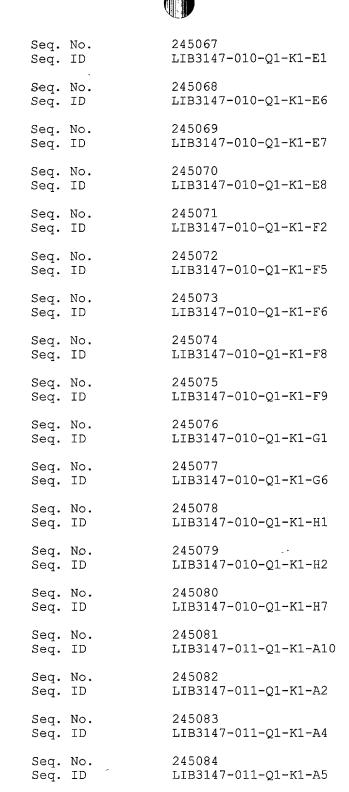
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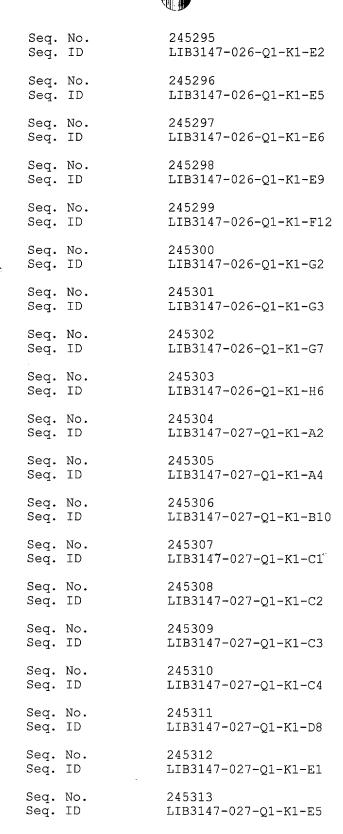
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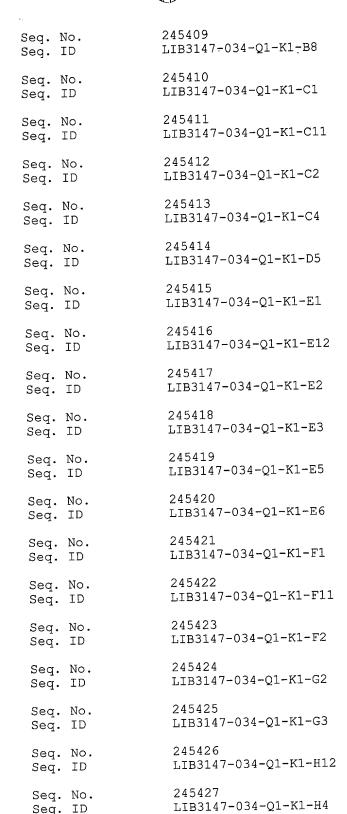


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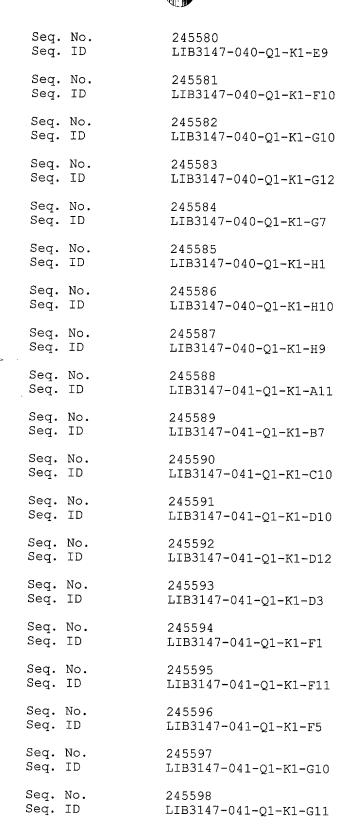
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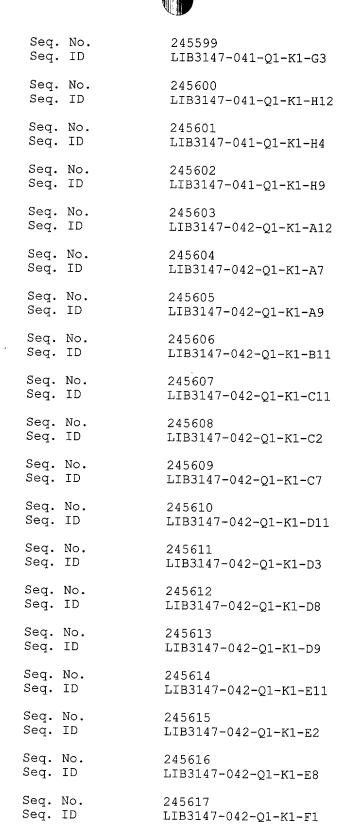


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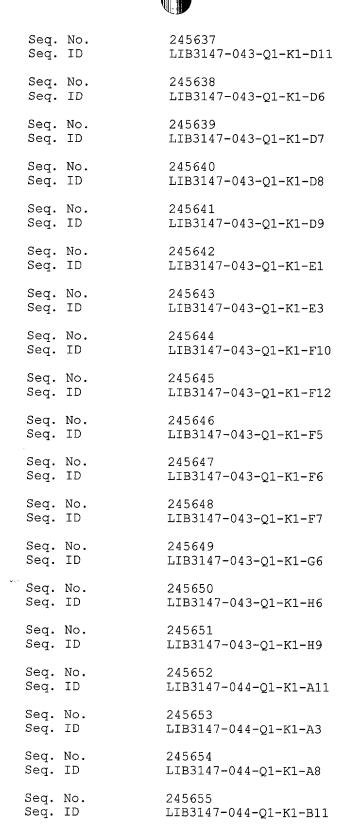


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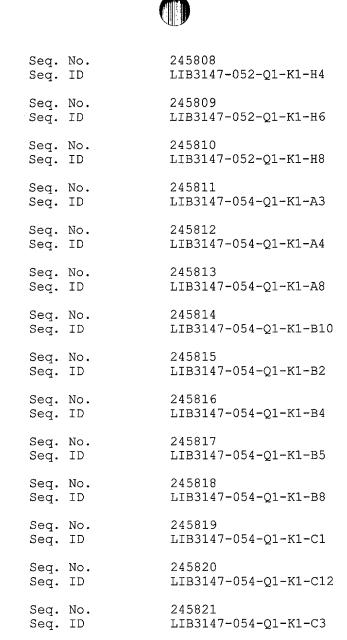
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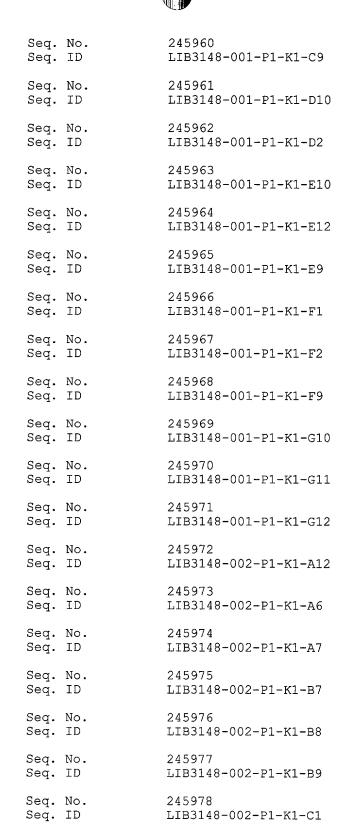
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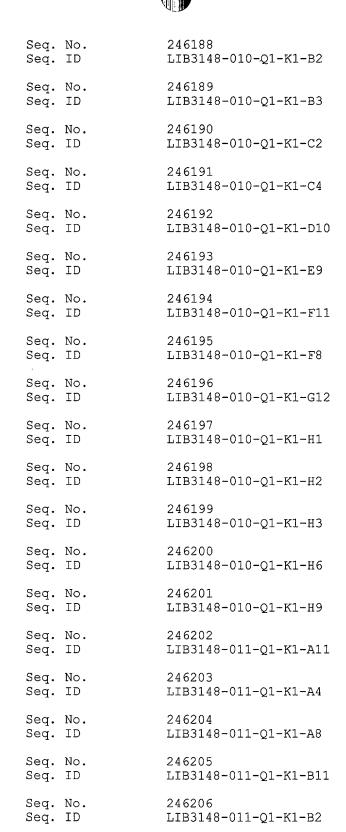
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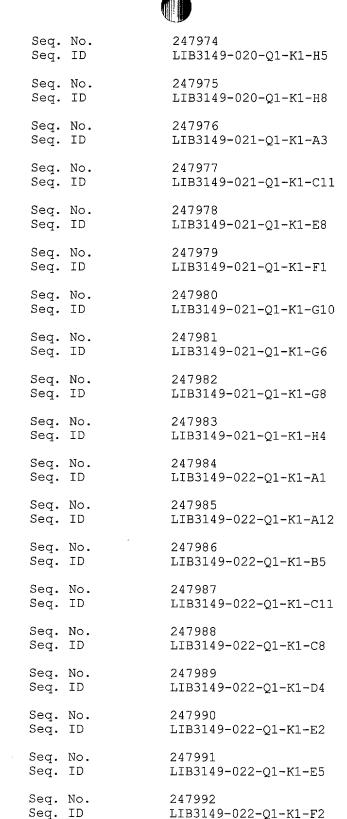
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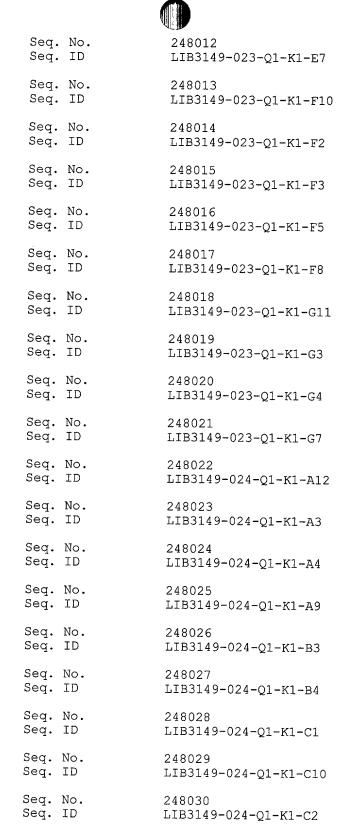
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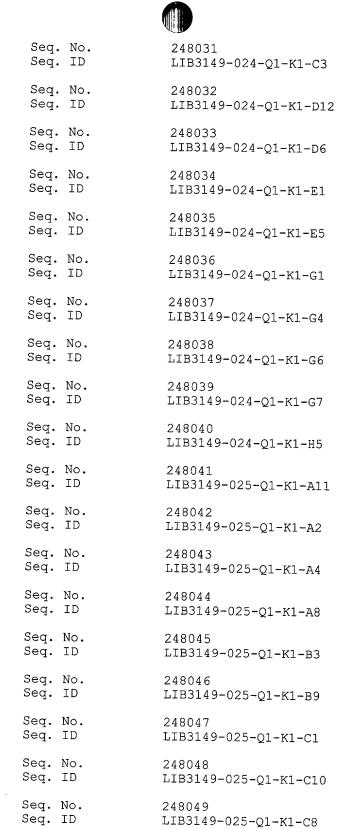


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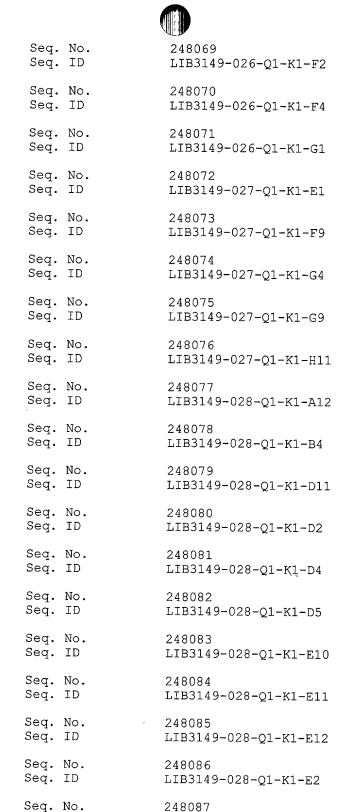
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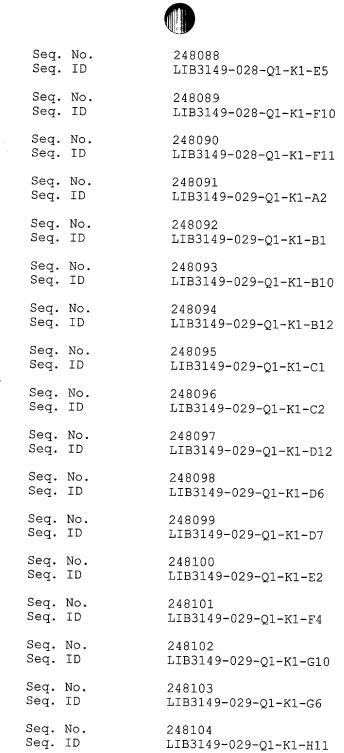
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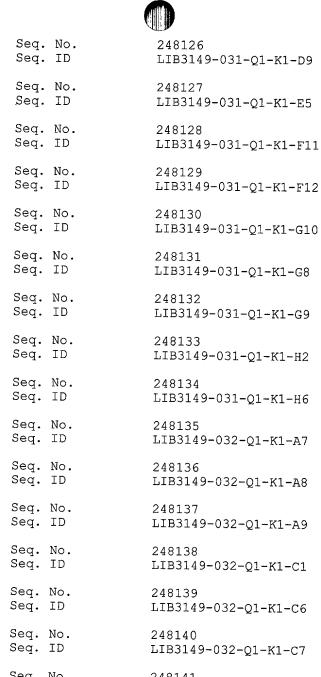
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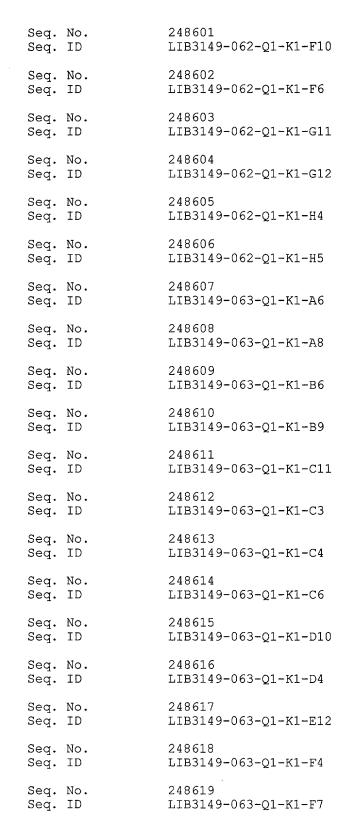
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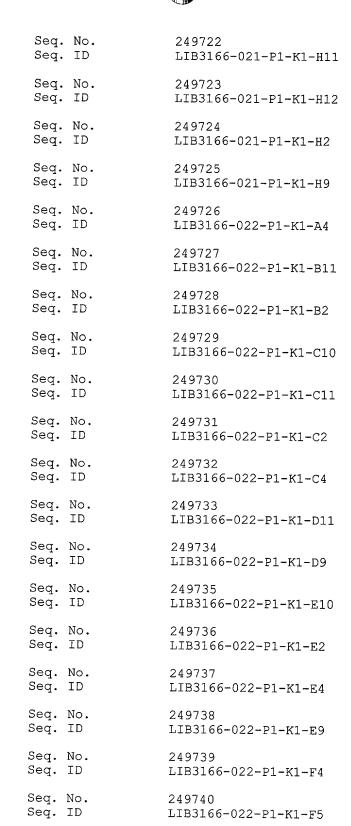
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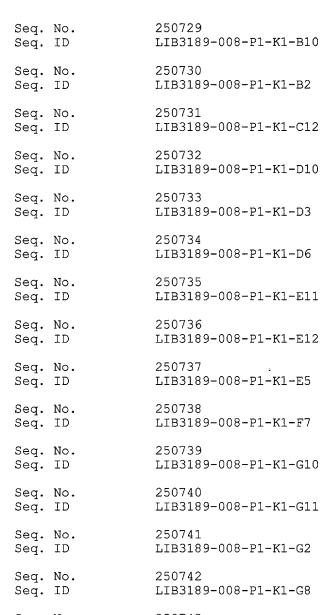
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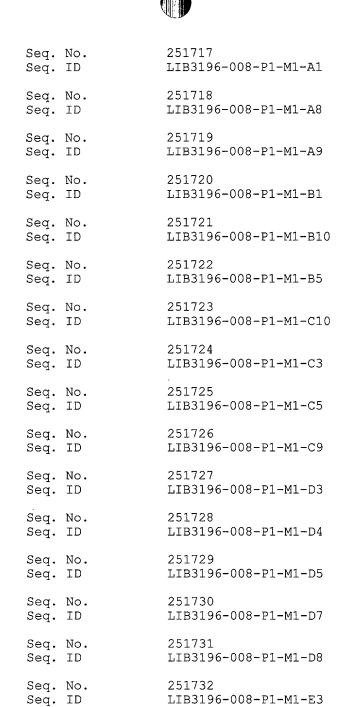
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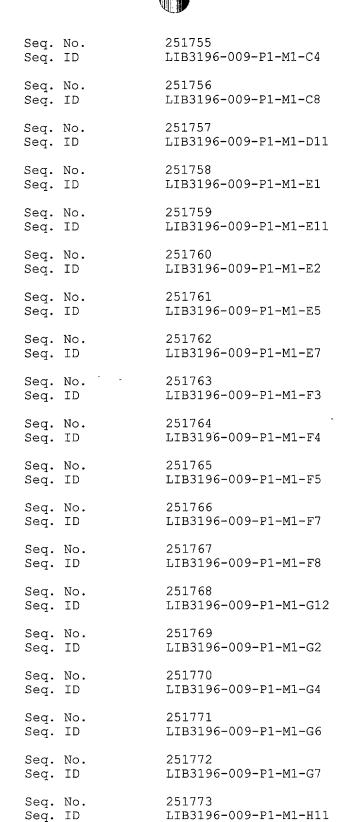
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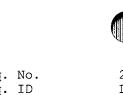
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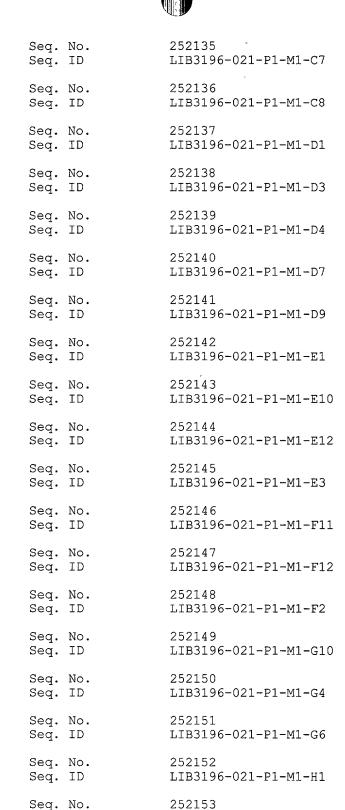


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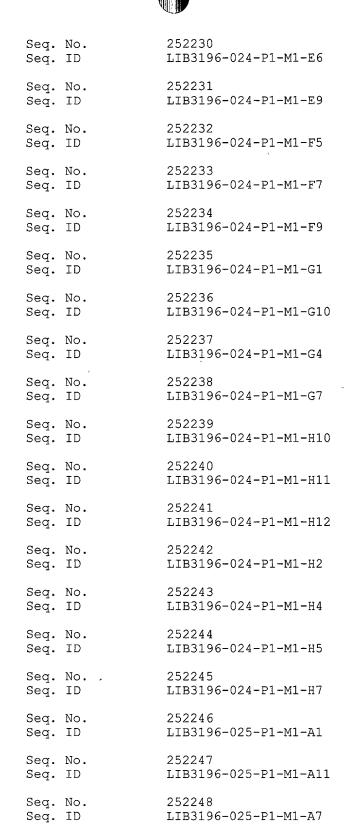
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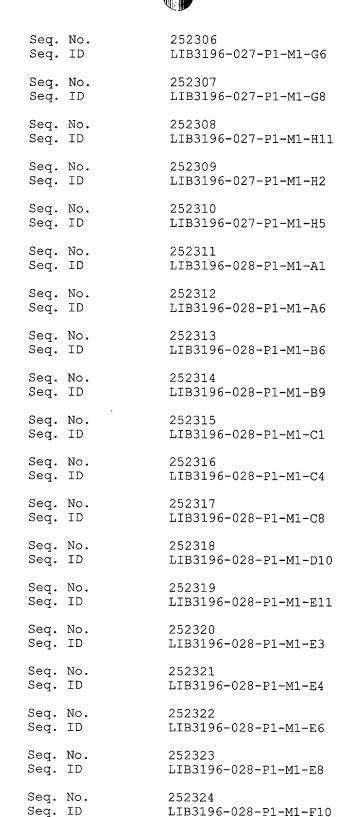
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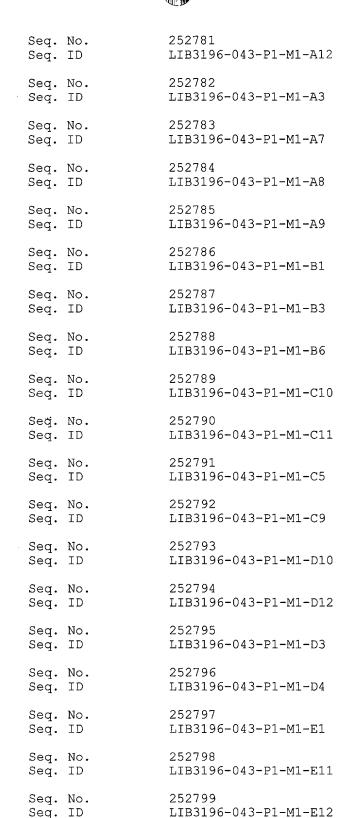
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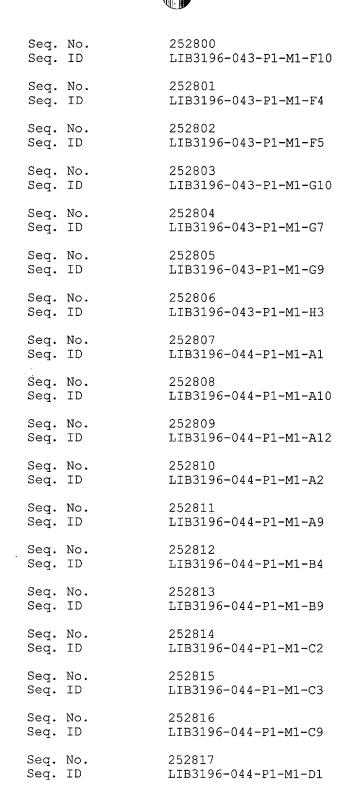


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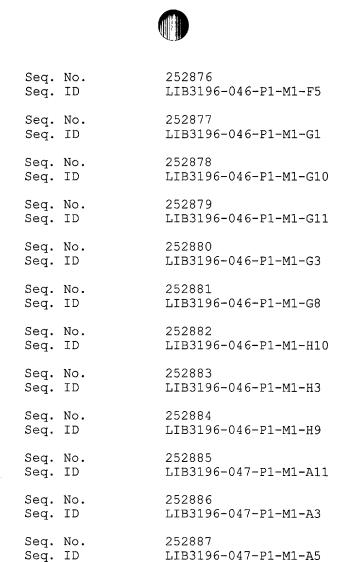
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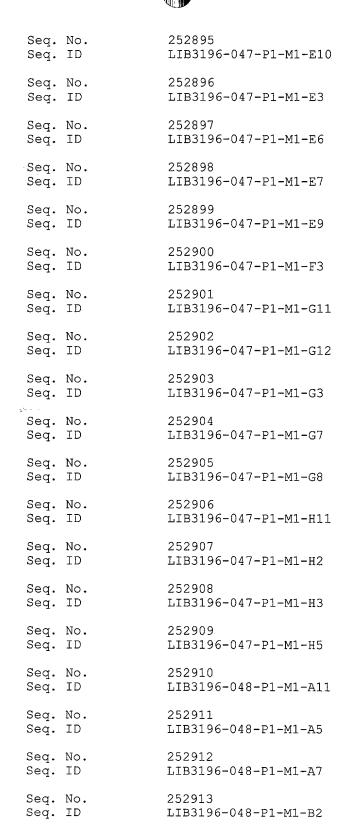
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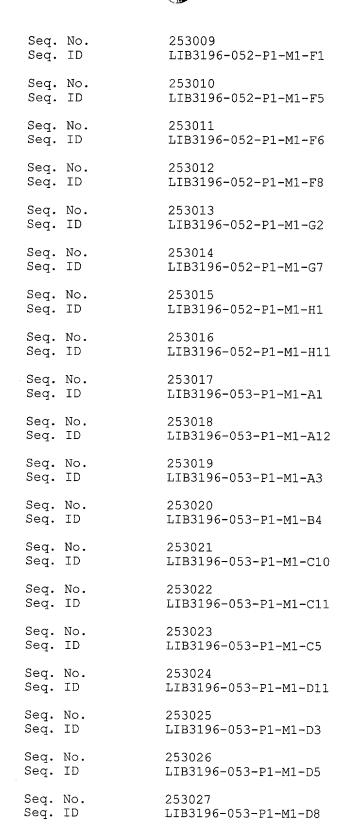
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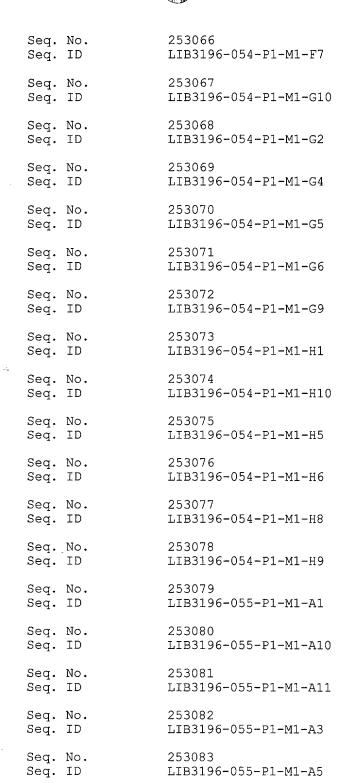


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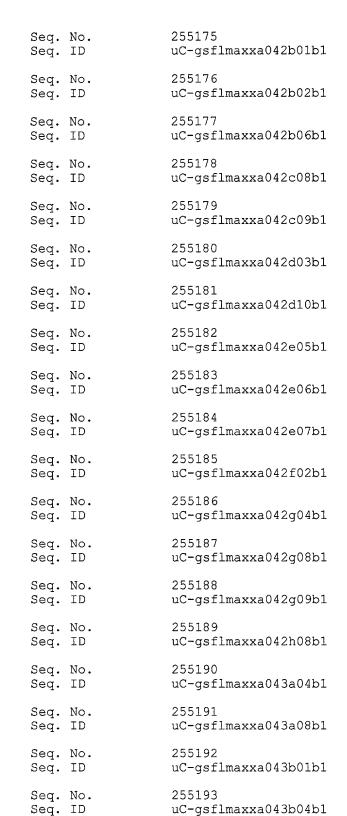
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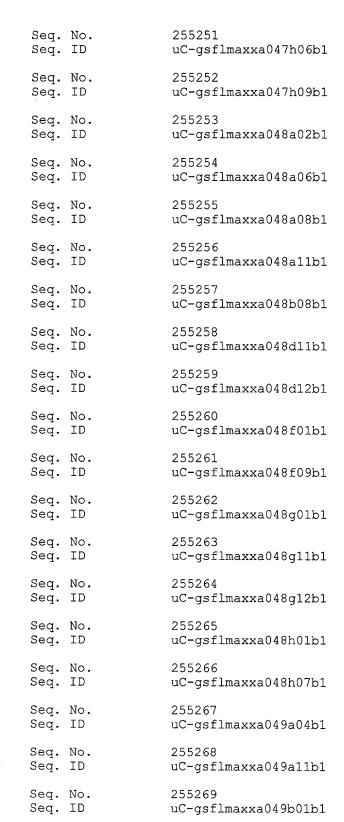
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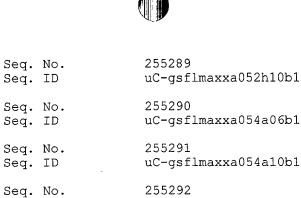


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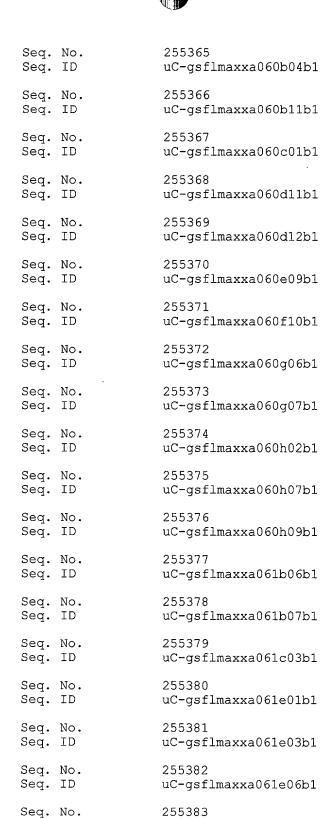


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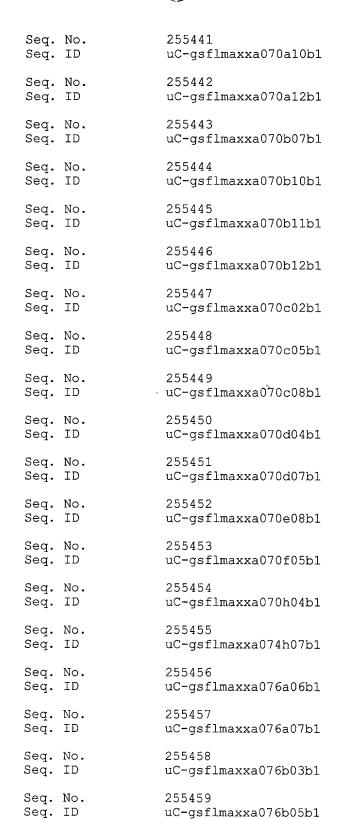
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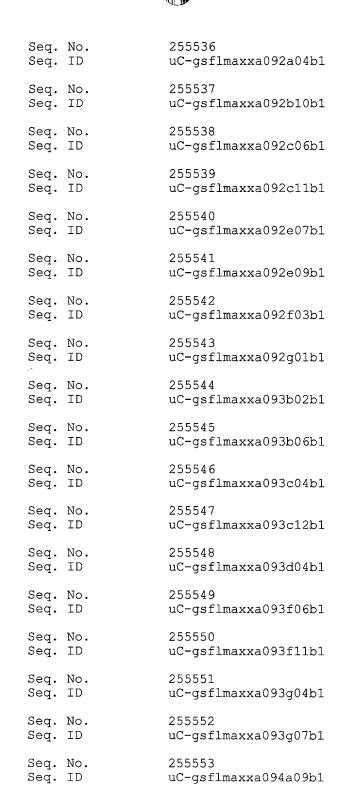


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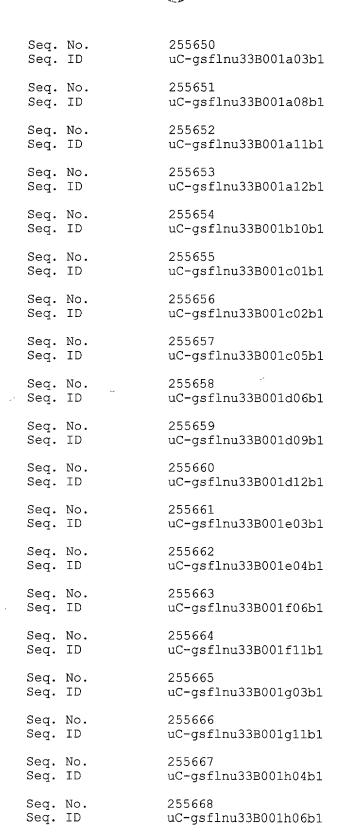


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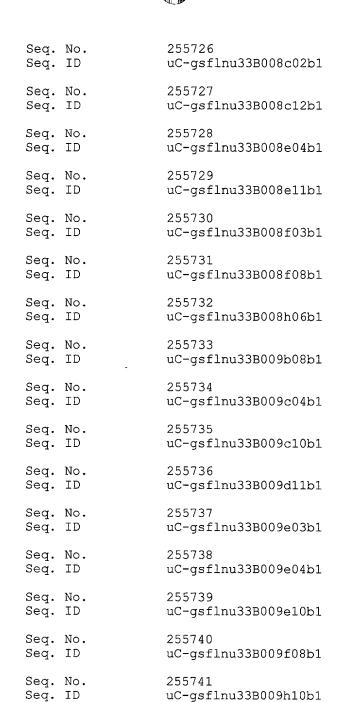
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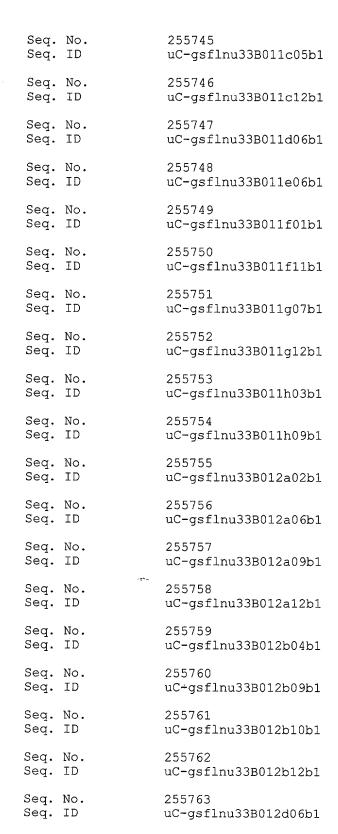
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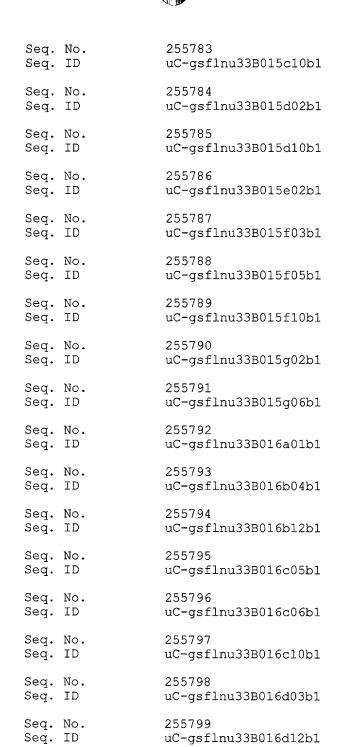
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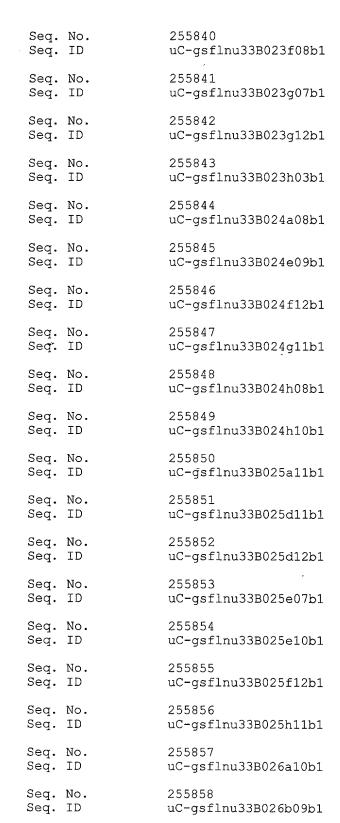
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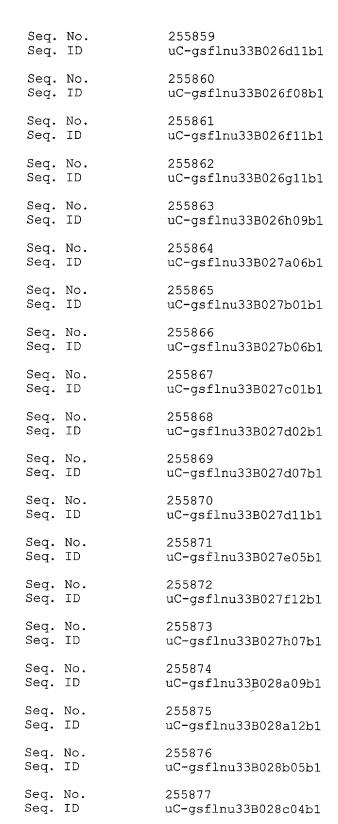
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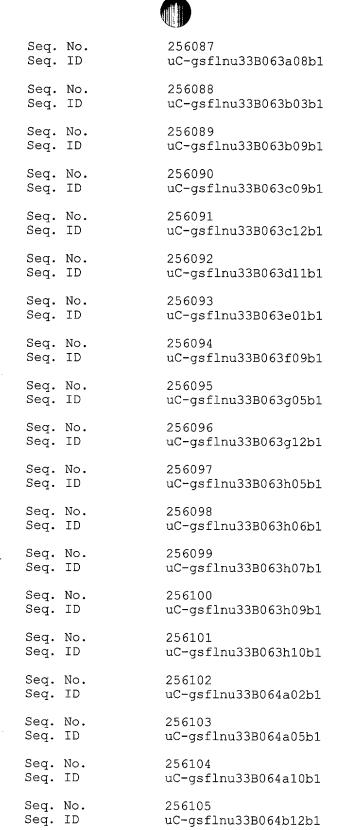
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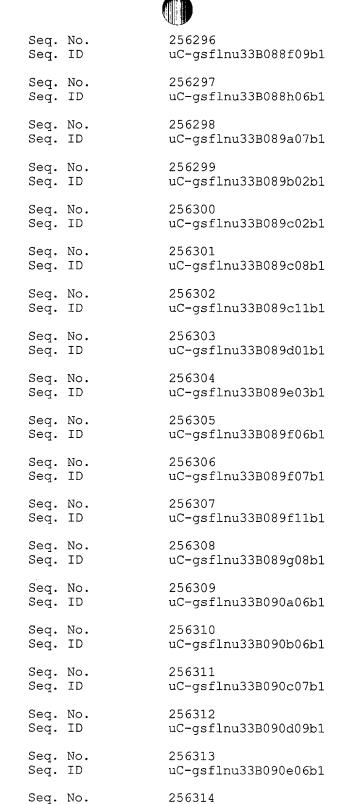


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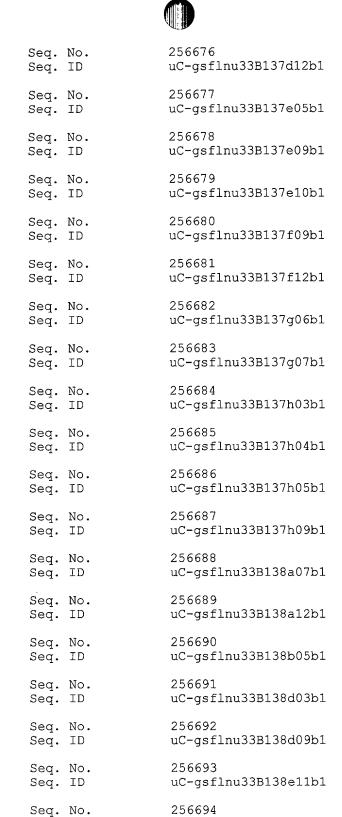


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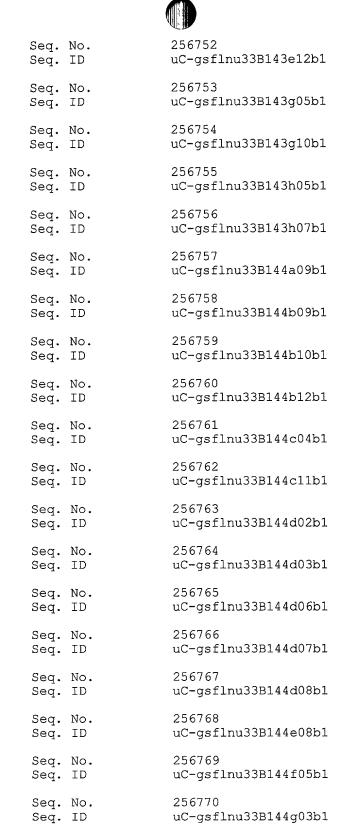
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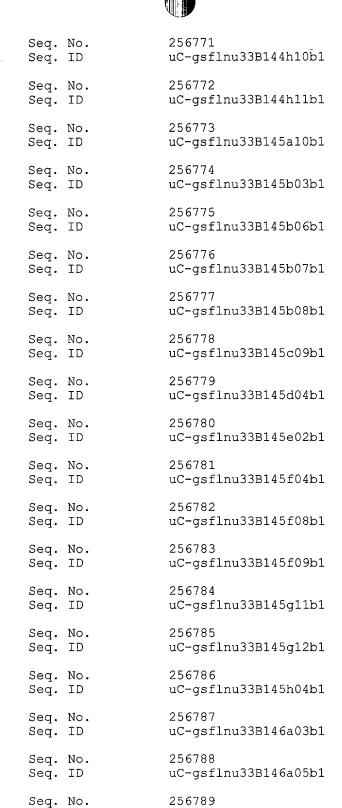


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Seq. No.	258085
Seq. ID	uC-gsronu33b025a10b1
Seq. No.	258086
Seq. ID	uC-gsronu33b025b02b1
Seq. No.	258087
Seq. ID	uC-gsronu33b025b03b1
Seq. No.	258088
Seq. ID	uC-gsronu33b025c06b1
Seq. No.	258089
Seq. ID	uC-ggronu33b025c07b1
Seq. No.	258090
Seq. ID	uC-gsronu33b025c12b1
Seq. No.	258091
Seq. ID	uC-gsronu33b025d01b1
Seq. No.	258092
Seq. ID	uC-gsronu33b025d04b1
Seq. No.	258093
Seq. ID	uC-gsronu33b025d07b1
Seq. No.	258094
Seq. ID	uC-gsronu33b025e06b1
Seq. No.	258095
Seq. ID	uC-gsronu33b025g05b1
Seq. No.	258096
Seq. ID	uC-gsronu33b025h04b1
Seq. No.	258097
Seq. ID	uC-gsronu33b025h05b1
Seq. No.	258098
Seq. ID	uC-gsronu33b112a01b1
Seq. No.	258099
Seq. ID	uC-gsronu33b112a06b1
Seq. No.	258100
Seq. ID	uC-gsronu33b112a08b1

Method

NCBI GI

BLASTX

q733454



```
Seq. No.
Seq. ID
                  uC-gsronu33b112b05b1
Seq. No.
                  258102
Seq. ID
                  uC-gsronu33b112c01b1
Seq. No.
                  258103
Seq. ID
                  uC-gsronu33b112c08b1
Seq. No.
                  258104
Seq. ID
                  uC-gsronu33b112d04b1
Seq. No.
                  258105
Seq. ID
                  uC-gsronu33b112f07b1
Seq. No.
                  258106
Seq. ID
                  uC-gsronu33b112g05b1
Seq. No.
                  258107
Seq. ID
                  uC-gsronu33b112h03b1
Seq. No.
                  258108
Seq. ID
                  uC-gsronu33b112h09b1
Zea mays
                  258109
Seq. No.
Contig ID
                  0 1.R1011
5'-most EST
                  >700042206.seq FL
Method
                  BLASTX
NCBI GI
                  g1488255
BLAST score
                  729
E value
                  5.0e-77
Match length
                  215
% identity
                  64
NCBI Description (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
                  >gi 2961381 emb CAA18128 (AL022141) ferulate-5-hydroxylase
                  (FAH1) [Arabidopsis thaliana] >gi 3925365 (AF068574)
                  ferulate-5-hydroxylase [Arabidopsis thaliana]
Seq. No.
                  258110
Contig ID
                  1 1.R1011
5'-most EST
                  LIB3078-038-Q1-K1-D7
Method
                 BLASTX
NCBI GI
                  g733456
BLAST score
                 1297
E value
                  1.0e-143
Match length
                  283
% identity
                  89
NCBI Description (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
                  258111
Seq. No.
Contig ID
                  1 4:R1011
5'-most EST
                  uC-zmflb73121g05a1
```



```
BLAST score
                   487
                   5.0e-49
E value
                   95
Match length
                   99
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   258112
Seq. No.
Contig ID
                   1 7.R1011
                   clt700041973.f1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q733454
BLAST score
                   696
                   2.0e-73
E value
Match length
                   158
% identity
                   85
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                   258113
                   1_8.R1011
Contig ID
                   fwa700098876.hl
5'-most EST
Method
                   BLASTX
NCBI GI
                   q733454
BLAST score
                   182
E value
                   9.0e-14°
                   38
Match length
                   100
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   258114
Seq. No.
Contig ID
                   2 1.R1011
5'-most EST
                   700087981H1.FSEQ_FL
Method
                   BLASTX
NCBI GI
                   g1518540
BLAST score
                   2312
E value
                   0.0e + 00
                   480
Match length
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   258115
Seq. No.
Contig ID
                   2 2.R1011
5'-most EST
                   700336783SEQ_FL
Method
                   BLASTX
NCBI GI
                   q1518540
BLAST score
                   2007
                   0.0e + 00
E value
Match length
                   428
                   92
% identity
```

NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max]

258116 Seq. No. 2 3.R1011 Contig ID

LIB3150-075-P1-N1-E6 5'-most EST

Method BLASTX



NCBI GI q1518540 BLAST score 2106 E value 0.0e+00Match length 459 % identity 88 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max] Seq. No. 258117 2 5.R1011 Contig ID 5'-most EST LIB3078-024-Q1-K1-B2 Method BLASTX NCBI GI g1518540 BLAST score 529 E value 8.0e-54 107 Match length % identity 89 NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max] Seq. No. 258118 Contig ID 2 6.R1011 5'-most EST xsy700211447.h1 Method BLASTX NCBI GI q1518540 BLAST score 464 E value 2.0e-46 Match length 98 % identity 9₽. NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max] Seq. No. 258119 2 7.R1011 Contig ID 5'-most EST LIB3066-013-Q1-K1-A11 Method BLASTX NCBI GI q1518540 BLAST score 504 4.0e-57 E value 136 Match length 85 % identity NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max] Seq. No. 258120 2 9.R1011 Contig ID LIB148-029-Q1-E1-C6 5'-most EST Method BLASTX NCBI GI q1518540 BLAST score 159 E value 1.0e-10 Match length 44 % identity NCBI Description (U53418) UDP-glucose dehydrogenase [Glycine max] 258121 Seq. No. Contig ID 3 1.R1011

5'-most EST xjt700093178.h1 BLASTX

Method q2827143 NCBI GI BLAST score 3361

```
E value
                   0.0e+00
Match length
                  816
% identity
                  77
NCBI Description (AF027174) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                  258122
Contig ID
                  3 2.R1011
5'-most EST
                  700210175H1.SEQ_FL
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  2442
E value
                  0.0e + 00
Match length
                  548
% identity
                  83
NCBI Description (AF027174) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                  258123
Contig ID
                  3 3.R1011
5'-most EST
                  LIB3062-041-Q1-K1-D12
Method
                  BLASTX
                  g2827143
NCBI GI
BLAST score
                  2193
E value
                  0.0e + 00
Match length
                  506
% identity
                  81
NCBI Description (AF027174) cellulose synthase catalytic subunit
                  [Arabidopsis thaliana]
                  258124
Seq. No.
Contig ID
                  3 4.R1011
5'-most EST
                  LIB3067-023-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q2827143
BLAST score
                  504
E value
                  6.0e-51
Match length
                  100
% identity
                  91
NCBI Description (AF027174) cellulose synthase catalytic subunit
                  [Arabidopsis thaliana]
Seq. No.
                  258125
Contig ID
                  3 5.R1011
```

5'-most EST uC-zmflmo17310d04a1

Method BLASTX NCBI GI g2827143 BLAST score 323 7.0e-30 E value Match length 64 % identity 89

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Sea. No. 258126 Contig ID 3 6.R1011

5'-most EST uC-zmroteosinte099f03b2

```
Method
                   BLASTX
NCBI GI
                   q1706958
BLAST score
                   503
E value
                   7.0e-51
Match length
                   121
% identity
                   76
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
Seq. No.
                   258127
Contig ID
                   4 1.R1011
5'-most EST
                  uC-zmflb73318a03b1
                   258128
Seq. No.
Contig ID
                   4 2.R1011
5'-most EST
                  pmx700086382.h1
Method
                  BLASTX
NCBI GI
                   q2117937
BLAST score
                   2008
                   0.0e+00
E value
Match length
                   471
% identity
                   83
NCBI Description
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
                   258129
Seq. No.
Contig ID
                   4_3.R1011
                  uC-zmflm017207d05b1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q3107931
BLAST score
                   539
E value
                   1.0e-54
Match length
                   122
% identity
                   86
NCBI Description
                  (AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]
                   258130
Seq. No.
Contig ID
                   6 1.R1011
                  LIB36-009-Q1-E1-H8
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1666173
BLAST score
                   521
                   1.0e-52
E value
Match length
                   153
% identity
                   67
NCBI Description
                  (Y09106) transcription factor [Nicotiana plumbaginifolia]
                   258131
Seq. No.
                   6 2.R1011
                   700167008 FL
                  BLASTX
                   g2982299
```

Contig ID 5'-most EST Method NCBI GI BLAST score 307 E value 9.0e-28 Match length 73

% identity

NCBI Description (AF051234) transcription factor BTF3 homolog [Picea

Seq. No. Contig ID

5'-most EST

## mariana]

```
Seq. No.
                   258132
Contig ID
                   6 3.R1011
5'-most EST
                   xsy700212157.h1
Method
                   BLASTX
NCBI GI
                   q1666173
BLAST score
                   427
E value
                   8.0e-42
Match length
                   93
% identity
NCBI Description
                  (Y09106) transcription factor [Nicotiana plumbaginifolia]
                   258133
Seq. No.
Contig ID
                   6 5.R1011
5'-most EST
                   tfd700574011.h1
                   258134
Seq. No.
Contig ID
                   7 1.R1011
5'-most EST
                   uC-zmflb73076a04b2
Method
                   BLASTX
NCBI GI
                   q3924612
BLAST score
                   1483
E value
                   0.0e + 00
Match length
                   443
% identity
                   76
NCBI Description
                   (AF069442) mitochondrial elongation factor Tu [Arabidopsis
                   thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial
                   elongation factor Tu [Arabidopsis thaliana]
Seq. No.
                   258135
Contig ID
                   7 2.R1011
5'-most EST
                   wyr700236844.h1
Method
                   BLASTX
NCBI GI
                   g1694621
BLAST score
                   1551
E value
                   1.0e-173
Match length
                   461
% identity
                   63
NCBI Description
                  (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
Seq. No.
                   258136
                   7 3.R1011
Contig ID
                   u\overline{C}-zmflmo17099b11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   q4504201
BLAST score
                   663
                   7.0e-69
E value
                   457
Match length
% identity
NCBI Description
                   general transcription factor IIH, polypeptide 4 (52kD
                   subunit) >gi 1514597 emb CAA68870 (Y07595) transcription
                   factor TFIIH [Homo sapiens]
                   258137
```

7 4.R1011

ymt700220389.h1



258138 Seq. No. Contig ID 7 5.R1011

5'-most EST uC-zmflb73305d04a1

BLASTX Method NCBI GI q3924612 BLAST score 253 1.0e-21 E value Match length 59 83 % identity

NCBI Description (AF069442) mitochondrial elongation factor Tu [Arabidopsis

thaliana] >gi\_4263511\_gb\_AAD15337\_ (AC004044) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No. 258139 7 7.R1011 Contig ID

uC-zmflb73273h01a1 5'-most EST

258140 Seq. No. Contig ID 7 10.R1011

uC-zmflmo17312g01b1 5'-most EST

BLASTX Method NCBI GI q3738297 BLAST score 604 E value 2.0e-62 Match length 322 23 % identity

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

258141 Seq. No. 7 11.R1011 Contig ID

 $u\overline{C}-zmflb73040a07b1$ 5'-most EST

Seq. No. 258142 Contig ID 7 12.R1011

5'-most EST LIB143-001-Q1-E1-B9

Method BLASTX NCBI GI g1351651 BLAST score 279 E value 2.0e-24170 Match length 37 % identity

HYPOTHETICAL 43.7 KD PROTEIN C24B11.08C IN CHROMOSOME I NCBI Description

>gi\_2130353\_pir\_\_S62553 hypothetical protein SPAC24B11.08c - fission yeast (Schizosaccharomyces pombe)

>gi 1061296 emb CAA91773 (Z67757) unknown

[Schizosaccharomyces pombe]

258143 Seq. No. Contig ID 7 13.R1011 5'-most EST xyt700343936.h1

258144 Seq. No. Contig ID 7 14.R1011 5'-most EST xsy700213359.h1

Method BLASTX NCBI GI q3360289



BLAST score 291 E value 6.0e-26 Match length 69 % identity 75

NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase

1 [Zea mays]

Seq. No. 258145 Contig ID 7\_16.R1011

5'-most EST LIB3115-017-P1-K1-D5

Method BLASTX
NCBI GI g4581114
BLAST score 302
E value 3.0e-27
Match length 79
% identity 72

NCBI Description (AC005825) putative HesB-like protein; required for

efficient nitrogen fixation in Cyanobacteria [Arabidopsis

thaliana]

Seq. No. 258146 Contig ID 7 17.R1011

5'-most EST  $u\overline{C}$ -zmflmo17324f09a1

Method BLASTN
NCBI GI g12470
BLAST score 85
E value 1.0e-39
Match length 113
% identity 94

NCBI Description Z.mays chloroplast rRNA-operon

 Seq. No.
 258148

 Contig ID
 7\_20.R1011

 5'-most EST
 ymt700219440.h1

Method BLASTX
NCBI GI g3702326
BLAST score 252
E value 3.0e-38
Match length 138
% identity 65

NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No. 258150 Contig ID 7 22.R1011

5'-most EST LIB3078-023-Q1-K1-E2

Seq. No. 258151 Contig ID 7 23.R1011

5'-most EST  $u\overline{C}$ -zmflmo17150e02b1



```
Method
                   BLASTX
NCBI GI
                   g3149952
BLAST score
                   987
E value
                   1.0e-159
Match length
                   350
% identity
                   81
```

NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]

Seq. No. 258152 Contig ID 7 24.R1011 5'-most EST wty700165924.h1

Seq. No. 258153 Contig ID 7 25.R1011

5'-most EST LIB3150-046-Q1-N1-G2

Method BLASTX NCBI GI g4506233 BLAST score 384 E value 1.0e-36 Match length 257 % identity 37

proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 NCBI Description

>gi\_1346766\_sp\_P48556\_PSD8\_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S14 (P31) >gi\_1362741\_pir\_\_S56108 multicatalytic endopeptidase complex (EC 3.4.99.46) regulatory chain 31 human >gi\_1037164\_dbj\_BAA07237\_ (D38047) 26S proteasome subunit p31 [Homo sapiens] >gi\_3702282 (AC005789)

PP31 HUMAN [Homo sapiens]

Seq. No. 258154 Contig ID 7 26.R1011

5'-most EST  $u\overline{C}$ -zmflb73078h10b2

Seq. No. 258155 Contig ID 7 27.R1011 5'-most EST qmh700026529.f1 Method BLASTX NCBI GI g3738297

BLAST score 197 E value 6.0e-15 Match length 63 % identity

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No. 258156 Contig ID 7 28.R1011

5'-most EST LIB3069-033-Q1-K1-H7

Seq. No. 258157 Contig ID 7 29.R1011

5'-most EST LIB3067-038-Q1-K1-H1

Seq. No. 258158 Contig ID 7 30.R1011

5'-most EST LIB3088-001-Q1-K1-E7

Seq. No. 258159



```
Contig ID
                   7 32.R1011
5'-most EST
                   pmx700082907.h1
                   258160
Seq. No.
                   7 33.R1011
Contig ID
5'-most EST
                   uC-zmflmo17128e03b1
Seq. No.
                   258161
Contig ID
                   7 34.R1011
5'-most EST
                  xsy700208454.h1
Method
                   BLASTX
NCBI GI
                   q1351722
BLAST score
                   236
E value
                   3.0e-19
Match length
                   101
% identity
                   46
NCBI Description
                  HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I
                   >gi 1122371 emb CAA92386 (Z68198) hypothetical protein
                   [Schizosaccharomyces pombe]
Seq. No.
                   258162
Contig ID
                   7 35.R1011
5'-most EST
                  uC-zmflb73022h04b1
Method
                  BLASTX
NCBI GI
                  q3738297
BLAST score
                   425
E value
                  9.0e-42
Match length
                  143
                   28
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  258163
Contig ID
                  7 38.R1011
5'-most EST
                  LIB3136-050-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  q4432857
BLAST score
                  273
E value
                  1.0e-23
Match length
                  103
% identity
                   48
NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  258164
Contig ID
                  7 39.R1011
5'-most EST
                  LIB3159-017-Q1-K1-G10
Method
                  BLASTX
NCBI GI
                  g1694621
BLAST score
                  642
E value
                  6.0e-67
Match length
                  174
% identity
                  72
NCBI Description (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.]
```

Seq. No. 258165 Contig ID 7\_40.R1011 5'-most EST wty700167141.h1

Method BLASTX



NCBI GI q3157941 BLAST score 281 E value 7.0e-25 Match length 101 % identity 49

NCBI Description (AC002131) Contains similarity to hypothetical protein

gb U95973 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 258166 Contig ID 7 42.R1011

5'-most EST uC-zmflmo17220f05b1

Seq. No. 258167 Contig ID 7 43.R1011

5'-most EST LIB3150-035-Q1-N1-B12

Method BLASTX NCBI GI g4506233 BLAST score 354 E value 4.0e-33 Match length 206 % identity 39

proteasome (prosome, macropain) 26S subunit, non-ATPase, 8 NCBI Description

>gi\_1346766\_sp\_P48556\_PSD8\_HUMAN 26S PROTEASOME REGULATORY SUBUNIT S14 (P31) >gi\_1362741\_pir\_\_S56108 multicatalytic endopeptidase complex (EC 3.4.99.46) regulatory chain 31 human >gi\_1037164\_dbj\_BAA07237 (D38047) 26S proteasome subunit p31 [Homo sapiens] >gi\_3702282 (AC005789)

PP31\_HUMAN [Homo sapiens]

Seq. No. 258168 7 44.R1011 Contig ID

5'-most EST LIB189-023-Q1-E1-A9

Seq. No. 258169 Contig ID 7 45.R1011

5'-most EST uC-zmroteosinte070b07b1

Method BLASTX NCBI GI g1351722 BLAST score 162 E value 6.0e-11 Match length 175 % identity 30

NCBI Description HYPOTHETICAL 29.7 KD PROTEIN C18G6.06 IN CHROMOSOME I

>gi\_1122371\_emb\_CAA92386\_ (Z68198) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 258170 Contig ID 7 46.R1011

5'-most EST LIB3067-025-Q1-K1-E6

Method BLASTX NCBI GI q3702326 BLAST score 474 E value 3.0e-47Match length 98 % identity

NCBI Description (AC005397) hypothetical protein [Arabidopsis thaliana]



Seq. No. 258171
Contig ID 7 47.R1011

5'-most EST  $u\overline{C}$ -zmrob73004g08b1

Method BLASTX
NCBI GI g3738297
BLAST score 184
E value 1.0e-13
Match length 53
% identity 64

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

 Seq. No.
 258172

 Contig ID
 7\_48.R1011

 5'-most EST
 uC-zmflmo17h11b1

Seq. No. 258173 Contig ID 7 49.R1011

5'-most EST LIB148-045-Q1-E1-D8

5'-most EST LĪB3067-007-Q1-K1-G7

Seq. No. 258175 Contig ID 7\_56.R1011

5'-most EST LIB143-042-Q1-E1-F6

Method BLASTX
NCBI GI g3149952
BLAST score 253
E value 1.0e-21
Match length 55
% identity 87

NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]

Seq. No. 258176 Contig ID 7 58.R1011

5'-most EST LIB3180-022-P2-M1-A10

Method BLASTX
NCBI GI g2494125
BLAST score 421
E value 8.0e-51
Match length 200
% identity 57

NCBI Description (AC002376) Strong similarity to Cucumis acetyl-CoA acyltransferase (gb\_D70895). [Arabidopsis thaliana]

Seq. No. 258177 Contig ID 7 59.R1011

5'-most EST LIB3150-100-P1-N1-A11

Seq. No. 258178 Contig ID 7\_61.R1011

5'-most EST uC-zmflmo17179a04a1

Seq. No. 258179 Contig ID 7\_62.R1011 5'-most EST tfd700575223.h1

E value

Match length

% identity

5.0e-85

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

284

56

```
Seq. No.
                   258180
Contig ID
                   7 63.R1011
5'-most EST
                   xjt700096568.hl
Method
                   BLASTX
NCBI GI
                   q3149952
BLAST score
                   340
E value
                   6.0e-32
Match length
                   107
% identity
                   62
NCBI Description (AB010259) DRH1 [Arabidopsis thaliana]
Seq. No.
                   258181
Contig ID
                   7 66.R1011
5'-most EST
                   nbm700476596.h1
Seq. No.
                   258182
Contig ID
                   7 68.R1011
5'-most EST
                   pwr700448842.h1
Seq. No.
                   258183
Contig ID
                   7 76.R1011
5'-most EST
                   pmx700091114.h1
                   258184
Seq. No.
Contig ID
                   9 1.R1011
5'-most EST
                   700193495 FL
Method
                   BLASTX
NCBI GI
                   g862644
BLAST score
                   246
E value
                   2.0e-20
Match length
                   133
                   47
% identity
NCBI Description (U20184) MADS-box protein AGL14 [Arabidopsis thaliana]
Seq. No.
                   258185
                   9 3.R1011
Contig ID
5'-most EST
                   u\overline{C}-zmflmo17066b05b1
Method
                   BLASTX
NCBI GI
                   g3759184
BLAST score
                   166
E value
                   2.0e-11
                   77
Match length
% identity
                   39
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   258186
                   9 4.R1011
Contig ID
5'-most EST
                   LIB3136-060-Q1-K1-E4
Method
                   BLASTX
NCBI GI
                   q3759184
BLAST score
                   663
```



 Seq. No.
 258187

 Contig ID
 9\_5.R1011

 5'-most EST
 hvj700621362.h1

Method BLASTN
NCBI GI g169818
BLAST score 100
E value 1.0e-48
Match length 124
% identity 95

NCBI Description Rice 25S ribosomal RNA gene

5'-most EST  $u\overline{C}$ -zmflmo17060g07a1

Method BLASTX
NCBI GI g3759184
BLAST score 305
E value 7.0e-28
Match length 74
% identity 74

NCBI Description (AB018441) phi-1 [Nicotiana tabacum]

Seq. No. 258189 Contig ID 9 7.R1011

5'-most EST LIB3088-008-Q1-K1-D6

Seq. No. 258190 Contig ID 9 8.R1011

5'-most EST LIB3066-033-Q1-K1-F10

Seq. No. 258191 Contig ID 9 9.R1011

5'-most EST uC-zmflb73110b09a1

Method BLASTN
NCBI GI g169818
BLAST score 335
E value 0.0e+00
Match length 391
% identity 96

NCBI Description Rice 25S ribosomal RNA gene

 Seq. No.
 258192

 Contig ID
 9\_10.R1011

5'-most EST LĪB3067-053-Q1-K1-D10

 Seq. No.
 258193

 Contig ID
 9\_11.R1011

 5'-most EST
 xsy700209434.h1

Method BLASTX
NCBI GI g1351222
BLAST score 1376
E value 1.0e-153
Match length 312

```
% identity
 NCBI Description
                    TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi 945087
                    (U31097) transcription factor TFIIB [Glycine max]
 Seq. No.
                    258195
 Contig ID
                    10 2.R1011
 5'-most EST
                    LIB3062-045-Q1-K1-B11
 Method
                    BLASTX
 NCBI GI
                    g1351222
 BLAST score
                    207
 E value
                    2.0e-16
 Match length
                    47
 % identity
                    83
 NCBI Description
                    TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi 945087
                    (U31097) transcription factor TFIIB [Glycine max]
 Seq. No.
                    258196
 Contig ID
                    10 3.R1011
 5'-most EST
                    hvj700618843.h1
 Method
                    BLASTX
 NCBI GI
                    g1351222
 BLAST score
                    216
 E value
                    1.0e-17
 Match length
                    45
 % identity
                    80
 NCBI Description TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi 945087
                    (U31097) transcription factor TFIIB [Glycine max]
Seq. No.
                    258197
 Contig ID
                    11 1.R1011
 5'-most EST
                    700201723_FL
 Seq. No.
                    258198
                    12 1.R1011
 Contig ID
 5'-most EST
                    700206101H1.SEQ_FL
 Method
                    BLASTX
 NCBI GI
                    g2924781
 BLAST score
                    489
 E value
                    4.0e-49
 Match length
                   175
 % identity
 NCBI Description (AC002334) putative cellulose synthase [Arabidopsis
                    thaliana]
 Seq. No.
                    258199
 Contig ID
                    13 1.R1011
 5'-most EST
                   ntr700071667.h1
 Method
                   BLASTX
 NCBI GI
                   g1362086
 BLAST score
                    3447
 E value
                    0.0e+00
```

Match length 766
% identity 87
NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_2129919\_pir\_\_S65957
5-methyltetrahydropteroyltriglutamate--homocysteine



S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase [Catharanthus roseus]

Contig ID 13 2.R1011 5'-most EST LIB3067-001-Q1-K1-C6 Method BLASTX NCBI GI g1362086 BLAST score 858 E value 3.0e-92

Match length 194 85 % identity

Seq. No.

NCBI Description 5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle

>gi\_2129919\_pir\_\_\$65957

5-methyltetrahydropteroyltriglutamate--homocysteine

S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle  $>gi_886471_emb_CAA58474_$  (X83499) methionine synthase

[Catharanthus roseus]

Seq. No. 258201 Contig ID 13\_3.R1011 5'-most EST xsy700208732.h1 Method BLASTX NCBI GI q1814403

BLAST score 593 E value 3.0e-67 Match length 150 % identity 81

NCBI Description (U84889) methionine synthase [Mesembryanthemum

crystallinum]

Seq. No. 258202 Contig ID 13 4.R1011 5'-most EST

LIB143-021-Q1-E1-F9

Seq. No. 258203 Contig ID 13 8.R1011 5'-most EST ymt700224308.h1 Method BLASTX

NCBI GI g1814403 BLAST score 713 E value 2.0e-75 Match length 151 % identity 87

NCBI Description (U84889) methionine synthase [Mesembryanthemum

crystallinum]

Seq. No. 258204

Contig ID 13 17.R1011 5'-most EST cyk700051461.f1 Method

BLASTX NCBI GI g2738248 BLAST score 464 E value 3.0e-46

Match length 198

Contig ID

```
% identity
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
Seq. No.
                   258205
Contig ID
                   13 21.R1011
5'-most EST
                   LIB143-027-Q1-E1-H3
Method
                   BLASTX
NCBI GI
                   q1814403
BLAST score
                   339
E value
                   4.0e-38
Match length
                   83
% identity
                   90
NCBI Description
                   (U84889) methionine synthase [Mesembryanthemum
                   crystallinum]
Seq. No.
                   258206
Contig ID
                   14 1.R1011
5'-most EST
                   700209062H1.SEQ FL
Method
                   BLASTX
NCBI GI
                   q2117937
BLAST score
                   2106
E value
                   0.0e + 00
Match length
                   473
% identity
                   87
                   UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                   barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                   pyrophosphorylase [Hordeum vulgare]
Seq. No.
                   258207
Contig ID
                   14 2.R1011
5'-most EST
                   uC-zmflb73185f09b1
Method
                   BLASTX
NCBI GI
                   g2117937
BLAST score
                   2106
E value
                   0.0e+00
Match length
                   473
% identity
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                   barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
Seq. No.
                   258208
Contig ID
                   14 3.R1011
5'-most EST
                  LIB3150-039-Q1-N1-C5
Method
                  BLASTX
NCBI GI
                  g2117937
BLAST score
                  1413
E value
                   1.0e-157
Match length
                  303
                   90
% identity
NCBI Description
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
Seq. No.
                   258209
```

35628

14 4.R1011

```
5'-most EST
                  uC-zmroteosinte102h03b2
Method
                  BLASTX
NCBI GI
                  g136739
BLAST score
                   610
E value
                   3.0e-63
Match length
                  138
% identity
                  85
NCBI Description
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi_218001_dbj_BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                  258210
Contig ID
                  14 6.R1011
5'-most EST
                  pwr700449014.h1
Method
                  BLASTX
NCBI GI
                  g2245108
BLAST score
                  513
E value
                  1.0e-51
Match length
                  139
% identity
                  63
NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
Seq. No.
                  258211
Contig ID
                  14 7.R1011
5'-most EST
                  uC-zmroteosinte001a12b1
Method
                  BLASTX
NCBI GI
                  g136739
BLAST score
                  231
E value
                  7.0e-19
Match length
                  67
% identity
                  66
NCBI Description UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                  258212
Contig ID
                  14 17.R1011
5'-most EST
                  uC-zmflmo17215h07b1
Method
                  BLASTX
NCBI GI
                  g2117937
BLAST score
                  437
                  8.0e-61
E value
Match length
                  133
% identity
                  89
NCBI Description
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  barley >gi_1212996 emb_CAA62689 (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
                  258213
Seq. No.
```

Contig ID 16\_1.R1011
5'-most EST 700219515\_FL
Method BLASTX
NCBI GI 94038471

NCBI GI

```
BLAST score
                   401
E value
                   1.0e-38
Match length
                   86
 % identity
                   88
NCBI Description (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
Seq. No.
                   258214
Contig ID
                   16 2.R1011
 5'-most EST
                   uC-zmflb73219a01b2
Method
                   BLASTX
NCBI GI
                   g4038471
BLAST score
                   283
E value
                   6.0e-25
Match length
                   51
% identity
                   100
NCBI Description (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
Seq. No.
                   258215
Contig ID
                   16 3.R1011
5'-most EST
                   LIB3116-006-Q1-K1-D10
Method
                   BLASTX
NCBI GI
                   q4038471
BLAST score
                   401
E value
                   5.0e-39
Match length
                   86
% identity
                   88
NCBI Description (AF111029) 40S ribosomal protein S27 homolog [Zea mays]
Seq. No.
                   258216
Contig ID
                   17 1.R1011
5'-most EST
                   700221310 FL
Method
                   BLASTX
NCBI GI
                   g1346790
BLAST score
                   780
E value
                   1.0e-82
Match length
                   443
% identity
                   42
NCBI Description
                  PATHOGENESIS-RELATED HOMEODOMAIN PROTEIN (PRHA) >gi 507220
                   (L21991) homeodomain protein [Arabidopsis thaliana]
                   >gi 2501810 (U48864) PRHA [Arabidopsis thaliana]
Seq. No.
                   258217
Contig ID
                   18 1.R1011
5'-most EST
                   uC-zmroteosinte075d04b1
Method
                   BLASTX
NCBI GI
                   g3264767
BLAST score
                   385
E value
                   1.0e-36
Match length
                   247
% identity
                   39
NCBI Description
                  (AF071893) AP2 domain containing protein [Prunus armeniaca]
Seq. No.
                   258218
Contig ID
                   18_2.R1011
5'-most EST
                  uC-zmflmo17282g03b1
Method
                  BLASTN
```

g2443456

Contig ID

Method

5'-most EST

```
BLAST score
E value
                   1.0e-10
Match length
                   88
                   85
% identity
NCBI Description Oryza sativa ethylene responsive element binding protein
                   (Os-EREBP1) mRNA, complete cds
Seq. No.
                   258219
                   18 3.R1011
Contig ID
5'-most EST
                   LIB189-022-Q1-E1-B5
Method
                   BLASTX
NCBI GI
                   g3264767
BLAST score
                   221
E value
                   1.0e-17
Match length
                   138
% identity
                   42
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
Seq. No.
                   258220
Contig ID
                   18 5.R1011
5'-most EST
                   dyk700104338.h1
Method
                   BLASTX
NCBI GI
                   g3264767
BLAST score
                   199
E value
                   3.0e-15
Match length
                   146
% identity
                   39
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
Seq. No.
                   258221
Contig ID
                   19 1.R1011
5'-most EST
                   CPR21928:2F700212293H1.seq FL
Method
                  BLASTX
NCBI GI
                   g2827141
BLAST score
                   3739
E value
                   0.0e + 00
Match length
                   963
% identity
                   71
NCBI Description (AF027173) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                   258222
Contig ID
                  19 2.R1011
5'-most EST
                  cyk700050280.f1
Method
                  BLASTX
                  q2827141
NCBI GI
BLAST score
                  1932
E value
                  0.0e + 00
Match length
                  694
% identity
                  (AF027173) cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  258223
```

35631

19 3.R1011

BLASTX

pmx700088647.h1

Match length

% identity

43

63

```
NCBI GI
                   g2827141
 BLAST score
                   3357
 E value
                   0.0e+00
 Match length
                   825
 % identity
NCBI Description (AF027173) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                   258224
 Contig ID
                   19 4.R1011
5'-most EST
                   LIB3158-010-Q1-K1-B4
                   258225
Seq. No.
Contig ID
                   19 6.R1011
5'-most EST
                  ntr700076906.h1
Method
                   BLASTX
                   g2252631
NCBI GI
BLAST score
                   199
E value
                   6.0e-15
Match length
                   120
% identity
                   46
NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   258226
Contig ID
                  19 7.R1011
5'-most EST
                  uC-zmflmo17158h12b1
Method
                  BLASTX
NCBI GI
                   g2827143
BLAST score
                  737
E value
                  3.0e-78
Match length
                  180
% identity
                  73
NCBI Description (AF027174) cellulose synthase catalytic subunit
                  [Arabidopsis thaliana]
Seq. No.
                  258227
Contig ID
                  19 8.R1011
5'-most EST
                  xsy700214883.h1
Method
                  BLASTX
NCBI GI
                  g1706958
BLAST score
                  177
E value
                  1.0e-12
Match length
                  69
% identity
                  49
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  258228
Contig ID
                  19 10.R1011
5'-most EST
                  uC-zmflmo17025d07a1
Method
                  BLASTX
NCBI GI
                  g3287270
BLAST score
                  148
E value
                  2.0e-09
```

35632

NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]

```
Seq. No.
                   258229
Contig ID
                   19 11.R1011
 5'-most EST
                   uC-zmflb73140a09b1
Seq. No.
                   258230
Contig ID
                   19 12.R1011
5'-most EST
                   uC-zmflb73214g05b1
Method
                   BLASTX
NCBI GI
                   q2827141
BLAST score
                   1631
E value
                   0.0e + 00
Match length
                   416
% identity
                   70
NCBI Description
                  (AF027173) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                   258231
Contig ID
                   19 13.R1011
5'-most EST
                   uC-zmflMo17093d02b1
Method
                   BLASTX
NCBI GI
                   g2827141
BLAST score
                   152
E value
                   1.0e-09
Match length
                   33
% identity
                   76
NCBI Description (AF027173) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                   258232
Contig ID
                   19 15.R1011
5'-most EST
                   LIB3069-022-Q1-K1-B7
Seq. No.
                   258233
Contig ID
                   19 17.R1011
5'-most EST
                  LIB3067-050-Q1-K1-G2
Seq. No.
                  258234
Contig ID
                  19 20.R1011
5'-most EST
                  LIB3136-017-Q1-K1-F6
Seq. No.
                  258235
Contig ID
                  19 24.R1011
5'-most EST
                  xsy700210709.h1
Method
                  BLASTX
NCBI GI
                  g1706958
BLAST score
                  447
E value
                  2.0e-44
Match length
                  113
% identity
                  70
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]
                  258236
```

 Seq. No.
 258236

 Contig ID
 22\_1.R1011

 5'-most EST
 700350212.SEQ\_FL

 Method
 BLASTX

 NCBI GI
 q1709205

BLAST score 312



E value 1.0e-28 Match length 82 % identity 70

NCBI Description MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE 3 (IMP 3) (INOSITOL

MONOPHOSPHATASE 3) >gi\_1098971 (U39059) myo-inositol

monophosphatase 3 [Lycopersicon esculentum]

Seq. No. 258237 Contig ID 23\_1.R1011

5'-most EST uC-zmflb73125f11a1

5'-most EST LIB3069-011-Q1-K1-E7

Seq. No. 258239 Contig ID 24\_1.R1011

5'-most EST uC-zmflb73156c09b1

Method BLASTX
NCBI GI g2827139
BLAST score 3903
E value 0.0e+00
Match length 856
% identity 82

NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi\_4049343\_emb\_CAA22568\_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 258240 Contig ID 24\_2.R1011

5'-most EST LIB3137-023-Q1-K1-B7

Method BLASTX
NCBI GI g1706956
BLAST score 1926
E value 0.0e+00
Match length 429
% identity 83

NCBI Description (U58283) cellulose synthase [Gossypium hirsutum]

5'-most EST uC-zmroteosinte058e03b2

Method BLASTX
NCBI GI g2827143
BLAST score 404
E value 4.0e-39
Match length 84
identity 87

NCBI Description (AF027174) cellulose synthase catalytic subunit

[Arabidopsis thaliana]

Method BLASTX NCBI GI g2781433



```
BLAST score
                   628
E value
                   4.0e-65
Match length
                   143
% identity
                   81
NCBI Description
                  (AF030052) RSW1-like cellulose synthase catalytic subunit
                   [Oryza sativa subsp. japonica]
Seq. No.
                   258243
Contig ID
                   24 5.R1011
5'-most EST
                  LIB3067-053-Q1-K1-C8
Method
                  BLASTX
                  g1706958
NCBI GI
BLAST score
                   310
E value
                   3.0e-28
Match length
                   75
% identity
                   77
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]
Seq. No.
                  258244
Contig ID
                  25 1.R1011
5'-most EST
                  LIB148-047-Q1-E1-D5
Method
                  BLASTX
NCBI GI
                  g2150002
BLAST score
                  931
E value
                  1.0e-100
Match length
                  203
% identity
                  79
NCBI Description (AF000940) ribonuclease [Hordeum vulgare]
                  258245
Seq. No.
Contig ID
                  26 1.R1011
                  LIB148-038-Q1-E1-H7
5'-most EST
Method
                  BLASTX
NCBI GI
                  q1864024
BLAST score
                  222
E value
                   1.0e-26
                  79
Match length
% identity
NCBI Description
                  (U35683) calcium-binding pollen allergen [Cynodon dactylon]
                  >gi_1871507_emb_CAA62634_ (X91256) calcium-binding pollen
                  allergen [Cynodon dactylon]
Seq. No.
                  258246
Contig ID
                  26 3.R1011
5'-most EST
                  LIB3066-048-Q1-K1-D2
Seq. No.
                  258247
                  26 4.R1011
Contig ID
5'-most EST
                  LIB3075-010-Q1-K1-C2
Method
                  BLASTX
NCBI GI
                  q1864024
BLAST score
                  185
```

E value 7.0e-23 Match length 72 % identity 83

NCBI Description (U35683) calcium-binding pollen allergen [Cynodon dactylon] >gi\_1871507\_emb\_CAA62634 (X91256) calcium-binding pollen



## allergen [Cynodon dactylon]

Method BLASTX
NCBI GI g1504052
BLAST score 2382
E value 0.0e+00
Match length 471
% identity 98

NCBI Description (D87042) Calcium-dependent protein kinase [Zea mays]

Seq. No. 258249 Contig ID 26 6.R1011

5'-most EST LIB3059-034-Q1-K1-C5

Method BLASTN
NCBI GI g4160401
BLAST score 155
E value 2.0e-81
Match length 303
% identity 88

NCBI Description Zea mays eIF-5 gene, exons 1-2

Seq. No. 258250 Contig ID 26 7.R1011

5'-most EST LIB148-049-Q1-E1-G3

Method BLASTN
NCBI GI g4160401
BLAST score 109
E value 3.0e-54
Match length 184
% identity 90

NCBI Description Zea mays eIF-5 gene, exons 1-2

Seq. No. 258251 Contig ID 26\_10.R1011

5'-most EST LIB3075-034-Q1-K1-C2

Method BLASTX
NCBI GI g1864024
BLAST score 373
E value 9.0e-36
Match length 80
% identity 90

NCBI Description (U35683) calcium-binding pollen allergen [Cynodon dactylon]

>gi\_1871507\_emb\_CAA62634\_ (X91256) calcium-binding pollen

allergen [Cynodon dactylon]

Seq. No. 258252 Contig ID 26 11.R1011

5'-most EST uC-zmroteosinte099c10b2

Method BLASTX
NCBI GI g1504052
BLAST score 507
E value 2.0e-51
Match length 96
% identity 100

```
NCBI Description (D87042) Calcium-dependent protein kinase [Zea mays]
Seq. No.
                   258253
                  26 16.R1011
Contig ID
5'-most EST
                  uC-zmflmo17405a02a1
Method
                  BLASTN
NCBI GI
                  q4160401
BLAST score
                  95
E value
                  7.0e-46
Match length
                  146
% identity
                  92
NCBI Description Zea mays eIF-5 gene, exons 1-2
Seq. No.
                  258254
Contig ID
                  26 17.R1011
5'-most EST
                  vux700157212.h1
Method
                  BLASTX
                  g2795876
                  345
                  1.0e-32
                  130
```

NCBI GI BLAST score E value Match length % identity

NCBI Description (AF020726) phosphoglucomutase [Tetrahymena thermophila]

Seq. No. 258255 Contig ID 27 1.R1011

5'-most EST LIB148-004-Q1-E1-D9

Method BLASTN NCBI GI g507770 BLAST score 53 E value 4.0e-20 Match length 174 % identity 89

NCBI Description Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete

Seq. No. 258256 Contig ID 27 2.R1011

5'-most EST uC-zmflmo17035d05a1

Method BLASTX NCBI GI g130582 BLAST score 186 E value 7.0e-14Match length 110 % identity 34

NCBI Description RETROVIRUS-RELATED POL POLYPROTEIN FROM TRANSPOSON TNT 1-94

[CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]

>gi\_100342\_pir\_\_S04273 hypothetical protein - common tobacco >gi\_20045\_emb\_CAA32025 (X13777) ORF [Nicotiana

tabacum]

Seq. No. 258257 Contig ID 27 3.R1011

5'-most EST LIB3066-043-Q1-K1-G10

Method BLASTX q3702317 NCBI GI BLAST score 150

E value 2.0e-09 Match length 34 % identity 85 (AC005397) unknown protein [Arabidopsis thaliana] NCBI Description >gi\_4559376\_gb\_AAD23036.1 AC006526 1 (AC006526) unknown protein [Arabidopsis thaliana] Seq. No. 258258 Contig ID 28 1.R1011 5'-most EST CPR10368consensus FL Method BLASTX

Method BLASTX
NCBI GI g121277
BLAST score 1430
E value 1.0e-159
Match length 349
% identity 83
NCBI Description GLYCININ

NCBI Description GLYCININ G2 PRECURSOR [CONTAINS: GLYCININ A2 SUBUNIT; GLYCININ B1A SUBUNIT] > gi\_99908\_pir\_\_S11002 glycinin G2 precursor - soybean > gi\_255222\_bbs\_112931 glycinin G2

subunit [soybeans, Peptide, 485 aa] >gi\_18637\_emb\_CAA33216

(X15122) glycinin subunit G2 [Glycine max]

>gi\_218265\_dbj\_BAA00154\_ (D00216) glycinin A2B1a subunit
[Glycine max] >gi\_295800\_emb\_CAA68460\_ (Y00398) glycinin
[Glycine max] >gi\_225863\_prf\_\_1402179A glycinin A2B1a

[Glycine max]

Seq. No. 258259 Contig ID 29\_1.R1011

5'-most EST CPR11053consensus FL

Method BLASTX
NCBI GI g20559
BLAST score 1342
E value 1.0e-149
Match length 347
% identity 93

NCBI Description (X13301) hsp70 (AA 6 - 651) [Petunia x hybrida]

Seq. No. 258260 Contig ID 29\_2.R1011

5'-most EST uC-zmflb73199a09b1

Method BLASTX
NCBI GI g123650
BLAST score 1814
E value 0.0e+00
Match length 462
% identity 78

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN >gi\_82245\_pir\_\_S03250 heat

shock protein 70 (clone pMON9743) - garden petunia >gi\_20557\_emb\_CAA30018\_ (X06932) heat shock protein 70

[Petunia x hybrida]

Seq. No. 258261 Contig ID 29 3.R1011

5'-most EST LIB148-044-Q1-E1-F12

Method BLASTX NCBI GI g2827002 BLAST score 1071

NCBI GI

BLAST score

```
E value
                   1.0e-117
Match length
                   260
 % identity
                   82
NCBI Description (AF005993) HSP70 [Triticum aestivum]
Seq. No.
                   258262
 Contig ID
                   30 1.R1011
 5'-most EST
                   CPR11054consensus FL
Method
                   BLASTX
NCBI GI
                   g2827002
BLAST score
                   1130
E value
                   1.0e-123
Match length
                   294
% identity
                   76
NCBI Description (AF005993) HSP70 [Triticum aestivum]
Seq. No.
                   258263
Contig ID
                   30 2.R1011
5'-most EST
                   LIB3150-017-Q1-N1-C9
Method
                   BLASTX
NCBI GI
                   g1076746
BLAST score
                   1922
E value
                   0.0e + 00
Match length
                   459
% identity
                   83
NCBI Description heat shock protein 70 - rice (fragment)
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                   258264
Contig ID
                   30_3.R1011
5'-most EST
                  uC-zmflb73050d09b1
Method
                  BLASTX
NCBI GI
                   g3264596
BLAST score
                   993
E value
                   1.0e-108
Match length
                  249
% identity
                   80
NCBI Description (AF057183) putative tonoplast aquaporin [Zea mays]
Seq. No.
                  258265
Contig ID
                  30 4.R1011
5'-most EST
                  uC-zmroteosintel19d06b2
Method
                  BLASTX
NCBI GI
                  q861170
BLAST score
                  423
E value
                  2.0e-41
Match length
                  108
% identity
                  78
NCBI Description (X03697) heat shock protein 70 [Zea mays]
Seq. No.
                  258266
Contig ID
                  30 5.R1011
5'-most EST
                  tzu700206071.h1
Method
                  BLASTX
```

35639

q1549339

```
E value
                   9.0e-36
 Match length
                   81
 % identity
                   89
NCBI Description (U58207) aquaporin homologue [Allium cepa]
 Seq. No.
                   258267
 Contig ID
                   30 6.R1011
 5'-most EST
                   uC-zmflmo17021h05b1
Method
                   BLASTX
NCBI GI
                   g2827002
BLAST score
                   1150
E value
                   1.0e-126
Match length
                   234
 % identity
                   95
NCBI Description (AF005993) HSP70 [Triticum aestivum]
Seq. No.
                   258268
Contig ID
                   30 7.R1011
5'-most EST
                   uC-zmflb73378e05a2
Method
                   BLASTX
NCBI GI
                   g3264596
BLAST score
                   935
E value
                   1.0e-101
Match length
                   261
% identity
                   74
NCBI Description (AF057183) putative tonoplast aquaporin [Zea mays]
Seq. No.
                   258269
Contig ID
                   30 8.R1011
5'-most EST
                   uC-zmroteosinte066a07b1
Method
                   BLASTX
NCBI GI
                   g3264596
BLAST score
                   474
E value
                   2.0e-47
Match length
                   132
% identity
                   73
NCBI Description (AF057183) putative tonoplast aquaporin [Zea mays]
Seq. No.
                   258270
Contig ID
                   30 9.R1011
5'-most EST
                  LIB143-030-Q1-E1-A12
                  BLASTX
Method
NCBI GI
                  g3128175
BLAST score
                  147
E value
                  5.0e-09
Match length
                  48
% identity
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  258271
Contig ID
                  30 10.R1011
5'-most EST
                  uC-zmflb73137b08a1
Method
                  BLASTN
NCBI GI
                  g3264595
BLAST score
                  66
E value
                  1.0e-28
Match length
                  136
```

Contig ID

5'-most EST

```
% identity
NCBI Description Zea mays putative tonoplast aquaporin mRNA, complete cds
Seq. No.
                   258272
Contig ID
                   30 13.R1011
5'-most EST
                   LIB3069-010-Q1-K1-B1
Seq. No.
                   258273
Contig ID
                   30 15.R1011
5'-most EST
                   ntr700072741.h1
Method
                   BLASTX
NCBI GI
                   q3264596
BLAST score
                   438
E value
                   2.0e-55
Match length
                   127
% identity
                   93
NCBI Description (AF057183) putative tonoplast aquaporin [Zea mays]
Seq. No.
                   258274
Contig ID
                   30 16.R1011
5'-most EST
                   dyk700106039.h1
Method
                   BLASTX
NCBI GI
                   q461929
BLAST score
                   272
E value
                   4.0e-24
Match length
                   83
% identity
                   67
NCBI Description
                  PROBABLE TONOPLAST INTRINSIC PROTEIN DIP
                   >gi_1076688_pir__S51781 integral membrane protein - garden
                   snapdragon >gi_414088_emb_CAA49854_ (X70417) integral
                  membrane protein [Antirrhinum majus]
Seq. No.
                   258275
Contig ID
                  30 17.R1011
5'-most EST
                  LIB3136-001-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  q3128176
BLAST score
                  317
E value
                  5.0e-29
Match length
                  106
% identity
                  57
NCBI Description (AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.
                  258276
                  30 18.R1011
Contig ID
5'-most EST
                  uC-zmflm017084c07b1
Method
                  BLASTX
NCBI GI
                  g224970
BLAST score
                  262
E value
                  5.0e-23
Match length
                  83
% identity
                  75
NCBI Description heat shock protein hsp70 [Zea mays]
Seq. No.
                  258277
```

35641

30 21.R1011

uC-zmflb73372b07a1

Seq. No.

Contig ID

258282

36 1.R1011

```
Method
                   BLASTN
NCBI GI
                   g22342
BLAST score
                   125
E value
                   5.0e-64
Match length
                   157
% identity
                   95
NCBI Description Maize gene for heat shock protein 70 exon 2 and 3'-UT
                   (hsp70; clone pMON 9502)
Seq. No.
                   258278
Contig ID
                   31 1.R1011
5'-most EST
                   CPR1375_700047754_FL
Method
                   BLASTX
NCBI GI
                   g3935138
BLAST score
                   777
E value
                   2.0e-82
Match length
                   340
% identity
                   43
NCBI Description (AC005106) T25N20.2 [Arabidopsis thaliana]
Seq. No.
                   258279
Contig ID
                   32 1.R1011
5'-most EST
                  uC-zmroteosinte069b07b1
Method
                  BLASTX
NCBI GI
                  g3135256
BLAST score
                   440
E value
                   5.0e-43
Match length
                  299
% identity
                   35
NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   258280
Contig ID
                  33 1.R1011
5'-most EST
                  CPR1377_700085012_FL
Method
                  BLASTX
                  q3540206
NCBI GI
BLAST score
                  504
E value
                  2.0e-50
Match length
                  244
% identity
                  41
NCBI Description (AC004260) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  258281
Contig ID
                  34 1.R1011
5'-most EST
                  LIB3076-055-Q1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3236235
BLAST score
                  892
E value
                  1.0e-103
Match length
                  455
% identity
NCBI Description
                  (AC004684) unknown protein [Arabidopsis thaliana]
                  >gi_4056501 (AC005896) unknown protein [Arabidopsis
                  thaliana]
```

5'-most EST

```
5'-most EST
                   LIB3066-008-Q1-K1-F10
Method
                   BLASTX
NCBI GI
                   q3935138
BLAST score
                   410
E value
                   3.0e-39
Match length
                   161
% identity
                   48
NCBI Description (AC005106) T25N20.2 [Arabidopsis thaliana]
Seq. No.
                   258283
Contig ID
                   37 1.R1011
5'-most EST
                   uC-zmrob73019b04b1
Method
                   BLASTX
NCBI GI
                   q4510418
BLAST score
                   1288
E value
                   1.0e-142
Match length
                   688
% identity
                   43
NCBI Description (AC006929) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   258284
Contig ID
                   39 1.R1011
5'-most EST
                   CPR1387_700441447_FL
Seq. No.
                   258285
Contig ID
                   39 2.R1011
5'-most EST
                   LIB84-012-Q1-E12-D4
Seq. No.
                   258286
Contig ID
                   39 3.R1011
5'-most EST
                   uC-zmflmo17100h09b1
Seq. No.
                   258287
Contig ID
                   40 1.R1011
5'-most EST
                  CPR1431FL 700166721 FL
Method
                  BLASTX
NCBI GI
                  g4539677
BLAST score
                  1880
E value
                  0.0e + 00
Match length
                  404
% identity
                   90
NCBI Description (AF061282) patatin-like protein [Sorghum bicolor]
Seq. No.
                  258288
Contig ID
                  40 2.R1011
5'-most EST
                  CPR1430consensus_FL
Method
                  BLASTX
NCBI GI
                  g4539677
BLAST score
                  1886
E value
                  0.0e+00
Match length
                  409
% identity
                  90
NCBI Description (AF061282) patatin-like protein [Sorghum bicolor]
Seq. No.
                  258289
Contig ID
                  45 2.R1011
```

LIB148-012-Q1-E1-F6



Method BLASTX NCBI GI g729944 BLAST score 1028 E value 1.0e-112 Match length 191 % identity 97

NCBI Description POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi\_478272 pir\_ JC1524 major allergen mI protein - maize >gi\_293902 (L14271) Zea

mI [Zea mays]

Seq. No. 258290 Contig ID 45 4.R1011

5'-most EST LIB3075-032-Q1-K1-G1

Method BLASTX NCBI GI g729944 BLAST score 297 E value 7.0e-27 Match length 57 % identity 96

NCBI Description POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi\_478272\_pir\_\_JC1524

major allergen mI protein - maize >gi 293902 (L14271) Zea

mI [Zea mays]

Seq. No. 258291 Contig ID 45 10.R1011

5'-most EST LIB3075-029-Q1-K1-G3

Method BLASTX NCBI GI g729944 BLAST score 891 E value 4.0e-96 Match length 181 % identity 92

NCBI Description POLLEN ALLERGEN ZEA M 1 (ZEA M I) >gi\_478272\_pir\_\_JC1524

major allergen mI protein - maize >gi\_293902 (L14271) Zea

mI [Zea mays]

Seq. No. 258292 Contig ID 46 1.R1011 5'-most EST

gct701176810.h1

Method BLASTX NCBI GI g563235 BLAST score 521 E value 7.0e-53 Match length 181 % identity

NCBI Description (U15964) xyloglucan endo-transglycosylase homolog; similar

to Triticum aestivum endo-xyloglucan transferase, PIR Accession Number E49539 [Zea mays] >gi\_563927 (U15781) xyloglucan endo-transglycosylase homolog [Zea mays]

>gi\_1097378\_prf\_\_2113418A xyloglucan endotransglycosylase

homolog [Zea mays]

Seq. No. 258293 Contig ID 47 1.R1011

5'-most EST CPR22012consensus FL

Method BLASTX NCBI GI g1890577

```
BLAST score
                    639
E value
                    1.0e-66
Match length
                    172
% identity
NCBI Description (X93175) xyloglucan endotransglycosylase (XET) [Hordeum
                    vulgare]
Seq. No.
                    258294
Contig ID
                    48 1.R1011
                   CPR22042consensus FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2960364
BLAST score
                   890
E value
                    8.0e-96
Match length
                    320
% identity
                   52
NCBI Description (AJ224986) cinnamoyl CoA reductase [Populus balsamifera
                   subsp. trichocarpa]
Seq. No.
                   258295
Contig ID
                   49 1.R1011
5'-most EST
                   pwr700450831.h1
Method
                   BLASTX
NCBI GI
                   q3603401
BLAST score
                   967.
E value
                   1.0e-105
Match length
                   341
% identity
NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
Seq. No.
                   258296
Contig ID
                   49 3.R1011
5'-most EST
                   uC-zmflb73092q10b2
Method
                   BLASTX
NCBI GI
                   q1168727
BLAST score
                   149
E value
                   2.0e-09
Match length
                   51
% identity
                   53
NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD)
                   >gi_474300_dbj_BAA03099_ (D13991) cinnamyl alcohol
dehydrogenase [Aralia cordata] >gi_745086_prf__2015401A
                   cinnamoyl alcohol dehydrogenase [Aralia cordata]
Seq. No.
                   258297
Contig ID
                   50 1.R1011
5'-most EST
                   CPR22074consensus FL
Method
                   BLASTX
NCBI GI
                   g1724110
BLAST score
                   975
E value
                   1.0e-106
Match length
                   342
% identity
                   53
NCBI Description
                  (U79770) cinnamyl-alcohol dehydrogenase Eli3
```

Seq. No. 258298

[Mesembryanthemum crystallinum]

Contig ID

```
Contig ID
                   51 1.R1011
 5'-most EST
                   uC-zmflb73040b09b1
Method
                   BLASTX
NCBI GI
                   q82496
BLAST score
                   3032
E value
                   0.0e + 00
Match length
                   701
% identity
                   85
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                   258299
Contig ID
                   51 2.R1011
5'-most EST
                   qmh700029234.f1
Method
                   BLASTX
NCBI GI
                   q1944573
BLAST score
                   777
E value
                   1.0e-82
Match length
                   210
% identity
                   71
NCBI Description
                  (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
Seq. No.
                   258300
Contig ID
                   51_3.R1011
5'-most EST
                   uC-zmflb73079b05b2
Method
                   BLASTX
NCBI GI
                   q3024363
BLAST score
                   1169
E value
                   1.0e-128
Match length
                   306
% identity
                   75
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 1483610_emb CAA68036
                   (X99705) phenylalanine ammonia-Tyase [Triticum aestivum]
Seq. No.
                   258301
Contig ID
                   51 4.R1011
5'-most EST
                   uC-zmflb73057a03b1
Method
                   BLASTX
NCBI GI
                   g1944573
BLAST score
                   649
E value
                   9.0e-68
Match length
                  162
% identity
                   75
NCBI Description
                  (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
Seq. No.
                   258302
Contig ID
                  51 5.R1011
5'-most EST
                  LIB3067-045-Q1-K1-A6
Method
                  BLASTX
NCBI GI
                  g168570
BLAST score
                  267
E value
                  3.0e-23
Match length
                  49
% identity
                  100
NCBI Description
                  (M95077) phenylalanine ammonia lyase [Zea mays]
Seq. No.
                  258303
```

35646

51 6.R1011

NCBI Description

```
5'-most EST
                    LIB3062-027-Q1-K1-D8
 Method
                    BLASTX
 NCBI GI
                    g3024363
 BLAST score
                    709
 E value
                    4.0e-90
Match length
                   211
 % identity
                   79
NCBI Description PHENYLALANINE AMMONIA-LYASE >gi 1483610 emb CAA68036
                   (X99705) phenylalanine ammonia-lyase [Triticum aestivum]
Seq. No.
                   258304
Contig ID
                   51_16.R1011
 5'-most EST
                   uC-zmflb73206f04b1
Method
                   BLASTX
NCBI GI
                   q82496
BLAST score
                   858
E value
                   3.0e-92
Match length
                   177
% identity
                   94
NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
Seq. No.
                   258305
Contig ID
                   52 1.R1011
5'-most EST
                   CPR22357consensus_FL
Method
                   BLASTX
NCBI GI
                   q99699
BLAST score
                   1740
E value
                   0.0e + 00
Match length
                   356
% identity
                   94
NCBI Description
                   glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone
                   lambdaAtgsr1) - Arabidopsis thaliana
Seq. No.
                   258306
Contig ID
                   54 1.R1011
5'-most EST
                   LIB189-024-Q1-E1-B5
Method
                   BLASTX
NCBI GI
                   q3913018
BLAST score
                   1819
E value
                   0.0e+00
Match length
                   388
% identity
                   92
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
Seq. No.
                  258307
Contig ID
                  54 2.R1011
5'-most EST
                  LIB3067-031-Q1-K1-B11
Method
                  BLASTX
NCBI GI
                  g2497748
BLAST score
                  261
E value
                  4.0e-22
Match length
                  91
% identity
                  55
```

NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4) >gi\_902058 (U29176) lipid transfer protein precursor [Oryza

```
sativa]
```

Seq. No. 258308 Contig ID 54 3.R1011 5'-most EST uwc700151354.h1 Method BLASTX NCBI GI g4096786 BLAST score 1651 E value 0.0e + 00Match length 566 % identity 90

NCBI Description (U39958) NADP-malic enzyme [Zea mays]

5'-most EST LIB189-032-Q1-E1-E7

Method BLASTX
NCBI GI g100506
BLAST score 1232
E value 1.0e-136
Match length 251
% identity 95

NCBI Description Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)

(EC 1.1.1.40) - Flaveria trinervia (fragment)

Seq. No. 258310 Contig ID 54 5.R1011

5'-most EST LIB3088-004-Q1-K1-A10

Method BLASTN
NCBI GI g902057
BLAST score 35
E value 6.0e-10
Match length 71
% identity 87

NCBI Description Oryza sativa lipid transfer protein precursor, mRNA,

partial cds

Seq. No. 258311 Contig ID 54 6.R1011

5'-most EST uC-zmflb73028e11b1

Method BLASTX
NCBI GI g3913018
BLAST score 1515
E value 1.0e-169
Match length 349
% identity 86

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

(ALDP) >gi\_218155\_dbj\_BAA02730\_ (D13513) chloroplastic

aldolase [Oryza sativa]

Seq. No. 258312 Contig ID 54\_7.R1011

5'-most EST  $LI\overline{B}3076-027-Q1-K1-G9$ 

Method BLASTX
NCBI GI g2497748
BLAST score 261
E value 3.0e-22

Match length 91 % identity

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4)

>gi 902058 (U29176) lipid transfer protein precursor [Oryza

satīva]

Seq. No. 258313 Contig ID 55 1.R1011

5'-most EST LIB83-011-Q1-E1-B8

Method BLASTX NCBI GI q1173347 BLAST score 1388 E value 1.0e-154 Match length 272 % identity 96

NCBI Description SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi\_100803 pir S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi 14265 emb CAA46507 (X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

Seq. No. 258314 Contig ID 56\_1.R1011

5'-most EST -CPR2836\_700046054 FL

Method BLASTX NCBI GI q3913641 BLAST score 680 E value 1.0e-71 Match length 134 % identity 96

NCBI Description

FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)

>gi\_3041777\_dbj\_BAA25423\_ (AB007194)

fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 258315 57 5.R1011 Contig ID 5'-most EST xyt700344779.h1

Method BLASTX NCBI GI g4098272 BLAST score 242 E value 2.0e-24 Match length 61 % identity 100

NCBI Description (U76558) alpha-tubulin [Triticum aestivum]

Seq. No. 258316 57 6.R1011 Contig ID

5'-most EST LIB3060-018-Q1-K1-C5

Method BLASTN NCBI GI g644492 BLAST score 1,60 E value 5.0e-85 Match length 233 % identity 97

NCBI Description Corn elongation factor lalpha gene, complete cds

Match length

63

```
Seq. No.
                   258317
                   57 7.R1011
Contig ID
5'-most EST
                   uC-zmflmo17118f05b1
Method
                   BLASTN
NCBI GI
                   g393400
BLAST score
                   149
E value
                   3.0e-78
Match length
                   197
% identity
                   94
NCBI Description Z.mays mRNA for alpha-tubulin
Seq. No.
                   258318
Contig ID
                   57 8.R1011
5'-most EST
                   uC-zmflb73038e08a1
Method
                   BLASTX
NCBI GI
                   g2282584
BLAST score
                   842
E value
                   1.0e-90
Match length
                   165
% identity
                   97
NCBI Description (U76259) elongation factor 1-alpha [Zea mays]
Seq. No.
                   258319
                   57 9.R1011
Contig ID
5'-most EST
                   xjt700092788.h1
Seq. No.
                   258320
                   57 10.R1011
Contig ID
5'-most EST
                  LIB3117-004-Q1-K1-A3
Method
                  BLASTN
NCBI GI
                  g485376
BLAST score
                  130
E value
                   5.0e-67
Match length
                  214
% identity
                   90
NCBI Description Zea mays alpha-3-tubulin gene, complete cds
Seq. No.
                  258321
Contig ID
                  57 11.R1011
5'-most EST
                  uC-zmroteosinte048f07b1
Method
                  BLASTN
NCBI GI
                  g602605
BLAST score
                  119
E value
                  2.0e-60
Match length
                  251
% identity
                  87
NCBI Description Zea mays tandem genes for alphal-tubulin and alpha2-tubulin
                  258322
Seq. No.
Contig ID
                  57 12.R1011
5'-most EST
                  wyr700236243.hl
Method
                  BLASTX
NCBI GI
                  g135417
BLAST score
                  253
E value
                  8.0e-22
```

```
% identity
NCBI Description · TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin
                   alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176)
                   Alpha-tubulin \#3 [Zea mays] >gi_485\overline{3}77 (M601\overline{7}1) alpha-3
                    tubulin [Zea mays]
Seq. No.
                   258323
Contig ID
                   57 13.R1011
5'-most EST
                   xyt700342615.h1
Seq. No.
                   258324
Contig ID
                   57 14.R1011
5'-most EST
                   hvj700621936.h1
Seq. No.
                   258325
                   57 15.R1011
Contig ID
5'-most EST
                   LIB3067-059-Q1-K1-D1
Seq. No.
                   258326
Contig ID
                   57 16.R1011
5'-most EST
                   vux700157845.h1
Method
                   BLASTN
NCBI GI
                   q485376
BLAST score
                   74
E value
                   1.0e-33
Match length
                   142
% identity
                   96
NCBI Description Zea mays alpha-3-tubulin gene, complete cds
Seq. No.
                   258327
Contig ID
                   57 17.R1011
5'-most EST
                   LIB3150-018-Q1-N1-B6
Method
                   BLASTX
NCBI GI
                   g232029
BLAST score
                   261
E value
                   9.0e-23
Match length
                   53
% identity
                   92
NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                   >gi_100154_pir__S21989 translation elongation factor eEF-1
                   alpha chain - carrot >gi_18339 emb_CAA42843 (X60302)
                   elongation factor 1A [Daucus carota]
Seq. No.
                   258328
Contig ID
                   57 18.R1011
5'-most EST
                   tzu700207016.h1
Method
                  BLASTX
NCBI GI
                  g135417
BLAST score
                   431
E value
                   1.0e-42
Match length
                   97
% identity
NCBI Description
                 TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin
```

tubulin [Zea mays]

alpha-3 chain - maize >gi\_22150\_emb\_CAA44861\_ (X63176) Alpha-tubulin #3 [Zea mays] >gi\_485377 (M60171) alpha-3

```
Seq. No.
                   258329
                   57 19.R1011
Contig ID
5'-most EST
                   uC-zmflmo17127e04b1
Seq. No.
                   258330
Contig ID
                   57 20.R1011
5'-most EST
                   LIB3150-113-P2-K1-C3
Method
                   BLASTX
NCBI GI
                   g2130149
BLAST score
                   152
E value
                   3.0e-10
Match length
                   30
% identity
                   100
NCBI Description translation elongation factor eEF-1 alpha chain - maize
                   (fragment)
Seq. No.
                   258331
Contig ID
                   57 21.R1011
5'-most EST
                   xsy700209686.h1
Method
                   BLASTX
NCBI GI
                   g1732359
BLAST score
                   309
E value
                   2.0e-28
Match length
                   69
% identity
                   88
NCBI Description (U80268) elongation factor 1 alpha [Malus domestica]
Seq. No.
                   258332
Contig ID
                   57 22.R1011
5'-most EST
                  LIB3078-024-Q1-K1-H12
Seq. No.
                   258333
Contig ID
                   57 23.R1011
5'-most EST
                  uC-zmflmo17376e03a1
Method
                  BLASTN
NCBI GI
                  g2282583
BLAST score
                  59
E value
                  2.0e-24
Match length
                  115
% identity
                  88
NCBI Description Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete
                  cds
Seq. No.
                  258334
Contig ID
                  57 24.R1011
5'-most EST
                  dyk700102612.h1
Method
                  BLASTN
NCBI GI
                  g644492
BLAST score
                  106
E value
                  1.0e-52
Match length
                  191
% identity
                  88
NCBI Description Corn elongation factor lalpha gene, complete cds
Seq. No.
                  258335
Contig ID
                  57 25.R1011
5'-most EST
                  uC-zmroteosintel17g10b1
```

```
Method
                   BLASTX
NCBI GI
                   q3850818
BLAST score
                   174
E value
                   2.0e-12
Match length
                   31
% identity
                   100
NCBI Description (Y18349) U2 snRNP auxiliary factor, small subunit [Oryza
Seq. No.
                   258336
Contig ID
                   58 1.R1011
5'-most EST
                   fwa700100427.h1
Method
                   BLASTX
NCBI GI
                   g2117700
BLAST score
                   2350
E value
                   0.0e+00
Match length
                   517
% identity
                   85
NCBI Description transketolase (EC 2.2.1.1) precursor - potato (fragment)
Seq. No.
                   258337
Contig ID
                   58 2.R1011
5'-most EST
                   uC-zmflmo17099c05b1
Method
                   BLASTX
NCBI GI
                   q1076746
BLAST score
                   2929
E value
                   0.0e + 00
Match length
                   649
% identity
                   89
NCBI Description
                  heat shock protein 70 - rice (fragment)
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza satīva]
Seq. No.
                   258338
Contig ID
                   58 3.R1011
5'-most EST
                   LIB3067-050-Q1-K1-E8
Method
                   BLASTX
NCBI GI
                   q1076746
BLAST score
                   2909
E value
                   0.0e+00
Match length
                   649
% identity
                   88
NCBI Description
                  heat shock protein 70 - rice (fragment)
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                   258339
Contig ID
                   58 4.R1011
5'-most EST
                  uC-zmroteosinte107f07b2
Method
                  BLASTX
NCBI GI
                  g4584342
BLAST score
                  816
E value
                  9.0e-88
Match length
                  276
% identity
NCBI Description
                  (AC007127) putative ubiquitin protein [Arabidopsis
                  thaliana]
```

```
Seq. No.
                   258340
Contig ID
                   58_5.R1011
5'-most EST
                   nbm700472754.h1
Method
                   BLASTX
NCBI GI
                   g1076746
BLAST score
                   419
E value
                   5.0e-66
Match length
                   160
% identity
                   83
                   heat shock protein 70 - rice (fragment)
NCBI Description
                   >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
Seq. No.
                   258341
Contig ID
                   58 7.R1011
5'-most EST
                   LIB3150-102-P2-K1-F10
Seq. No.
                   258342
Contig ID
                   58 8.R1011
5'-most EST
                   uC-zmflb73084f02b2
Method
                   BLASTX
NCBI GI
                   g2979565
BLAST score
                   470
E value
                   1.0e-46
Match length
                   124
% identity
                   73
NCBI Description
                  (AC003680) putative sin3 associated polypeptide (SAP18)
                   [Arabidopsis thaliana]
Seq. No.
                   258343
Contig ID
                   58 9.R1011
                   LIB3150-057-Q1-N1-C6
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2979565
BLAST score
                   460
E value
                   1.0e-45
Match length
                   124
% identity
                   71
NCBI Description
                   (AC003680) putative sin3 associated polypeptide (SAP18)
                   [Arabidopsis thaliana]
Seq. No.
                   258344
Contig ID
                   58 10.R1011
5'-most EST
                  uC-zmflB73042c05b1
Method
                  BLASTX
NCBI GI
                  g2979565
BLAST score
                   392
E value
                   5.0e-38
Match length
                  95
                  76
% identity
NCBI Description
                  (AC003680) putative sin3 associated polypeptide (SAP18)
                   [Arabidopsis thaliana]
Seq. No.
                  258345
Contig ID
                  58 11.R1011
5'-most EST
                  gct701167471.h1
```

```
Seq. No.
                   258346
Contig ID
                   58 12.R1011
5'-most EST
                   LIB3078-050-Q1-K1-B5
Method
                   BLASTX
NCBI GI
                   g2979565
BLAST score
                   335
E value
                   5.0e-31
Match length
                   96
% identity
                   69
NCBI Description (AC003680) putative sin3 associated polypeptide (SAP18)
                   [Arabidopsis thaliana]
Seq. No.
                   258347
Contig ID
                   58 15.R1011
5'-most EST
                   uC-zmflmo17042b02b1
Method
                   BLASTX
                   g1181673
NCBI GI
BLAST score
                   472
E value
                   1.0e-59
Match length
                   129
% identity
                   87
NCBI Description (U41652) heat shock protein cognate 70 [Sorghum bicolor]
Seq. No.
                   258348
Contig ID
                   58_18.R1011
5'-most EST
                   uC-zmflb73053g12b2
Method
                   BLASTX
NCBI GI
                   g629844
BLAST score
                   640
E value
                   9.0e-67
Match length
                   170
% identity
                   78
NCBI Description
                  heat shock protein hsp70-5 - maize (fragment)
                   >gi_498775_emb_CAA55184_ (X78415) heat shock protein 70 kDa
                   [Zea mays]
Seq. No.
                   258349
Contig ID
                  58 19.R1011
5'-most EST
                  uC-zmflmo17322f02a1
Seq. No.
                   258350
Contig ID
                  59 1.R1011
5'-most EST
                  CPR2864 700208152 FL
Method
                  BLASTX
NCBI GI
                  g1673456
BLAST score
                  900
E value
                  4.0e-97
Match length
                  170
% identity
                  98
NCBI Description (Y09214) rubisco small subunit [Zea mays]
Seq. No.
                  258351
Contig ID
                  59 2.R1011
5'-most EST
                  LIB36-010-Q1-E1-A10
Method
                  BLASTX
NCBI GI
                  g132147
```



BLAST score 916 E value 6.0e-99 Match length 170 % identity 99

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 68089 pir RKZMS

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - maize >gi\_22474\_emb\_CAA29784\_ (X06535)
ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor
[Zea mays] >gi\_217964\_dbj\_BAA00120 (D00170) ribulose

1,5-bisphosphate carboxylase small subunit [Zea mays]
>gi\_359512 prf 1312317A ribulosebisphosphate carboxylase

[Zea mays]

Seq. No. 258352 Contig ID 59\_3.R1011

Method BLASTX
NCBI GI g132147
BLAST score 917
E value 4.0e-99
Match length 170
% identity 100

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi 68089 pir RKZMS

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - maize >gi\_22474\_emb\_CAA29784 (X06535)

ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi\_217964\_dbj\_BAA00120\_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi\_359512\_prf\_\_1312317A ribulosebisphosphate carboxylase

[Zea mays]

258353

Seq. No.
Contig ID
5'-most EST

59\_4.R1011

hbs701185535.h1

Method BLASTX
NCBI GI g132147
BLAST score 464
E value 2.0e-69
Match length 132
% identity 98

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_68089\_pir\_\_RKZMS

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - maize >gi\_22474\_emb\_CAA29784\_ (X06535)

ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi\_217964\_dbj\_BAA00120\_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi\_359512\_prf\_\_1312317A ribulosebisphosphate carboxylase

[Zea mays]

Seq. No.
Contig ID

258354 59\_9.R1011

5'-most EST

LIB3078-006-Q1-K1-A3

Method NCBI GI BLASTX g132147

BLAST score 188
E value 7.0e-14
Match length 45
% identity 80
NCBI Description RIBULOS
(RUBISC
ribulos
precurs
ribulos

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR

(RUBISCO SMALL SUBUNIT) >gi\_68089\_pir\_ RKZMS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

precursor - maize >gi\_22474\_emb\_CAA29784 (X06535)

ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor [Zea mays] >gi\_217964\_dbj\_BAA00120\_ (D00170) ribulose 1,5-bisphosphate carboxylase small subunit [Zea mays] >gi\_359512\_prf\_\_1312317A ribulosebisphosphate carboxylase

[Zea mays]

Seq. No. 258355 Contig ID 63\_1.R1011

5'-most EST LIB3069-020-Q1-K1-B3

Method BLASTX
NCBI GI g4262236
BLAST score 709
E value 1.0e-74
Match length 233
% identity 63

NCBI Description (AC006200) putative ribose 5-phosphate isomerase

[Arabidopsis thaliana]

Method BLASTX
NCBI GI g4262236
BLAST score 409
E value 1.0e-39
Match length 144
% identity 58

NCBI Description (AC006200) putative ribose 5-phosphate isomerase

[Arabidopsis thaliana]

Seq. No. 258357 Contig ID 63\_3.R1011

5'-most EST LIB143-041-Q1-E1-C3

Method BLASTX
NCBI GI g3420051
BLAST score 623
E value 8.0e-65
Match length 110
% identity 98

NCBI Description (AC004680) unknown protein [Arabidopsis thaliana]

 Seq. No.
 258358

 Contig ID
 63\_4.R1011

5'-most EST uC-zmflmo17160h09b1

Method BLASTX
NCBI GI g3420051
BLAST score 552
E value 1.0e-59
Match length 110



% identity 98 (AC004680) unknown protein [Arabidopsis thaliana] NCBI Description 258359 Seq. No. Contig ID 64 1.R1011 5'-most EST LIB3150-005-Q1-N1-A7 BLASTX Method g1351270 NCBI GI BLAST score 986 E value 1.0e-107 . 251 Match length 75 % identity TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) NCBI Description >gi\_478410\_pir\_\_JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi 169821 (M87064) triosephosphate isomerase [Oryza sativa] 258360 Seq. No. Contig ID 64 2.R1011 5'-most EST LIB3150-118-P2-K1-C1 Method BLASTX NCBI GI g1351279 BLAST score 173 2.0e-12 E value Match length 40 % identity 85 TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) NCBI Description >gi 602590 emb\_CAA58230\_ (X83227) triosephosphate isomerase [Petunia x hybrida] Seq. No. 258361 65 1.R1011 Contig ID uC-zmflb73197d09b1 5'-most EST Method BLASTX NCBI GI q3080369 BLAST score 327 E value 7.0e-30 Match length 196 39 % identity NCBI Description (AL022580) putative protein [Arabidopsis thaliana] Seq. No. 258362 65 2.R1011 Contig ID 5'-most EST uC-zmflb73193a08a1 Method BLASTN NCBI GI q2351069 BLAST score 44 E value 2.0e-15 Match length 188 81 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No. 258363 Contig ID 65\_3.R1011

5'-most EST uC-zmflb73143c08b1

Method BLASTX



```
q3080369
NCBI GI
BLAST score
                   258
E value
                   3.0e-22
                  105
Match length
% identity
                   49
                  (AL022580) putative protein [Arabidopsis thaliana]
NCBI Description
                  258364
Seq. No.
                  65_7.R1011
Contig ID
5'-most EST
                  wty700162838.h1
                  258365
Seq. No.
Contig ID
                   66 1.R1011
5'-most EST
                  CPR2848_700093371_FL
Method
                  BLASTX
NCBI GI
                  q1362078
BLAST score
                  596
                  5.0e-74
E value
Match length
                  251
                  59
% identity
NCBI Description
                  endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1)
                  - common nasturtium >gi_311835 emb CAA48324 (X68254)
                  cellulase [Tropaeolum majus]
                  258366
Seq. No.
                  67 1.R1011
Contig ID
5'-most EST
                  LIB3137-033-Q1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1890575
BLAST score
                  1255
E value
                  1.0e-138
Match length
                  274
% identity
                  81
NCBI Description
                  (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
Seq. No.
                  258367
Contig ID
                  67 2.R1011
5'-most EST
                  xjt700095989.h1
Method
                  BLASTX
NCBI GI
                  g1890577
BLAST score
                  853
E value
                  1.0e-91
Match length
                  193
% identity
                  79
NCBI Description
                  (X93175) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
                  258368
Seq. No.
                  67 3.R1011
Contig ID
5'-most EST
                  uC-zmflmo17297g03b1
Method
                  BLASTX
NCBI GI
                  g1890575
```

BLAST score 606

E value 6.0e-63 Match length 140 76 % identity



```
NCBI Description (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
Seq. No.
                  258369
Contig ID
                  67 4.R1011
5'-most EST
                  xsy700217090.h1
Seq. No.
                  258370
Contig ID
                  67 6.R1011
5'-most EST
                  LIB3062-004-Q1-K1-G9
Seq. No.
                  258371
Contig ID
                  67 7.R1011
5'-most EST
                  LIB3079-052-Q1-K1-A4
Method
                  BLASTX
NCBI GI
                  q1890575
BLAST score
                  541
E value
                  3.0e-55
Match length
                  141
% identity
NCBI Description
                  (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
Seq. No.
                  258372
Contig ID
                  67 8.R1011
5'-most EST
                  uC-zmflB73007e01b1
Method
                  BLASTX
NCBI GI
                  q1890577
BLAST score
                  510
E value
                  5.0e-73
Match length
                  185
                  75
% identity
NCBI Description
                 (X93175) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
Seq. No.
                  258373
                  67 9.R1011
Contig ID
5'-most EST
                  LIB3150-104-P2-K1-D4
Method
                  BLASTX
NCBI GI
                  g3860323
BLAST score
                  359
                  7.0e-34
E value
                  77
Match length
                  88
% identity
NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                  258374
                  67 10.R1011
Contig ID
5'-most EST
                  LIB3116-006-Q1-K1-H7
Method
                  BLASTX
                  g3860323
```

NCBI GI g3860323 BLAST score 320 E value 2.0e-29 Match length 77

% identity 81

NCBI Description (AJ012688) hypothetical protein [Cicer arietinum]

% identity

78



```
258375
Seq. No.
Contig ID
                   67_14.R1011
5'-most EST
                   uC-zmflb73075a11a1
Method
                   BLASTX
                   q3860323
NCBI GI
BLAST score
                   348
E value
                   1.0e-32
Match length
                   77
% identity
                   87
NCBI Description
                  (AJ012688) hypothetical protein [Cicer arietinum]
Seq. No.
                   258376
Contig ID
                   68 1.R1011
5'-most EST
                   CPR2865 700208768 FL
Method
                   BLASTX
NCBI GI
                   q125580
BLAST score
                   1898
                   0.0e+00
E value
Match length
                   405
% identity
                   89
NCBI Description
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
                   (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC
                   2.7.1.19) - wheat
                   258377
Seq. No.
Contig ID
                   69 1.R1011
5'-most EST
               LIB3137-033-Q1-K1-D5
Method
                   BLASTX
NCBI GI
                   q4105561
BLAST score
                   1126
E value
                   1.0e-123
Match length
                   255
% identity
                   88
NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
Seq. No.
                   258378
Contig ID
                   69 2.R1011
5'-most EST
                   uC-zmflb73177f12b1
Method
                   BLASTX
NCBI GI
                   g4105561
BLAST score
                   553
E value
                   2.0e-56
Match length
                   134
% identity
                   80
NCBI Description
                  (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
Seq. No.
                   258379
Contig ID
                   69 3.R1011
5'-most EST
                  LIB189-001-Q1-E1-F4
Method
                  BLASTX
NCBI GI
                  g4105561
BLAST score
                   419
E value
                   4.0e-41
Match length
                  111
```

NCBI Description (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]



Seq. No. 258380 Contig ID 70\_1.R1011

5'-most EST LIB3116-009-Q1-K1-B10

Method BLASTX
NCBI GI g120657
BLAST score 198
E value 3.0e-15
Match length 38
% identity 95

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,

CHLOROPLAST >gi\_66024\_pir\_\_DEZMG3

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - maize >gi\_168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi\_763035\_emb\_CAA33455\_ (X15408)

glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 258381 Contig ID 70\_2.R1011

5'-most EST LIB3066-033-Q1-K1-A12

Method BLASTX
NCBI GI g2459445
BLAST score 583
E value 1.0e-59
Match length 229
% identity 52

NCBI Description (AC002332) putative ribonucleoprotein [Arabidopsis

thalianal

5'-most EST LIB3066-051-Q1-K1-F3

Seq. No. 258383 Contig ID 70\_4.R1011

5'-most EST LIB84-023-Q1-E1-A11

Method BLASTN
NCBI GI g22294
BLAST score 187
E value 1.0e-100
Match length 211
% identity 96

NCBI Description Maize Gpal gene for glyceraldehyde-3-phosphate

dehydrogenase subunit A >gi\_168478\_gb\_M18976\_MZEG3PD Zea mays chloroplast glyceraldehyde-3-phosphate dehydrogenase

gene, complete cds, clone lambda-gapA1

 Seq. No.
 258384

 Contig ID
 71\_1.R1011

 5'-most EST
 clt700042787.f1

Method BLASTX
NCBI GI g120663
BLAST score 1565
E value 0.0e+00
Match length 423
% identity 78

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,



CHLOROPLAST >gi\_66027\_pir\_\_DEPMNB glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B precursor, chloroplast -garden pea >gi\_309671 (M55147) glyceraldehyde-3-phosphate dehydrogenase B subunit [Pisum sativum]

Seq. No. 258385 71 2.R1011 Contiq ID LIB3060-002-Q1-K2-G6 5'-most EST Method BLASTX NCBI GI q120663 BLAST score 1726 0.0e+00E value Match length 448 76 % identity

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE B PRECURSOR,

CHLOROPLAST >gi 66027 pir DEPMNB

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) B precursor, chloroplast - garden pea >gi\_309671 (M55147) glyceraldehyde-3-phosphate

dehydrogenase B subunit [Pisum sativum]

Seq. No. 258386 Contig ID 71 3.R1011

5'-most EST LIB3115-031-P1-K1-A2

Method BLASTX
NCBI GI g22240
BLAST score 736
E value 4.0e-78
Match length 180
% identity 82

NCBI Description (X07157) GADPH (383 AA) [Zea mays]

 Seq. No.
 258387

 Contig ID
 71\_5.R1011

5'-most EST LIB3137-012-Q1-K1-A11

Method BLASTX
NCBI GI g82166
BLAST score 575
E value 5.0e-59
Match length 158
% identity 72

NCBI Description glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) B, chloroplast - common

tobacco (fragment)

 Seq. No.
 258388

 Contig ID
 71\_6.R1011

 5'-most EST
 mwy700441070.h1

Seq. No. 258389 Contig ID 72\_1.R1011

Method BLASTX
NCBI GI g2407233
BLAST score 252
E value 7.0e-21



Match length 101 50 % identity

(AF017750) similar to Haemophilus influenzae product NCBI Description encoded by Genbank Accession Number U32796 [Haemophilus

ducreyi]

258390 Seq. No. 72 2.R1011 Contig ID

LIB3062-047-Q1-K1-H12 5'-most EST

258391 Seq. No. 74 1.R1011 Contig ID

CPR2856\_700098056\_FL 5'-most EST

BLASTX Method q3287693 NCBI GI 466 BLAST score E value 2.0e-46 Match length 141 68 % identity

(AC003979) Similar to LIM17 gene product gb\_1653769 from NCBI Description

the genome of Synechocystis sp. gb D90916. [Arabidopsis

thaliana]

258392 Seq. No. 81 1.R1011 Contig ID 5'-most EST xsy700210157.h1

BLASTX Method g136063 NCBI GI BLAST score 1181 1.0e-130 E value 250 Match length 93 % identity

TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) NCBI Description

>gi\_68426\_pir\_\_ISZMT triose-phosphate isomerase (EC 5.3.1.1) - maize >gi\_168647 (L00371) triosephosphate isomerase 1 [Zea mays] >gi\_217974\_dbj\_BAA00009\_ (D00012)

triosephosphate isomerase [Zea mays]

258393 Seq. No. Contig ID 81 2.R1011

LIB3078-020-Q1-K1-C9 5'-most EST

Method BLASTX q136063 NCBI GI BLAST score 1172 1.0e-129 E value 253 Match length % identity 91

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)

> >gi\_68426\_pir\_\_ISZMT triose-phosphate isomerase (EC 5.3.1.1) - maize >gi\_168647 (L00371) triosephosphate isomerase 1 [Zea mays] >gi\_217974\_dbj\_BAA00009\_ (D00012) triosephosphate isomerase [Zea mays]

258394 Seq. No. Contig ID 82 1.R1011 5'-most EST wen700334366.hl

Method BLASTX



```
NCBI GI
                   g4559304
BLAST score
                    1426
E value
                    1.0e-175
Match length
                   343
                   89
 % identity
                   (AF127021) T7-like RNA polymerase [Zea mays]
NCBI Description
                   258395
 Seq. No.
                   83 1.R1011
 Contig ID
                   LIB3061-052-Q1-K1-H7
 5'-most EST
Method
                   BLASTX
NCBI GI
                   g4126695
                    184
 BLAST score
                    4.0e-13
 E value
Match length
                   116
 % identity
                    38
                   (AB016505) prolamin [Oryza sativa]
 NCBI Description
                    258396
 Seq. No.
 Contig ID
                    83 2.R1011
                   LIB3152-009-P1-K1-H1
 5'-most EST
 Seq. No.
                    258397

√Contig ID

                    83 4.R1011
                    ypc700803072.h1
 5'-most EST
                    258398
 Seq. No.
 Contig ID
                    84 1.R1011
                    CPR3443 700447718 FL
 5'-most EST
                    258399
 Seq. No.
                    85 1.R1011
 Contig ID
 5'-most EST
                    CPR3449 700184970 FL
 Method
                    BLASTX
 NCBI GI
                    g121472
 BLAST score
                    306
 E value
                    2.0e-27
 Match length
                    109
                    56
 % identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
 NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                    maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                    [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                    mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
 Seq. No.
                    258400
 Contig ID
                    85_2.R1011
 5'-most EST
                    uC-zmflmo17303d08b1
 Method
                    BLASTX
 NCBI GI
                    q4507857
 BLAST score
                    302
```

Method BLASTX
NCBI GI 94507857
BLAST score 302
E value 1.0e-26
Match length 420
% identity 27
NCBI Description Herpes v.

Herpes virus-associated ubiquitin-specific protease >gi\_2501460\_sp\_Q93009\_UBPH\_HUMAN PROBABLE UBIQUITIN

BLAST score

E value

258

1.0e-143



CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) >gi\_1545952\_emb\_CAA96580\_(Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]

```
258401
Seq. No.
                  85 3.R1011
Contig ID
                  LIB3151-040-Q1-K1-G9
5'-most EST
                  BLASTX
Method
NCBI GI
                  g168695
                  267
BLAST score
                  6.0e-23
E value
Match length
                  105
% identity
                  52
                  (M16218) gamma zein [Zea mays] >gi 225315 prf 1211356A
NCBI Description
                  zein gamma [Zea mays]
                  258402
Seq. No.
                  85 4.R1011
Contig ID
5'-most EST
                  LIB3151-034-Q1-K1-E9
Method
                  BLASTX
NCBI GI
                  q141617
                  478
BLAST score
                  7.0e-48
E value
                  119
Match length
% identity
                  75
                  ZEIN-BETA PRECURSOR (ZEIN 2) (16 KD) (ZEIN ZC1)
NCBI Description
                  >gi_100941_pir__S12140 zein Zc1 - maize
                  >gi_100945_pir__B29017 zein 2 - maize
                  >gi 22515 emb CAA37595 (X53515) zein Zc1 [Zea mays]
                  >gi 168666 (M16460) 16-kDa zein protein [Zea mays]
                  258403
Seq. No.
                  85 5.R1011
Contig ID
5'-most EST
                  LIB3059-045-Q1-K1-F10
Method
                  BLASTX
                  g121472
NCBI GI
BLAST score
                   333
                   1.0e-30
E value
Match length
                  90
% identity
                   79
                  GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                  >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                  maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                   [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                  mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
                   258404
Seq. No.
Contig ID
                   85 6.R1011
5'-most EST
                  LIB3152-001-01-K1-A7
Method
                  BLASTN
NCBI GI
                   q168484
```



```
423
Match length
                  69
% identity
                  Maize endosperm glutelin-2 gene, complete cds
NCBI Description
                  258405
Seq. No.
                  85 7.R1011
Contig ID
                  LIB3061-006-Q1-K1-A8
5'-most EST
                  BLASTX
Method
                  g2832243
NCBI GI
                  258
BLAST score
                  3.0e-22
E value
Match length
                  85
                  69
% identity
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
Seq. No.
                  258406
                  85 8.R1011
Contig ID
                  LIB3151-041-Q1-K1-C9
5'-most EST
Method
                  BLASTX
                  q121472
NCBI GI
                  198
BLAST score
                  4.0e-15
E value
Match length
                  55
% identity
                  71
                  GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                   (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                  >gi 72326 pir ZMZM19 glutelin 2 precursor (clone pME119) -
                  maize >gi 22289 emb CAA26149 (X02230) glutelin-2 precursor
                   [Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
                  mays] >gi 168485 (M16066) glutelin-2 [Zea mays]
                  258407
Seq. No.
                  85 10.R1011
Contig ID
                  LIB3061-031-Q1-K1-G10
5'-most EST
                  BLASTN
Method
                  g22514
NCBI GI
BLAST score
                  256
E value
                  1.0e-142
                   299
Match length
                   97
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                   258408
Seq. No.
                   85 11.R1011
Contig ID
                  LIB3151-038-Q1-K1-C9
5'-most EST
Method
                   BLASTX
NCBI GI
                   q168695
BLAST score
                   427
E value
                   1.0e-41
Match length
                   110
                   75
% identity
NCBI Description
                  (M16218) gamma zein [Zea mays] >gi 225315 prf 1211356A
                   zein gamma [Zea mays]
```

35667

258409

85\_13.R1011

hrx700704064.h1

Seq. No.

Contig ID 5'-most EST



```
Method
                   BLASTX
                   g2668742
NCBI GI
BLAST score
                   200
                   2.0e-15
E value
                   50
Match length
                   80
% identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   258410
Seq. No.
                   85 14.R1011
Contig ID
                   LIB3150-109-P2-K1-B2
5'-most EST
                   BLASTX
Method
                   g168695
NCBI GI
BLAST score
                   156
                   3.0e-10
E value
                    46
Match length
                    70
% identity
                    (M16218) gamma zein [Zea mays] >gi_225315_prf__1211356A
NCBI Description
                    zein gamma [Zea mays]
                    258411
Seq. No.
                    85 15.R1011
Contig ID
                    LIB3061-049-Q1-K1-B10
5'-most EST
Method
                    BLASTX
                    q121472
NCBI GI
BLAST score
                    206
                    2.0e-16
E value
Match length
                    42
                    90
% identity
                   GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
NCBI Description
                    (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)
                    >gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) -
                    maize >gi_22289_emb_CAA26149_ (X02230) glutelin-2 precursor
                    [Zea mays] >gi_\overline{2}251\overline{7}_emb_CAA\overline{3}7594_ (X53514) zein Zc2 [Zea
                    mays] >gi_1684\overline{8}5 (M1\overline{6}066) gluteli\overline{n}-2 [Zea mays]
                    258412
Seq. No.
                    85 16.R1011
Contig ID
                    LIB3151-012-Q1-K1-D5
5'-most EST
                    BLASTX
Method
                    g168695
NCBI GI
                    203
BLAST score
                    9.0e-16
E value
                    69
Match length
                    65
% identity
                   (M16218) gamma zein [Zea mays] >gi 225315 prf 1211356A
NCBI Description
                    zein gamma [Zea mays]
Seq. No.
                    258413
                    85 18.R1011
Contig ID
                    LIB3151-016-Q1-K1-D4
5'-most EST
                    BLASTX
Method
NCBI GI
                    q121472
                    163
BLAST score
                    6.0e-11
E value
                    74
Match length
```

35668

53

% identity



NCBI Description GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN) (ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2) >gi 72326\_pir\_\_ZMZM19 glutelin 2 precursor (clone pME119) maize >gi\_22289 emb\_CAA26149 (X02230) glutelin-2 precursor [Zea mays] >gi\_ $\overline{2}251\overline{7}$ \_emb\_CAA $\overline{3}7594$ \_ (X53514) zein Zc2 [Zea mays]  $>gi_1684\overline{8}5$  (M1 $\overline{6}066\overline{)}$  gluteli $\overline{n}$ -2 [Zea mays] 258414 Seq. No. 85 20.R1011 Contig ID ypc700804208.h1 5'-most EST BLASTN Method NCBI GI g168694 197 BLAST score 1.0e-106 E value Match length 343 99 % identity Maize gamma zein mRNA, partial cds NCBI Description 258415 Seq. No. 85 21.R1011 Contiq ID LIB3059-054-Q1-K1-C7 5'-most EST BLASTN Method NCBI GI g22514 147 BLAST score 7.0e-77 E value 194 Match length 94 % identity NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2) 258416 Seq. No. 85 25.R1011 Contig ID ypc700801541.h1 5'-most EST BLASTN Method g168484 NCBI GI 177 BLAST score 8.0e-95 E value 229 Match length % identity 98 NCBI Description Maize endosperm glutelin-2 gene, complete cds 258417 Seq. No. 85 26.R1011 Contig ID LIB3059-012-Q1-K1-B1 5'-most EST BLASTN Method q168484 NCBI GI 88 BLAST score 7.0e-42 E value Match length 88 100 % identity NCBI Description Maize endosperm glutelin-2 gene, complete cds 258418 Seq. No. 85 34.R1011

Contig ID LIB3059-046-Q1-K1-G4 5'-most EST

BLASTN Method g22516 NCBI GI

BLAST score 125



E value 6.0e-64 228 Match length % identity 97 Maize Zc2 gene for zein Zc2 (28 kD glutelin-2) NCBI Description 258419 Seq. No. Contig ID 87 1.R1011 CPR3490 HS5R-139-Q1-A2-C3\_FL 5'-most EST BLASTN Method g598955 NCBI GI

BLAST score E value 0.0e+00Match length 1227 99 % identity

1177

Human mRNA for hepatoma-derived growth factor, complete cds NCBI Description

258420 Seq. No. Contig ID 88 1.R1011

CPR3495 HS5R-152-Q1-A1-A11\_FL 5'-most EST

BLASTX Method g337767 NCBI GI BLAST score 212 3.0e-16 E value Match length 34 100 % identity

(M60258) cerebroside sulfate activator protein [Homo NCBI Description

sapiens]

258421 Seq. No. 89 1.R1011 Contig ID

uC-zmf1b73091h02b25'-most EST

BLASTX Method NCBI GI g1706374 1729 BLAST score 0.0e+00 E value 348 Match length 96 % identity

DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL NCBI Description

4-REDUCTASE) >gi 313678\_emb\_CAA28734\_ (X05068) 40.1 kD A1

protein [Zea mays]

258422 Seq. No. 89 2.R1011 Contig ID

uC-zmflm017084c09b1 5'-most EST

BLASTX Method g4096099 NCBI GI 526 BLAST score 1.0e-55 E value 120 Match length % identity

(U23161) NADPH-dependent reductase [Zea mays] NCBI Description

Seq. No. 258423 89 3.R1011 Contig ID

uC-zmflb73222c05b1 5'-most EST

BLASTX Method NCBI GI g1706374



```
849
BLAST score
E value
                   5.0e-91
                   219
Match length
                   79
% identity
                   DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
NCBI Description
                   4-REDUCTASE) >gi_313678_emb_CAA28734_ (X05068) 40.1 kD A1
                   protein [Zea mays]
                   258424
Seq. No.
                   89 5.R1011
Contig ID
                   uC-zmflmo17317d02a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q1706374
BLAST score
                   375
                   7.0e-36
E value
                   73
Match length
                   100
% identity
                   DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
NCBI Description
                   4-REDUCTASE) >gi_313678_emb_CAA28734 (X05068) 40.1 kD A1
                   protein [Zea mays]
                   258425
Seq. No.
Contig ID
                   89 6.R101<del>1</del>
5'-most EST
                   uC-zmflb73360d02a1
                   BLASTN
Method
                   g22102
NCBI GI
                   353
BLAST score
                   0.0e + 00
E value
Match length
                   377
% identity
                   98
                   Zea mays Al gene for 40.1kd Al protein (NADPH-dependent
NCBI Description
                   reductase)
                   258426
Seq. No.
Contig ID
                   90 1.R1011
                   CPR3842 700550431 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g3241943
BLAST score
                   207
                   7.0e-16
E value
Match length
                   44
                   82
% identity
                   (AC004625) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   258427
Seq. No.
                   91 1.R1011
Contig ID
                   uC-zmflb73073d01b3
5'-most EST
                   BLASTX
Method
NCBI GI
                   g1946371
                   421
BLAST score
                   5.0e-59
E value
Match length
                   325
                   43
% identity
```

Seq. No. 258428

NCBI Description

[Arabidopsis thaliana]

(U93215) regulatory protein Viviparous-1 isolog



```
91 3.R1011
Contig ID
5'-most EST
                     uC-zmflb73212c12a1
                     258429
Seq. No.
                     94 1.R1011
Contig ID
                     CPR3845 700551981 FL
5'-most EST
                     258430
Seq. No.
                     95 1.R1011
Contig ID
5'-most EST
                     gct701176283.h1
Method
                     BLASTX
NCBI GI
                     g4206306
BLAST score
                     218
E value
                     2.0e-17
Match length
                     119
                     43
% identity
NCBI Description (AF049110) prpol [Zea mays]
Seq. No.
                     258431
                     95 2.R1011
Contig ID
5'-most EST
                     rvt700553143.h1
Method
                     BLASTX
                     g70772
NCBI GI
BLAST score
                     410
                     7.0e-40
E value
Match length
                     82
                     100
% identity
                     histone H4 - wheat >gi 70773 pir HSPM4 histone H4 - garden
NCBI Description
                     258432
Seq. No.
                     95 3.R1011
Contig ID
                     LIB3088-029-Q1-K1-G10
5'-most EST
Method
                     BLASTX
NCBI GI
                     g122106
BLAST score
                     363
E value
                     1.0e-39
Match length
                     102
% identity
                     86
                     HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana
NCBI Description
                     >gi_2119028_pir__S60475 histone H4 - garden pea
                     >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum
                     aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >di_166742 (M17133) histone H4 [Arabidopsis thaliana]
                      thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
                      >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503
                      (M13377) histone H4 [Zea mays] >gi 498898 (\overline{\text{U10042}}) histone
                     H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata]
                      >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                      >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4
                      [Arabidopsis thaliana] >gi 225838 prf 1314298A histone H4
```

Seq. No. 258433 Contig ID 95 4.R1011

35672

[Arabidopsis thaliana]



```
LIB3070-002-Q1-N1-C3
5'-most EST
Method
                  BLASTX
                  g122106
NCBI GI
BLAST score
                   301
                   3.0e-27
E value
                   60
Match length
                   100
% identity
                  HISTONE H4 >gi 70771 pir HSZM4 histone H4 - maize
NCBI Description
                   >qi 81642 pir \(^{\text{S06904}}\) histone H4 - Arabidopsis thaliana
                   >gi 2119028 pir S60475 histone H4 - garden pea
                   >gi 21795 emb CAA24924 (X00043) histone H4 [Triticum
                   aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis
                   thaliana] >gi 166742 (M17133) histone H4 [Arabidopsis
                   thaliana] >gi 168499 (M36659) histone H4 (H4C13) [Zea mays]
                   >qi 168501 (M13370) histone H4 [Zea mays] >gi 168503
                   (M1\overline{3}377) histone H4 [Zea mays] >gi 498898 (U10042) histone
                   H4 homolog [Pisum sativum] >gi 1806285 emb CAB01914_
                   (Z79638) histone H4 homologue [Sesbania rostrata]
                   >qi 3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                   >gi 4580385 gb AAD24364.1_AC007184_4 (AC007184) histone H4
                   [Arabidopsis thaliana] >gi 225838 prf 1314298A histone H4
                   [Arabidopsis thaliana]
```

 Seq. No.
 258434

 Contig ID
 96\_1.R1011

 5'-most EST
 CPR5984\_700044242\_FL

 Method
 BLASTX

 NCBI GI
 g399307

 BLAST score
 684

BLAST score 684
E value 6.0e-72
Match length 235
% identity 57

NCBI Description PRENYL TRANSFERASE > gi 99282 pir A40433 prephytoene

pyrophosphatase dehydrogenase (crtE) homolog - Cyanophora paradoxa >gi\_336639 (M37111) prephytoene pyrophosphate dehydrogenase [Cyanophora paradoxa] >gi\_1016130 (U30821)

prenyl transferase [Cyanophora paradoxa]

Seq. No. 258435 Contig ID 100 1.R1011 5'-most FST LIB3137-020-01

5'-most EST LIB3137-020-Q1-K1-B4

 Seq. No.
 258436

 Contig ID
 101\_1.R1011

5'-most EST LIB3069-020-Q1-K1-E12

Method BLASTX
NCBI GI 94105772
BLAST score 804
E value 7.0e-86
Match length 183
% identity 53

NCBI Description (AF049917) PGP9B [Petunia x hybrida]

 Seq. No.
 258437

 Contig ID
 101\_2.R1011

 5'-most EST
 cyk700049473.f1

Method BLASTX



```
NCBI GI
                  g4105772
                   379
BLAST score
                   3.0e-36
E value
                   92
Match length
                   42
% identity
                  (AF049917) PGP9B [Petunia x hybrida]
NCBI Description
                   258438
Seq. No.
                   101 3.R1011
Contig ID
                   LIB3061-021-Q1-K1-D2
5'-most EST
                   BLASTX
Method
                   g4105772
NCBI GI
BLAST score
                   232
                   2.0e-21
E value
Match length
                   99
                   54
% identity
                  (AF049917) PGP9B [Petunia x hybrida]
NCBI Description
                   258439
Seq. No.
Contia ID
                   101 4.R1011
                   LIB3062-030-Q1-K1-A5
5'-most EST
Seq. No.
                   258440
Contig ID
                   102 1.R1011
                   CPR6257_LIB81-015-Q1-E1-D5 FL
5'-most EST
                   BLASTX
Method
                   q2529421-
NCBI GI
BLAST score
                   1079
E value
                   1.0e-118
Match length
                   446
                   49
% identity
                  (U73935) unknown [Shewanella sp. SCRC-2738]
NCBI Description
                   258441
Seq. No.
                   105 1.R1011
Contig ID
                   CPR6635 700802282 FL
5'-most EST
                   BLASTX
Method
NCBI GI
                   g100939
                   595
BLAST score
                   5.0e-80
E value
                   244
Match length
                   68
% identity
                  zein precursor - maize
NCBI Description
                   258442
Seq. No.
                   105_2.R1011
Contig ID
                   uC-zmflb73304a01a1
5'-most EST
                   BLASTX
Method
                   q4105798
NCBI GI
BLAST score
                   855
                   1.0e-91
E value
                   246
Match length
                   54
% identity
                  (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                   258443
Seq. No.
```

105\_3.R1011

Contig ID

Match length

% identity

167 26



5'-most EST LIB3180-013-P2-M1-D8 Method BLASTX NCBI GI q141606 BLAST score 634 6.0e-66 E value 240 Match length 58 % identity ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1) NCBI Description >gi\_72309\_pir\_\_ZIZMD1 19K zein precursor (clone cZ19D1) maize >gi\_168682 (M12144) 19 kDa zein protein [Zea mays] 258444 Seq. No. 105 4.R1011 Contig ID LIB3059-058-Q1-K1-H12 5'-most EST Method BLASTX NCBI GI q141606 BLAST score 493 E value 2.0e-49 Match length 183 59 % identity ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1) NCBI Description >gi\_72309\_pir\_\_ZIZMD1 19K zein precursor (clone cZ19D1) maize >gi\_168682 (M12144) 19 kDa zein protein [Zea mays] 258445 Seq. No. 105 5.R1011 Contig ID LIB3061-021-Q1-K1-E7 5'-most EST BLASTX Method NCBI GI q141606 699 BLAST score 1.0e-73 E value 240 Match length 66 % identity ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1) NCBI Description >gi\_72309\_pir\_\_ZIZMD1 19K zein precursor (clone cZ19D1) maize >gi 168682 (M12144) 19 kDa zein protein [Zea mays] Seq. No. 258446 105\_6.R1011 Contig ID LIB3117-010-Q1-K1-F7 5'-most EST Method BLASTX NCBI GI g2832243 BLAST score 684 1.0e-71 E value 237 Match length 68 % identity (AF031569) 22-kDa alpha zein 4 [Zea mays] NCBI Description 258447 Seq. No. 105 7.R1011 Contig ID LIB3059-002-Q1-K2-F3 5'-most EST Method BLASTN NCBI GI q4140643 130 BLAST score 1.0e-66 E value

```
Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
                  258448
Seq. No.
Contig ID
                  105 8.R1011
                  LIB3061-037-Q1-K1-B6
5'-most EST
                  BLASTX
Method
NCBI GI
                  q468516
                  451
BLAST score
                  2.0e-44
E value
                  223
Match length
                  83
% identity
NCBI Description
                  (X55724) zein [Zea mays]
Seq. No.
                  258449
                  105 9.R1011
Contig ID
5'-most EST
                  LIB3061-048-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                   q141613
                   589
BLAST score
                   5.0e-61
E value
                   140
Match length
                   88
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                  >gi 72305 pir ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]
                   258450
Seq. No.
Contig ID
                   105 10.R1011
5'-most EST
                   LIB3117-015-Q1-K1-C4
                   BLASTX
Method
NCBI GI
                   q2832243
BLAST score
                   655
E value
                   2.0e-68
Match length
                   171
                   80
% identity
                  (AF031569) 22-kDa alpha zein 4 [Zea mays]
NCBI Description
Seq. No.
                   258451
                   105 12.R1011
Contig ID
                   LIB3061-006-Q1-K1-H10
5'-most EST
                   BLASTX
Method
                   q72307
NCBI GI
                   343
BLAST score
                   5.0e-32
E value
                   144
Match length
                   60
% identity
                  22K zein precursor (clone pZ22.3) - maize >gi_168686
NCBI Description
                   (J01246) 26.99 kd zein protein [Zea mays]
```

Seq. No. 258452 Contig ID 105\_14.R1011

5'-most EST LIB3061-046-Q1-K1-B8

Method BLASTX
NCBI GI g141612
BLAST score 238
E value 7.0e-20



```
Match length
                  84
                  95
% identity
                  ZEIN-ALPHA PRECURSOR (22 KD) (CLONE 22C2)
NCBI Description
                  >gi 72306_pir__ZIZMC2 22K zein precursor (clone cZ22C2) -
                  maize (fragment) >gi_168688 (M12141) 22 kDa zein protein
                  [Zea mays]
                  258453
Seq. No.
                  105 18.R1011
Contig ID
                  LIB3181-008-P1-K2-F8
5'-most EST
                  BLASTX
Method
NCBI GI
                  g22220
BLAST score
                  191
                  2.0e-14
E value
Match length
                  85
                  52
% identity
                  (X55723) 22 kD zein [Zea mays]
NCBI Description
                  258454
Seq. No.
                  105 19.R1011
Contig ID
                  LIB3151-062-Q1-K1-H6
5'-most EST
Method
                  BLASTX
NCBI GI
                  g141606
BLAST score
                  291
                  1.0e-34
E value
Match length
                  133
% identity
                  67
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
NCBI Description
                  >gi 72309 pir__ZIZMD1 19K zein precursor (clone cZ19D1) -
                  maize >qi 168682 (M12144) 19 kDa zein protein [Zea mays]
                  258455
Seq. No.
                  105 20.R1011
Contig ID
                  LIB3152-042-P1-K1-C2
5'-most EST
                  BLASTN
Method
                  g168681
NCBI GI
BLAST score
                   216
E value
                   1.0e-118
                   352
Match length
% identity
                   91
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                  >gi 270686 gb I03333 Sequence 8 from Patent US
                   258456
Seq. No.
                   105 27.R1011
Contig ID
                   uC-zmflmo17290c02b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   q4105798
BLAST score
                   410
E value
                   8.0e-40
                   201
Match length
                   54
% identity
```

Seq. No. 258457 Contig ID 105 28.R1011

NCBI Description

5'-most EST LIB3151-049-P1-K1-H6

(AF049930) PGP237-11 [Petunia x hybrida]



```
BLASTX
Method
NCBI GI
                  g141606
                  392
BLAST score
                  8.0e-38
E value
Match length
                   127
                   65
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
NCBI Description
                  >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) -
                  maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]
                   258458
Seq. No.
                   105 29.R1011
Contig ID
                   LIB3151-062-Q1-K1-A1
5'-most EST
                   BLASTX
Method
                   g141606
NCBI GI
                   280
BLAST score
                   4.0e-36
E value
Match length
                   159
% identity
                   58
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19D1)
NCBI Description
                   >gi_72309_pir__ZIZMD1 19K zein precursor (clone cZ19D1) -
                   maize >gi_168682 (M12144) 19 kDa zein protein [Zea mays]
                   258459
Seq. No.
                   105 30.R1011
Contig ID
                   LIB3059-015-Q1-K1-C11
5'-most EST
                   BLASTX
Method
                   g141613
NCBI GI
BLAST score
                   206
                   3.0e-16
E value
                   51
Match length
                   82
% identity
                   ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
NCBI Description
                   >gi 72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) -
                   maize >gi_22532_emb_CAA24725_ (V01478) zein [Zea mays]
                   258460
Seq. No.
                   105 37.R1011
Contig ID
                   LIB3076-042-Q1-K1-A11
5'-most EST
                   BLASTN
Method
                   q4185305
NCBI GI
                   166
BLAST score
                   1.0e-88
E value
                   174
Match length
                   99
 % identity
                   Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                   protein, polyprotein, and copia protein genes, complete
                   cds; and unknown genes
                   258461
 Seq. No.
                   105 41.R1011
 Contig ID
                   ypc700804679.h1
 5'-most EST
```

BLASTN

Method g168681 NCBI GI 46 BLAST score 4.0e-17 E value



Match length 121 % identity 92

NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds. >gi 270686\_gb\_I03333\_ Sequence 8 from Patent US

Seq. No. 258462 Contig ID 106\_1.R1011

5'-most EST LIB3136-011-Q1-K1-H10

Method BLASTX
NCBI GI g1353135
BLAST score 305
E value 2.0e-27
Match length 140
% identity 43

% identity 43 NCBI Description PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN

CHROMOSOME II PRECURSOR >gi\_3874887\_emb\_CAA88100\_ (Z48045) similar to serine/threonine kinase; cDNA EST EMBL:D26974 comes from this gene; cDNA EST EMBL:D26978 comes from this gene; cDNA EST EMBL:D26977 comes from this gene; cDNA EST

EMBL: D26976 comes from this gene; cDNA EST E

Seq. No. 258463

Contig ID 106 2.R1011

5'-most EST LIB83-016-Q1-E1-H9

Method BLASTX
NCBI GI g1353135
BLAST score 410
E value 1.0e-39
Match length 201
% identity 42

NCBI Description PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN

CHROMOSOME II PRECURSOR >gi\_3874887\_emb\_CAA88100\_ (Z48045) similar to serine/threonine kinase; cDNA EST EMBL:D26974 comes from this gene; cDNA EST EMBL:D26978 comes from this gene; cDNA EST EMBL:D26977 comes from this gene; cDNA EST

EMBL: D26976 comes from this gene; cDNA EST E

Seq. No. 258464 Contig ID 107 1.R1011

Method BLASTX
NCBI GI g2735764
BLAST score 515
E value 7.0e-52
Match length 203
% identity 52

NCBI Description (AF008651) MADS transcriptional factor; STMADS16 [Solanum

tuberosum]

Seq. No. 258465 Contig ID 109\_1.R1011

Method BLASTX
NCBI GI g2735764
BLAST score 465
E value 5.0e-46
Match length 200



```
% identity
                   (AF008651) MADS transcriptional factor; STMADS16 [Solanum
NCBI Description
                  tuberosum]
                  258466
Seq. No.
                  109 2.R1011
Contig ID
                  LIB189-012-Q1-E1-F6
5'-most EST
Method
                  BLASTX
                  q2735764
NCBI GI
                   424
BLAST score
                   3.0e-41
E value
                   190
Match length
                   47
% identity
                   (AF008651) MADS transcriptional factor; STMADS16 [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   258467
                   111 1.R1011
Contig ID
5'-most EST
                   pmx700083990.h1
                   BLASTX
Method
                   q4322475
NCBI GI
                   287
BLAST score
                   3.0e-25
E value
Match length
                   90
                   64
% identity
                   (AF086642) putative MADS box transcription factor ETL
NCBI Description
                   [Eucalyptus globulus subsp. globulus]
Seq. No.
                   258468
Contig ID
                   112 1.R1011
                   uC-zmflb73200b03b1
5'-most EST
                   BLASTX
Method
                   q2979566
NCBI GI
BLAST score
                   458
                   3.0e-45
E value
Match length
                   210
                   50
% identity
                  (AC003680) MADS box protein AGL20 [Arabidopsis thaliana]
NCBI Description
                   258469
Seq. No.
                   112 3.R1011
Contig ID
                   yyf700348009.h1
5'-most EST
                   BLASTX
Method
                   g695690
NCBI GI
                   284
BLAST score
                   2.0e-25
E value
                   61
Match length
                   92
% identity
                  (X79281) DAL3 protein [Picea abies]
NCBI Description
                   258470
Seq. No.
                   113_1.R1011
Contig ID
                   CPR6875_700282564_FL
 5'-most EST
                   BLASTX
Method
                   g1905930
NCBI GI
                   1013
BLAST score
```

35680

1.0e-110

E value



Match length 240 % identity 83

(U31994) MADS box protein [Oryza sativa] NCBI Description

Seq. No. 258471 113 2.R1011 Contig ID

uC-zmflmo17263a07b1 5'-most EST

Method BLASTX q3851333 NCBI GI BLAST score 1180 1.0e-130 E value Match length 231 % identity 97

(Y09302) putative MADS-domain transcription factor [Zea NCBI Description

mays]

Seq. No. 258472 113 3.R1011 Contig ID

5'-most EST CPR6888 700468216 FL

BLASTX Method q1483232 NCBI GI BLAST score 594 4.0e-61 E value Match length 248 54 % identity

(X99655) MADS5 protein [Betula pendula] NCBI Description

258473 Seq. No. Contig ID 113 4.R1011

CPR6882\_700350443\_FL 5'-most EST

BLASTX Method g3851333 NCBI GI BLAST score 1155 1.0e-127 E value 230 Match length

97 % identity

(Y09302) putative MADS-domain transcription factor [Zea NCBI Description

mays]

258474 Seq. No. 113 5.R1011 Contig ID

 $uC-\overline{z}mflB73045d06b1$ 5'-most EST

BLASTX Method q4204232 NCBI GI BLAST score 768 2.0e-81 E value 245 Match length 65 % identity

(AF035378) MADS-box protein 1 [Lolium temulentum] NCBI Description

258475 Seq. No. 113 6.R1011 Contig ID

5'-most EST LIB3068-061-Q1-K1-D4

BLASTX Method g3851333 NCBI GI BLAST score 1155 1.0e-127 E value

Match length

104



```
230
Match length
                   97
% identity
                   (Y09302) putative MADS-domain transcription factor [Zea
NCBI Description
                   mays]
                   258476
Seq. No.
                   113 7.R1011
Contig ID
                   uC-\overline{z}mflmo17035a10b1
5'-most EST
                   BLASTX
Method
                   g4204232
NCBI GI
                   762
BLAST score
                   8.0e-81
E value
                   244
Match length
                   65
% identity
                   (AF035378) MADS-box protein 1 [Lolium temulentum]
NCBI Description
                   258477
Seq. No.
Contig ID
                   113 8.R1011
                   uC-zmflmo17030g11b1
5'-most EST
Method
                   BLASTX
                   g2286111
NCBI GI
                   280
BLAST score
                   1.0e-24
E value
                   89
Match length
                   64
% identity
                   (U78891) MADS box protein [Oryza sativa]
NCBI Description
Seq. No.
                   258478
Contig ID
                   116 1.R1011
                   CPR6892 700612251_FL
5'-most EST
                   BLASTX
Method
                   q886401
NCBI GI
                   999
BLAST score
                   1.0e-108
E value
                   209
Match length
                   91
% identity
                   (L37526) MADS box protein [Oryza sativa]
NCBI Description
                   258479
Seq. No.
                   119 1.R1011
Contig ID
                   uC-\overline{z}mf1b73020h04b1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g939785
BLAST score
                   281
                   9.0e-30
E value
                   132
Match length
                    61
% identity
NCBI Description
                   (L46400) MADS box protein [Zea mays]
                    258480
Seq. No.
                   120 1.R1011
Contig ID
                   LIB3088-005-Q1-K1-C12
5'-most EST
Method
                   BLASTX
                    g3892652
NCBI GI
BLAST score
                    390
                    3.0e-37
E value
```

NCBI GI

E value

BLAST score

g3646324 417

3.0e-58



% identity (Y09303) putative MADS-domain transcription factor [Zea NCBI Description 258481 Seq. No. 120 2.R1011 Contig ID LIB3067-059-Q1-K1-A11 5'-most EST Method BLASTX NCBI GI q3892652 BLAST score 639 1.0e-66 E value Match length 155 % identity 83 (Y09303) putative MADS-domain transcription factor [Zea NCBI Description mays] 258482 Seq. No. Contig ID 120 3.R1011 LIB3067-032-Q1-K1-B1 5'-most EST BLASTX Method NCBI GI q3892652 BLAST score 419 E value 2.0e-41 Match length 103 84 % identity (Y09303) putative MADS-domain transcription factor [Zea NCBI Description mays] 258483 Seq. No. 123 1.R1011 Contig ID fdz701160751.h1 5'-most EST BLASTX Method g2961437 NCBI GI 907 BLAST score 7.0e-98E value 212 Match length 80 % identity NCBI Description (L37527) MADS box protein [Oryza sativa] 258484 Seq. No. 124 1.R1011 Contig ID CPR6886\_700434680\_FL 5'-most EST BLASTX Method g3493647 NCBI GI 217 BLAST score 3.0e-17 E value 126 Match length 42 % identity (AF082531) transcription activator [Pimpinella brachycarpa] NCBI Description Seq. No. 258485 126\_1.R1011 Contig ID uC-zmflb73062g04b1 5'-most EST Method BLASTX



```
239
Match length
                   58
% identity
                  (AJ000761) MADS-box protein [Malus domestica]
NCBI Description
                   258486
Seq. No.
                   129 1.R1011
Contig ID
                   pwr700450237.h1
5'-most EST
Method
                   BLASTX
                   g2281705
NCBI GI
BLAST score
                   2200
                   0.0e + 00
E value
Match length
                   539
% identity
                   81
                  (AF013979) ethylene responsive factor [Oryza sativa]
NCBI Description
Seq. No.
                   258487
                   129 2.R1011
Contig ID
                   uC-zmflmo17059f05a1
5'-most EST
Seq. No.
                   258488
                   130 1.R1011
Contig ID
                   xsy700212586.h1
5'-most EST
Method
                   BLASTX
                   g4105633
NCBI GI
BLAST score
                   1127
                   1.0e-123
E value
                   549
Match length
% identity
                   46
                   (AF048982) putative ethylene receptor [Arabidopsis
NCBI Description
                   thaliana]
                   258489
Seq. No.
                   130 2.R1011
Contig ID
                   tzu700203005.h1
5'-most EST
                   BLASTX
Method
                   g4105633
NCBI GI
                   195
BLAST score
                   3.0e-15
E value
                   97
Match length
                   45
% identity
                   (AF048982) putative ethylene receptor [Arabidopsis
NCBI Description
                   thaliana]
                   258490
Seq. No.
                   132 1.R1011
Contig ID
                   LIB3076-044-Q1-K1-E5
5'-most EST
                   BLASTX
Method
                   g3913427
NCBI GI
                   2087
BLAST score
                   0.0e + 00
E value
                   400
Match length
                   100
% identity
NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
```

S-adenosylmethionine decarboxylase [Zea mays]

Seq. No.

258491

(SAMDC) >gi 1532073 emb\_CAA69075\_ (Y07767)

```
Contig ID
                  132 2.R1011
5'-most EST
                  LIB189-030-Q1-E1-D11
Method
                  BLASTX
                  q3913427
NCBI GI
BLAST score
                  1111
                  1.0e-122
E value
                  242
Match length
                  87
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >qi 1532073 emb CAA69075_ (Y07767)
                  S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.
                  258492
                  132 3.R1011
Contig ID
                  LIB3137-035-Q1-K1-B5
5'-most EST
                  BLASTX
Method
NCBI GI
                  q2129921
BLAST score
                  163
                   9.0e-11
E value
                   36
Match length
                   83
% identity
                  hypothetical protein 1 - Madagascar periwinkle >gi_758694
NCBI Description
                   (U12573) putative [Catharanthus roseus]
                   258493
Seq. No.
                   132 4.R1011
Contig ID
                   qmh700029323.f1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q1532072
BLAST score
                   289
                   1.0e-161
E value
                   301
Match length
                   99
% identity
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
                   258494
Seq. No.
                   132 6.R1011
Contig ID
                   uC-zmflmo17336b03b1
5'-most EST
                   BLASTX
Method
                   q2129921
NCBI GI
BLAST score
                   165
                   3.0e-11
E value
Match length
                   43
                   70
% identity
                   hypothetical protein 1 - Madagascar periwinkle >gi_758694
```

NCBI Description (U12573) putative [Catharanthus roseus]

258495 Seq. No. 132 8.R1011 Contig ID

uC-zmflmo17125d12b15'-most EST

BLASTX Method g2131329 NCBI GI 157 BLAST score 5.0e-10 E value 56 Match length 50 % identity

NCBI Description hypothetical protein YDL087c - yeast (Saccharomyces



cerevisiae) >gi\_1431114\_emb\_CAA98653\_ (Z74135) ORF YDL087c [Saccharomyces cerevisiae]

 Seq. No.
 258496

 Contig ID
 132\_9.R1011

 5'-most EST
 tfd700572020.h1

 Method
 BLASTX

 NCBI GI
 g3913427

 BLAST score
 706

 E value
 4.0e-74

E value 4.0e-Match length 144 % identity 94

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi\_1532073\_emb\_CAA69075\_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

Seq. No. 258497 Contig ID 132 10.R1011

5'-most EST uC-zmflMo17002c08b1

Method BLASTX
NCBI GI g2131329
BLAST score 152
E value 1.0e-09
Match length 48
% identity 58

% identity 58 NCBI Description hypothetical protein YDL087c - yeast (Saccharomyces

cerevisiae) >gi\_1431114\_emb\_CAA98653\_ (Z74135) ORF YDL087c

[Saccharomyces cerevisiae]

Seq. No. 258498 Contig ID 132\_11.R1011

5'-most EST yyf700351472.h1

Method BLASTX
NCBI GI g2213558
BLAST score 157
E value 1.0e-09
Match length 88
% identity 45

NCBI Description (Z97052) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 258499

Contig ID 132\_12.R1011

5'-most EST LIB3067-035-Q1-K1-H9

Method BLASTX
NCBI GI g3913427
BLAST score 625
E value 2.0e-65
Match length 125
% identity 97

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi\_1532073\_emb\_CAA69075\_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

Seq. No. 258500 Contig ID 132\_14.R1011

5'-most EST uC-zmflMo17010b07b1

Method BLASTX



NCBI GI g2129921 152 BLAST score 1.0e-09 E value 34 Match length 79 % identity hypothetical protein 1 - Madagascar periwinkle >gi\_758694 NCBI Description (U12573) putative [Catharanthus roseus] 258501 Seq. No. 132 16.R1011 Contig ID uC-zmflmo17288d05b1 5'-most EST 258502 Seq. No. 132 17.R1011 Contig ID uC-zmrob73076g12b1 5'-most EST BLASTX Method g2129921 NCBI GI BLAST score 167 2.0e-11 E value Match length 36 83 % identity hypothetical protein 1 - Madagascar periwinkle >gi 758694 NCBI Description (U12573) putative [Catharanthus roseus] 258503 Seq. No. 132 20.R1011 Contig ID LIB3069-042-Q1-K1-A11 5'-most EST BLASTN Method NCBI GI g1532072 191 BLAST score 1.0e-103 E value 234 Match length 96 % identity NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase 258504 Seq. No. 132 22.R1011 Contig ID 5'-most EST uC-zmflmo17061d09b1 Method BLASTX g3913427 NCBI GI 648 BLAST score 1.0e-78 E value 182 Match length 88 % identity S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) NCBI Description (SAMDC) >gi\_1532073\_emb\_CAA69075\_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays] 258505 Seq. No. 132\_26.R1011 Contig ID LIB3137-028-Q1-K1-A3 5'-most EST BLASTN Method NCBI GI q1532072

115 BLAST score 6.0e-58 E value

139 Match length 96 % identity



```
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
                  258506
Seq. No.
                  132 28.R1011
Contig ID
5'-most EST
                  uC-zmflmo17221d07a1
                  258507
Seq. No.
                  132 29.R1011
Contig ID
                  uC-zmflMo17004c08b1
5'-most EST
                  258508
Seq. No.
                  132 30.R1011
Contig ID
                  uC-zmflb73064a03b1
5'-most EST
                  BLASTX
Method
NCBI GI
                  g3913427
BLAST score
                   564
                   9.0e-58
E value
Match length
                   116
                   98
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi 1532073 emb CAA69075_ (Y07767)
                   S-adenosylmethionine decarboxylase [Zea mays]
                   258509
Seq. No.
                   132 32.R1011
Contig ID
                   LIB3069-036-Q1-K1-A4
5'-most EST
Seq. No.
                   258510
                   132 40.R1011
Contig ID
                   LIB3150-055-Q1-N1-C2
5'-most EST
                   BLASTN
Method
                   g1532072
NCBI GI
                   34
BLAST score
                   1.0e-09
E value
                   38
Match length
                   97
% identity
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
                   258511
Seq. No.
                   132 42.R1011
Contig ID
5'-most EST
                   qw1700616273.h1
                   BLASTN
Method
                   g1532072
NCBI GI
                   127
BLAST score
                   4.0e-65
E value
                   135
Match length
                   99
% identity
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
Seq. No.
                   258512
                   134 1.R1011
Contig ID
                   uC-zmflb73028q02b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2580499
BLAST score
                   2113
```

35688

0.0e+00

565

E value Match length



% identity (U67186) NADPH: ferrihemoprotein oxidoreductase NCBI Description [Eschscholzia californica] Seq. No. 258513 134 2.R1011 Contig ID uC-zmflmo17341a07b1 5'-most EST 258514 Seq. No. 134 3.R1011 Contig ID LIB3078-040-Q1-K1-E8 5'-most EST BLASTX Method g2809385 NCBI GI 677 BLAST score 5.0e-71E value 155 Match length 79 % identity (AF024634) NADPH cytochrome P450 reductase [Petroselinum NCBI Description crispum] 258515 Seq. No. 134 5.R1011 Contig ID xsy700208936.h1 5'-most EST BLASTX Method NCBI GI g2809385 603 BLAST score 2.0e-62 E value 144 Match length 76 % identity (AF024634) NADPH cytochrome P450 reductase [Petroselinum NCBI Description crispum] 258516 Seq. No. Contig ID 134 9.R1011 5'-most EST LIB3067-037-Q1-K1-H12 258517 Seq. No. 134 14.R1011 Contig ID ypc700798870.hl 5'-most EST Method BLASTX NCBI GI g1006694 BLAST score 246 2.0e-21 E value Match length 62 69 % identity (Z49767) NADPH-cytochrome P450 reductase [Pseudotsuga NCBI Description menziesii] 258518 Seq. No. Contig ID 135\_6.R1011 uwc700154463.hl 5'-most EST 258519

Seq. No. 258519
Contig ID 135\_7.R1011
5'-most EST cyk700049132.f1

Method BLASTX NCBI GI g1173055



```
244
BLAST score
                  3.0e-34
E value
                  82
Match length
% identity
                  94
                  60S RIBOSOMAL PROTEIN L11 (L5) >gi_541961_pir__S42497
NCBI Description
                  ribosomal protein L11.e - alfalfa >gi_1076504_pir__S51819
                  RL5 ribosomal protein - alfalfa >gi 463252 emb_CAA55090_
                  (X78284) RL5 ribosomal protein [Medicago sativa]
                  258520
Seq. No.
Contig ID
                  135 8.R1011
```

5'-most EST LIB143-052-Q1-E1-A1
Method BLASTX
NCBI GI g1173055
BLAST score 342
E value 2.0e-32
Match length 66

% identity 98

NCBI Description 60S RIBOSOMAL PROTEIN L11 (L5) >gi\_541961\_pir\_\_S42497 ribosomal protein L11.e - alfalfa >gi\_1076504\_pir\_\_S51819 RL5 ribosomal protein - alfalfa >gi\_463252\_emb\_CAA55090\_

(X78284) RL5 ribosomal protein [Medicago sativa]

 Seq. No.
 258521

 Contig ID
 135\_9.R1011

 5'-most EST
 uC-zmroteosinte047f12b2

Seq. No. 258522

Contig ID 135\_10.R1011 5'-most EST LIB3067-033-Q1-K1-G6

Seq. No. 258523

Contig ID 135\_11.R1011 5'-most EST wty700167572.h1

Method BLASTX
NCBI GI g3377851
BLAST score 163
E value 4.0e-11
Match length 49
% identity 65

NCBI Description (AF076274) contains similarity to ATPases associated with various cellular activities (Pfam: AAA.hmm, score: 155.05)

[Arabidopsis thaliana]

 Seq. No.
 258524

 Contig ID
 135\_12.R1011

 5'-most EST
 wty700171561.h1

 Method
 BLASTX

 NCBI GI
 g462013

 BLAST score
 221

E value 3.0e-18
Match length 47
% identity 96

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi\_542022\_pir\_\_S39558 HSP90 homolog - Madagascar periwinkle >gi\_348696 (L14594) heat shock protein 90

[Catharanthus roseus]



```
258525
Seq. No.
Contig ID
                  135 13.R1011
                  nbm700466246.hl
5'-most EST
Method
                  BLASTX
                  g3123270
NCBI GI
                  283
BLAST score
                  2.0e-33
E value
                  82
Match length
                  91
% identity
                  40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)
NCBI Description
                  >qi 2463335 emb CAA75242 (Y15009) ribosomal protein S4
                   [Oryza sativa]
                  258526
Seq. No.
                  135 14.R1011
Contig ID
5'-most EST
                  gct701178281.hl
                  BLASTX
Method
NCBI GI
                  q4006914
                   302
BLAST score
                  2.0e-27
E value
                   66
Match length
                   80
% identity
                  (Z99708) serine C-palmitoyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   258527
Seq. No.
                   135 15.R1011
Contig ID
5'-most EST
                   LIB3067-023-Q1-K1-D4
Method
                   BLASTX
                   g4455246
NCBI GI
                   195
BLAST score
                   7.0e-15
E value
                   59
Match length
                   59
% identity
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
                   258528
Seq. No.
                   135 16.R1011
Contig ID
                   uC-zmflmo17035c10b1
5'-most EST
                   258529
Seq. No.
                   135 17.R1011
Contig ID
                   hvj700623950.hl
5'-most EST
                   258530
Seq. No.
                   135_18.R1011
Contig ID
                   LIB143-030-Q1-E1-H5
5'-most EST
Seq. No.
                   258531
                   135 19.R1011
Contig ID
                   uC-zmflmo17128h07b1
5'-most EST
                   BLASTX
Method
                   q2980794
NCBI GI
                   391
BLAST score
```

35691

6.0e-38

90

E value

Match length



% identity (AL022197) myb - like protein [Arabidopsis thaliana] NCBI Description Seq. No. 258532 Contig ID 135 20.R1011 LIB3060-035-Q1-K1-F9 5'-most EST BLASTX Method NCBI GI g1172817 BLAST score 293 2.0e-26 E value 74 Match length 77 % identity 60S RIBOSOMAL PROTEIN L11B (L16B) >gi 550547 emb CAA57396 NCBI Description (X81800) ribosomal protein L16 [Arabidopsis thaliana] >gi\_4539392\_emb\_CAB37458.1\_ (AL035526) ribosomal protein L11, cytosolic [Arabidopsis thaliana] Seq. No. 258533 135 21.R1011 Contig ID uC-zmflmo17293c11b1 5'-most EST 258534 Seq. No. Contig ID 135 22.R1011 mwy700439712.h15'-most EST BLASTN Method NCBI GI g22614 39 BLAST score 2.0e-12 E value Match length 63 90 % identity S.vulgare pepC gene for PEP carboxylase NCBI Description 258535 Seq. No. 135 23.R1011 Contig ID LIB3088-002-Q1-K1-B2 5'-most EST 258536 Seq. No. 135 24.R1011 Contig ID 5'-most EST fwa700100017.h1 BLASTX Method q729442 NCBI GI 194 BLAST score 8.0e-15 E value 75 Match length 52 % identity PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR NCBI Description >gi\_166380 (M80235) glucose-regulated endoplasmic reticular protein precursor [Medicago sativa] 258537 Seq. No. 135\_25.R1011 Contig ID uC-zmflb73359e06a2 5'-most EST

5'-most EST uC-zmflb73359
Method BLASTX
NCBI GI g3687389
BLAST score 207
E value 2.0e-16
Match length 67

5'-most EST



```
% identity
                  (Y16124) putative cullin protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  258538
Contig ID
                  135 26.R1011
                  LIB3062-027-Q1-K1-F7
5'-most EST
Seq. No.
                  258539
                  135 27.R1011
Contig ID
                  ymt700221253.h1
5'-most EST
Seq. No.
                  258540
                  135 28.R1011
Contig ID
                  ntr700077051.h1
5'-most EST
                  BLASTX
Method
                  g4249419
NCBI GI
BLAST score
                  198
                   5.0e-15
E value
Match length
                  82
% identity
                   50
                   (AC006072) hypothetical protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   258541
                   135 29.R1011
Contig ID
5'-most EST
                  pmx700083985.h1
                   258542
Seq. No.
Contig ID
                   135 30.R1011
                   LIB3279-057-P1-K1-F4
5'-most EST
Method
                   BLASTX
                   q4006914
NCBI GI
                   409
BLAST score
E value
                   8.0e-40
                   150
Match length
                   55
% identity
                  (Z99708) serine C-palmitoyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   258543
Seq. No.
                   135 31.R1011
Contig ID
                   uC-zmflb73204h08b1
5'-most EST
                   258544
Seq. No.
                   135 32.R1011
Contig ID
                   wty700163472.hl
5'-most EST
                   BLASTN
Method
                   g529093
NCBI GI
                   67
BLAST score
                   5.0e-29
E value
                   184
Match length
                   84
% identity
NCBI Description Rice mRNA for proteasome C2 subunit, complete cds
                   258545
Seq. No.
                   135 33.R1011
Contig ID
```

35693

LIB3151-048-P1-K1-D3



Method BLASTX
NCBI GI g4455349
BLAST score 195
E value 9.0e-15
Match length 151
% identity 34
NCBL Description (AL03552)

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 258546

Contig ID 135\_34.R1011

5'-most EST uC-zmflb73100f09b1

Method BLASTX
NCBI GI g3377851
BLAST score 175
E value 2.0e-12
Match length 44
% identity 75

NCBI Description (AF076274) contains similarity to ATPases associated with

various cellular activities (Pfam: AAA.hmm, score: 155.05)

[Arabidopsis thaliana]

Seq. No. 258547

Contig ID 135\_35.R1011 50-most EST mwy700439817.h1

Method BLASTX
NCBI GI g1709758
BLAST score 306
E value 4.0e-47
Match length 107
% identity 93

NCBI Description PROTEASOME COMPONENT C2 (MACROPAIN SUBUNIT C2)

(MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C2)

>gi 1066151\_dbj\_BAA07128\_ (D37886) proteasome C2 subunit

[Oryza sativa]

Seq. No. 258548

Contig ID 135\_36.R1011 5'-most EST xdb700341364.h1

Seq. No. 258549

Contig ID 135\_37.R1011 5'-most EST vux700160160.h1 Method BLASTN

NCBI GI g2832242 BLAST score 80 E value 7.0e-37 Match length 141 % identity 96

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 258550

Contig ID 135\_38.R1011

5'-most EST uC-zmflb73067g08a1

Method BLASTX
NCBI GI g2689720
BLAST score 288
E value 6.0e-26



Match length 113 % identity 52

NCBI Description (AF037168) DnaJ homologue [Arabidopsis thaliana]

Seq. No. 258551

Contig ID 135\_39.R1011

5'-most EST uC-zmflmo17397d07a1 Method BLASTX

NCBI GI g544242
BLAST score 236
E value 7.0e-20
Match length 57
% identity 84

NCBI Description ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)

>gi\_485498\_pir\_\_S33533 heat shock protein 90 homolog
precursor - barley >gi\_22652\_emb\_CAA48143\_ (X67960) GRP94

homologue [Hordeum vulgare]

Seq. No. 258552

Contig ID 135\_40.R1011 5'-most EST rv1700455748.h1 Method BLASTX

Method BLASTX
NCBI GI g3377851
BLAST score 161
E value 1.0e-10
Match length 38
% identity 79

NCBI Description (AF076274) contains similarity to ATPases associated with various cellular activities (Pfam: AAA.hmm, score: 155.05)

[Arabidopsis thaliana]

Seq. No. 258553

Contig ID 135\_41.R1011

5'-most EST LIB3075-043-Q1-K1-A6

Method BLASTX
NCBI GI g3914899
BLAST score 331
E value 2.0e-30
Match length 90
% identity 76

NCBI Description 40S RIBOSOMAL PROTEIN S4 >gi\_2331301 (AF013487) ribosomal

protein S4 type I [Zea mays]

Seq. No. 258554

Contig ID 135 42.R1011

5'-most EST uC-zmflb73051f02b1

Seq. No. 258555

Contig ID 135\_43.R1011 5'-most EST xmt700266058.h1

Seq. No. 258556

Contig ID 135\_44.R1011 5'-most EST fdz701164992.h1

Method BLASTX
NCBI GI g3549652
BLAST score 212



2.0e-16 E value 67 Match length 64 % identity (AJ224982) MAP3K epsilon protein kinase [Arabidopsis NCBI Description thaliana] Seq. No. 258557 135 45.R1011 Contig ID uC-zmflmo17283b03b1 5'-most EST BLASTX Method q3914899 NCBI GI 428 BLAST score 6.0e-42 E value 94 Match length 88 % identity 40S RIBOSOMAL PROTEIN S4 >gi\_2331301 (AF013487) ribosomal NCBI Description protein S4 type I [Zea mays] 258558 Seq. No. 135 46.R1011 Contig ID LIB143-026-Q1-E1-F3 5'-most EST BLASTX Method q3549652 NCBI GI 581 BLAST score 9.0e-60 E value 298 Match length 48 % identity (AJ224982) MAP3K epsilon protein kinase [Arabidopsis NCBI Description thaliana] 258559 Seq. No. 135 47.R1011 Contig ID mwy700441514.hl 5'-most EST BLASTX Method NCBI GI g1488521 321 BLAST score 3.0e-29E value 241 Match length 54 % identity (X99938) RNA helicase [Arabidopsis thaliana] NCBI Description Seq. No. 258560 135 48.R1011 Contig ID  $uC-\overline{z}mflb73346e10a2$ 5'-most EST BLASTX Method g544242 NCBI GI 507 BLAST score 2.0e-51 E value 128 Match length 81 % identity ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) NCBI Description >gi\_485498\_pir\_\_S33533 heat shock protein 90 homolog precursor - barley >gi\_22652\_emb\_CAA48143\_ (X67960) GRP94

Seq. No. 258561 Contig ID 135\_49.R1011

homologue [Hordeum vulgare]



LIB3115-015-P1-K1-H6 5'-most EST BLASTX Method g4204293 NCBI GI BLAST score 158 2.0e-10 E value 118 Match length % identity (AC003027) lcl\_prt\_seq No definition line found NCBI Description [Arabidopsis thaliana] 258562 Seq. No. 135 50.R1011 Contig ID 5'-most EST LIB189-004-Q1-E1-G5 Method BLASTX q462013 NCBI GI BLAST score 165 4.0e-11 E value 34 Match length 100 % identity ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) NCBI Description >qi 542022 pir S39558 HSP90 homolog - Madagascar periwinkle >gi\_348696 (L14594) heat shock protein 90 [Catharanthus roseus] 258563 Seq. No. 135 51.R1011 Contig ID LIB3069-005-Q1-K1-F10 5'-most EST BLASTX Method NCBI GI g3549652 BLAST score 384 6.0e - 37E value 92 Match length 83 % identity (AJ224982) MAP3K epsilon protein kinase [Arabidopsis NCBI Description thaliana] 258564 Seq. No. 135 52.R1011 Contig ID nbm700472333.h1 5'-most EST BLASTX Method g544242 NCBI GI 423 BLAST score 2.0e-41 E value 93 Match length 90 % identity ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) NCBI Description >gi\_485498\_pir\_\_S33533 heat shock protein 90 homolog precursor - barley >gi\_22652\_emb\_CAA48143\_ (X67960) GRP94 homologue [Hordeum vulgare] 258565 Seq. No. 135 53.R1011 Contig ID

 Seq. No.
 258565

 Contig ID
 135\_53.R1011

 5'-most EST
 xsy700217062.h1

 Method
 BLASTX

 NCBI GI
 g3377805

 BLAST score
 699

E value

2.0e-73



```
254
Match length
                  53
% identity
                  (AF075597) contains similarity to several apoptosis or
NCBI Description
                  programmed cell death proteins such as rat apoptosis
                  protein RP-8 (GB:M80601) [Arabidopsis thaliana]
                  >gi_3912928_gb_AAC78712.1_ (AF001308) putative zinc finger
                  protein [Arabidopsis thaliana]
                  258566
Seq. No.
                  135 54.R1011
Contig ID
                  ntr700074435.h1
5'-most EST
                  BLASTX
Method
                  g4006914
NCBI GI
BLAST score
                  161
                  9.0e-11
E value
                  81
Match length
                   47
% identity
                   (Z99708) serine C-palmitoyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
                   258567
Seq. No.
                   135 55.R1011
Contig ID
                   ypc700803409.h1
5'-most EST
                   BLASTX
Method
                   g1167955
NCBI GI
                   201
BLAST score
                   2.0e-15
E value
                   116
Match length
                   38
% identity
                   (U43497) putative 32.7 kDa jasmonate-induced protein
NCBI Description
                   [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein
                   [Hordeum vulgare]
                   258568
Seq. No.
                   135 56.R1011
Contig ID
                   LIB3136-056-Q1-K1-G1
5'-most EST
                   BLASTN
Method
                   g2345153
NCBI GI
BLAST score
                   53
                   1.0e-20
E value
                   115
Match length
                   96
% identity
                   Zea mays ribsomal protein S4 (rps4) mRNA, complete cds
NCBI Description
Seq. No.
                   258569
Contig ID
                   135 57.R1011
                   wty700168530.h1
5'-most EST
                   BLASTX
Method
                   g1488647
NCBI GI
BLAST score
                   187
                   1.0e-13
E value
Match length
                   103
                   38
 % identity
```

Seq. No. 258570 Contig ID 135 58.R1011

NCBI Description

35698

(X99937) RNA helicase [Spinacia oleracea]

NCBI Description

thaliana]

```
uC-zmrob73049d01a1
5'-most EST
                  BLASTX
Method
                  q4455246
NCBI GI
BLAST score
                  201
                   4.0e-15
E value
                  59
Match length
                   63
% identity
                  (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                   258571
Seq. No.
                  135 59.R1011
Contig ID
                  LIB143-063-Q1-E1-A11
5'-most EST
                   BLASTX
Method
                   g3377805
NCBI GI
                   581
BLAST score
                   3.0e-73
E value
                   255
Match length
                   55
% identity
                   (AF075597) contains similarity to several apoptosis or
NCBI Description
                   programmed cell death proteins such as rat apoptosis
                   protein RP-8 (GB:M80601) [Arabidopsis thaliana]
                   >gi 3912928 gb AAC78712.1 (AF001308) putative zinc finger
                   protein [Arabidopsis thaliana]
                   258572
Seq. No.
                   135 60.R1011
Contig ID
                   ntr700072029.h1
5'-most EST
                   BLASTN
Method
                   q2832242
NCBI GI
BLAST score
                   99
                   6.0e-48
E value
Match length
                   213
                   92
% identity
                  Zea mays 22-kDa alpha zein gene cluster, complete sequence
NCBI Description
                   258573
Seq. No.
                   141 1.R1011
Contig ID
                   CPR9116consensus FL
5'-most EST
                   BLASTX
Method
                   g3618320
NCBI GI
BLAST score
                   171
                   1.0e-11
E value
Match length
                   100
                   40
 % identity
                   (AB001888) zinc finger protein [Oryza sativa]
NCBI Description
                   258574
Seq. No.
                   142 1.R1011
 Contig ID
                   xmt700264303.h1
 5'-most EST
                   BLASTX
Method
                   q4539315
NCBI GI
                   514
 BLAST score
                   9.0e-52
 E value
                   202
 Match length
                   51
 % identity
                   (AL035679) putative zinc finger protein [Arabidopsis
```

```
258575
Seq. No.
                  142 2.R1011
Contig ID
5'-most EST
                  CPR9117consensus FL
                  BLASTX
Method
                  q4539315
NCBI GI
                  518
BLAST score
                  4.0e-52
E value
Match length
                  206
% identity
                  (AL035679) putative zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
                   258576
Seq. No.
                   142 5.R1011
Contig ID
                   dyk700104747.hl
5'-most EST
                   BLASTX
Method
                   q2052090
NCBI GI
BLAST score
                   363
                   1.0e-34
E value
                   89
Match length
                   80
% identity
                  (Z49145) phenylalanine ammonia-lyase [Hordeum vulgare]
NCBI Description
                   258577
Seq. No.
                   143 1.R1011
Contig ID
                   CPR9150_700620948_FL
5'-most EST
                   BLASTN
Method
NCBI GI
                   g500852
BLAST score
                   53
                   6.0e-21
E value
Match length
                   73
                   93
% identity
                   Zea mays (clone pAKHSDH2) aspartate kinase-homoserine
NCBI Description
                   dehydrogenase mRNA, complete cds
                   258578
Seq. No.
                   144 1.R1011
Contig ID
                   CPR9153_7001180088_FL
5'-most EST
                   BLASTX
Method
                   g1362086
NCBI GI
                   324
BLAST score
                   5.0e-30
E value
Match length
                   68
                   93
% identity
                   5-methyltetrahydropteroyltriglutamate--homocysteine
NCBI Description
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
                   >gi 2129919_pir__$65957
                   5-methyltetrahydropteroyltriglutamate--homocysteine
                   S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle
```

Seq. No. 258579

Contig ID 145\_1.R1011

5'-most EST CPR917\_700209591\_FL

[Catharanthus roseus]

Method BLASTX

>gi\_886471\_emb\_CAA58474\_ (X83499) methionine synthase



50

90

Match length

% identity

```
g1850968
NCBI GI
                   596
BLAST score
                   2.0e-61
E value
                   222
Match length
                   53
% identity
                  (U79733) Hs1pro-1 [Beta procumbens]
NCBI Description
                   258580
Seq. No.
                   145 2.R1011
Contia ID
                   CPR919_700104751_FL
5'-most EST
                   258581
Seq. No.
                   148 1.R1011
Contig ID
                   uC\text{-}zmf1b73283e03b2
5'-most EST
                   BLASTX
Method
                   g4376158
NCBI GI
BLAST score
                   194
                   2.0e-24
E value
                   124
Match length
                   56
% identity
                   (X98873) aspartate kinase [Arabidopsis thaliana]
NCBI Description
                   258582
Seq. No.
                   149_1.R1011
Contig ID
                   CPR9204_700096779_FL
5'-most EST
                   BLASTX
Method
                   g1351904
NCBI GI
                   2626
BLAST score
                   0.0e+00
E value
                   920
Match length
                   99
% identity
                   ASPARTOKINASE 1 / HOMOSERINE DEHYDROGENASE 1 CHLOROPLAST
NCBI Description
                   PRECURSOR (AK-HSDH 1) (AKHSDH1) >gi 500851 (L33912)
                   aspartate kinase-homoserine dehydrogenase [Zea mays]
                   258583
Seq. No.
                   150 1.R1011
Contig ID
                   CPR9205_700086788_FL
 5'-most EST
                   BLASTX
Method
                   g2198851
NCBI GI
BLAST score
                   2138
                   0.0e + 00
E value
Match length
                   483
                    98
 % identity
                   (AF007785) cystathionine gamma-synthase [Zea mays]
 NCBI Description
                    258584
 Seq. No.
                    150 3.R1011
 Contig ID
                    uC-zmrob73061b04a1
 5'-most EST
                    BLASTX
 Method
                    q2198851
 NCBI GI
                    208
 BLAST score
                    3.0e-16
 E value
```

NCBI Description (AF007785) cystathionine gamma-synthase [Zea mays]



```
258585
Seq. No.
                  151 1.R1011
Contig ID
                  LIB3279-005-P1-K1-C2
5'-most EST
                  BLASTX
Method
NCBI GI
                  g1170937
                  1952
BLAST score
                   0.0e + 00
E value
Match length
                   396
                   94
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   258586
Seq. No.
                   151 2.R1011
Contig ID
                   uC-zmflmo17057d08b1
5'-most EST
                   BLASTN
Method
NCBI GI
                   q22091
                   316
BLAST score
                   1.0e-177
E value
                   608
Match length
                   38
% identity
                   Z.diploperennis gene for hydroxyproline-rich glycoprotein
NCBI Description
                   258587
Seq. No.
                   151 3.R1011
Contig ID
                   uC-zmflmo17070b11b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1170937
                   1955
BLAST score
                   0.0e + 00
E value
                   396
Match length
                   95
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   258588
 Seq. No.
                   151 4.R1011
 Contig ID
                   uC-zmflmo17267g02a1
 5'-most EST
                   BLASTN
Method
                   q22091
 NCBI GI
                   299
 BLAST score
                   1.0e-167
 E value
                   415
 Match length
                   95
 % identity
NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein
                   258589
 Seq. No.
                   151 5.R1011
 Contig ID
```

5'-most EST uC-zmflb73152h01b1

BLASTX Method g1076316 NCBI GI 279 BLAST score 3.0e-24E value



```
218
Match length
% identity
                  33
                  drought-induced protein Di19 - Arabidopsis thaliana
NCBI Description
                  >gi 469110 emb_CAA55321_ (X78584) Di19 [Arabidopsis
                  thaliana]
                  258590
Seq. No.
                  151 6.R1011
Contig ID
                  LIB3060-035-Q1-K1-H3
5'-most EST
                  BLASTX
Method
                  q1170937
NCBI GI
BLAST score
                   1945
                   0.0e+00
E value
                   396
Match length
                   94
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   258591
Seq. No.
                   151 7.R1011
Contig ID
                   uC-zmflmo17030b05b1
5'-most EST
                   BLASTN
Method
                   g22332
NCBI GI
                   436
BLAST score
                   0.0e + 00
E value
                   729
Match length
% identity
                   50
NCBI Description Z.mays HRGP gene
                   258592
Seq. No.
                   151 8.R1011
Contig ID
                   uC-zmflmo17335f11b1
5'-most EST
                   BLASTN
Method
                   g257040
NCBI GI
                   499
BLAST score
                   0.0e + 00
E value
                   1051
Match length
                   55
% identity
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
                   258593
Seq. No.
                   151 9.R1011
Contig ID
                   bdu700382902.h1
5'-most EST
                   BLASTX
Method
                   g1495251
NCBI GI
                   1751
BLAST score
                   0.0e+00
E value
                   529
Match length
% identity
                   66
                   (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
```

 Seq. No.
 258594

 Contig ID
 151\_10.R1011

 5'-most EST
 uC-zmflb73001e08b1

Method BLASTX



NCBI GI g1495251 1412 BLAST score 1.0e-157 E value 491 Match length 59 % identity (Z70314) heat-shock protein [Arabidopsis thaliana] NCBI Description 258595 Seq. No. 151 11.R1011 Contig ID tzu700203924.h1 5'-most EST

Method BLASTX
NCBI GI g1495251
BLAST score 2005
E value 0.0e+00
Match length 612
% identity 68

NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No. 258597 Contig ID 151 13.R1011

5'-most EST uC-zmflmo17335a04b1

Method BLASTX
NCBI GI g2129677
BLAST score 208
E value 3.0e-16
Match length 79
% identity 54

NCBI Description probablel N-acetyltransferase hookless 1 - Arabidopsis

thaliana >gi\_1277090 (U50399) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi\_1277092 (U50400) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi\_4468983\_emb\_CAB38297\_ (AL035605) probable N-acetyltransferase hookless 1 [Arabidopsis thaliana]

Seq. No. 258598

Contig ID 151 14.R1011

5'-most EST uC-zmflmo17046g11b1

Method BLASTN
NCBI GI g22332
BLAST score 312
E value 1.0e-175
Match length 383
% identity 95

NCBI Description Z.mays HRGP gene

Seq. No. 258599 Contig ID 151\_15.R1011

5'-most EST LIB3078-032-Q1-K1-D1

Method BLASTX
NCBI GI g1170937
BLAST score 651
E value 5.0e-68
Match length 149

35704



```
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549_emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  258600
Contig ID
                  151 16.R1011
                  uC-zmflB73004h10b1
5'-most EST
                  BLASTN
Method
NCBI GI
                  g22507
BLAST score
                   457
                  0.0e+00
E value
                  502
Match length
                  98
% identity
                  Maize (strain W64A) mRNA for cell wall glycoprotein
NCBI Description
                  258601
Seq. No.
Contig ID
                  151 17.R1011
5'-most EST
                  qw1700616344.h1
                  BLASTX
Method
                  g3941289
NCBI GI
BLAST score
                  814
E value
                   6.0e-87
Match length
                   266
                   56
% identity
                  (AF018093) similarity to SCAMP37 [Pisum sativum]
NCBI Description
Seq. No.
                   258602
                   151 18.R1011
Contig ID
                   wty700167803.h1
5'-most EST
Method
                   BLASTX
                   q1076316
NCBI GI
                   250
BLAST score
                   8.0e-21
E value
                   188
Match length
                   34
% identity
                   drought-induced protein Di19 - Arabidopsis thaliana
NCBI Description
                   >gi 469110 emb CAA55321 (X78584) Di19 [Arabidopsis
                   thaliana]
                   258603
Seq. No.
                   151 19.R1011
Contig ID
                   uC-zmroteosinte069f12b1
5'-most EST
                   BLASTX
Method
                   g1170937
NCBI GI
                   596
BLAST score
                   1.0e-61
E value
Match length
                   124
                   94
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
```

Seq. No. 258604 Contig ID 151\_20.R1011



LIB3069-006-Q1-K1-D5 5'-most EST BLASTX Method g1170937 NCBI GI BLAST score 364 1.0e-34 E value 74 Match length 95 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi\_450549\_emb\_CAA81481\_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 258605 Seq. No. 151 21.R1011 Contig ID uC-zmflmo17151b05b1 5'-most EST Method BLASTN g22268 NCBI GI 287 BLAST score 1.0e-160 E value 394 Match length 96 % identity Maize (strain E41) mRNA for cell wall glycoprotein NCBI Description (partial) >gi\_168458\_gb\_M36914\_MZECWAC Z.mays cell wall protein mRNA, 3' end 258606 Seq. No. 151 22.R1011 Contig ID uC-zmflmo17186c12b1 5'-most EST BLASTX Method g1170937 NCBI GI 664 BLAST score 1.0e-69 E value 129 Match length 98 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi\_450549\_emb\_CAA81481\_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 258607 Seq. No. 151 23.R1011 Contig ID 5'-most EST LIB3067-008-Q1-K1-E2 Method BLASTX NCBI GI q3915131 BLAST score 346 3.0e-32 E value Match length 112 % identity THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) NCBI Description >gi\_426442\_dbj\_BAA04864\_ (D21836) thioredoxin h [Oryza
sativa] >gi\_454882\_dbj\_BAA05546\_ (D26547) rice thioredoxin h [Oryza sativa] >gi 1930072 (U92541) thioredoxin h [Oryza sativa]

258608 Seq. No. 151 24.R1011 Contig ID

5'-most EST

LIB3150-094-P2-K1-D9

Contig ID

Method

NCBI GI

5'-most EST



258609 Seq. No. 151\_25.R1011 Contig ID 5'-most EST uC-zmflmo17297f07b1 BLASTN Method a4007864 NCBI GI 304 BLAST score 1.0e-170 E value 644 Match length 32 % identity Zea mays HRGP gene, AC1503 line NCBI Description 258610 Seq. No. Contig ID 151 27.R1011 uC-zmflmo17202a02b1 5'-most EST BLASTX Method NCBI GI g1170937 BLAST score 381 E value 2.0e-36 71 Match length 97 % identity S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi 450549\_emb\_CAA81481\_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa] 258611 Seq. No. 151 29.R1011 Contig ID 5'-most EST LIB3068-042-Q1-K1-F7 Method BLASTN q22091 NCBI GI 280 BLAST score 1.0e-156 E value 389 Match length % identity 94 NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein 258612 Seq. No. Contig ID 151 30.R1011 5'-most EST zla700380237.h1 Seq. No. 258613 Contig ID 151 31.R1011 uC-zmflb73120h01b1 5'-most EST Method BLASTN NCBI GI g22091 360 BLAST score 0.0e+00E value 830 Match length % identity 30 NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein 258614 Seq. No.

35707

151 34.R1011

BLASTN

g22091

uC-zmflb73413e11a1



```
BLAST score
                  268
                   1.0e-149
E value
Match length
                   440
% identity
                   94
                  Z.diploperennis gene for hydroxyproline-rich glycoprotein
NCBI Description
                   258615
Seq. No.
                   151 38.R1011
Contig ID
                   tzu700206801.h1
5'-most EST
                  BLASTX
Method
                   g1495251
NCBI GI
BLAST score
                   814
                   3.0e-87
E value
                   230
Match length
                   64
% identity
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   258616
Seq. No.
                   151 39.R1011
Contig ID
                   LIB3180-019-P2-M1-B12
5'-most EST
                   BLASTX
Method
                   g1495251
NCBI GI
BLAST score
                   463
                   3.0e-46
E value
                   106
Match length
                   81
% identity
                  (270314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   258617
                   151 40.R1011
Contig ID
                   LIB3137-039-Q1-K1-G5
5'-most EST
Method
                   BLASTX
                   g1170937
NCBI GI
BLAST score
                   445
                   3.0e-44
E value
                   87
Match length
                   98
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   258618
Seq. No.
                   151 41.R1011
Contig ID
                   uC-zmrob73055h06b1
5'-most EST
                   BLASTX
Method
                   q1495251
NCBI GI
                   272
BLAST score
                   7.0e-30
E value
Match length
                   83
                   82
 % identity
```

NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]

258619 Seq. No. 151 43.R1011 Contig ID

uC-zmroteosinte031f03b1 5'-most EST

BLASTX Method

NCBI Description



```
g1495251
NCBI GI
BLAST score
                  632
                   1.0e-102
E value
                  258
Match length
                  71
% identity
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   258620
                   151 44.R1011
Contig ID
                   uC-zmflmo17042h02b1
5'-most EST
                   BLASTN
Method
                   q22091
NCBI GI
BLAST score
                   311
                   1.0e-175
E value
                   446
Match length
                   94
% identity
                  Z.diploperennis gene for hydroxyproline-rich glycoprotein
NCBI Description
Seq. No.
                   258621
                   151 49.R1011
Contig ID
                   nbm700464838.hl
5'-most EST
Seq. No.
                   258622
                   151 52.R1011
Contig ID
                   LIB3078-037-Q1-K1-C6
5'-most EST
                   BLASTX
Method
                   q1495251
NCBI GI
                   238
BLAST score
                   1.0e-19
E value
Match length
                   121
                   50
% identity
                  (Z70314) heat-shock protein [Arabidopsis thaliana]
NCBI Description
                   258623
Seq. No.
                   151 53.R1011
Contig ID
                   xyt700343661.h1
5'-most EST
Method
                   BLASTX
                   g1170937
NCBI GI
BLAST score
                   487
                   6.0e-49
E value
Match length
                   125
                   82
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                   synthetase [Oryza sativa]
                   258624
Seq. No.
                   151_63.R1011
Contig ID
                   uC-zmflmo17404d03a1
5'-most EST
                   BLASTN
Method
NCBI GI
                   g22091
                   230
BLAST score
                   1.0e-126
E value
                   259
Match length
                   97
% identity
```

Z.diploperennis gene for hydroxyproline-rich glycoprotein



258625 Seq. No. 151 64.R1011 Contig ID 5'-most EST uC-zmflmo17090g08a1 Method BLASTN g22091 NCBI GI BLAST score 262 E value 1.0e-145 Match length 327 % identity 95 Z.diploperennis gene for hydroxyproline-rich glycoprotein NCBI Description 258626 Seq. No. 151 67.R1011 Contig ID LIB36-017-Q1-E1-E1 5'-most EST

 Seq. No.
 258627

 Contig ID
 151\_71.R1011

 5'-most EST
 LIB3068-044-Q1-K1-E7

 Method
 BLASTN

 NCBI GI
 g22091

NCBI GI g22091
BLAST score 148
E value 1.0e-77
Match length 177
% identity 96
NCBI Description 7 diplo

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

 Seq. No.
 258628

 Contig ID
 151\_81.R1011

 5'-most EST
 mwy700443224.h2

 Method
 BLASTX

 NCBI GI
 g3914019

 BLAST score
 140

 E value
 2.0e-14

 Match length
 61

Match length 61 % identity 72

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi\_2305014

(AF004317) S-adenosyl-L-methionine synthetase homolog [Musa

acuminata]

Seq. No. 258629

Contig ID 151\_84.R1011

5'-most EST LIB3180-030-P2-M2-F8

Seq. No. 258630

Contig ID 151 94.R1011

5'-most EST LIB3069-048-Q1-K1-H1

Method BLASTN
NCBI GI g22091
BLAST score 262
E value 1.0e-145
Match length 307
% identity 96

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 258631



Contig ID 151 100.R1011 uC-zmflmo17031c06a1 5'-most EST Method BLASTN NCBI GI g22091 BLAST score 215 1.0e-117 E value Match length 338 % identity 93 Z.diploperennis gene for hydroxyproline-rich glycoprotein NCBI Description 258632 Seq. No. 151 103.R1011 Contig ID 5'-most EST uC-zmflmo17316h05a1 BLASTN Method NCBI GI q22091 BLAST score 157 4.0e-83 E value Match length 214 % identity 94 Z.diploperennis gene for hydroxyproline-rich glycoprotein NCBI Description 258633 Seq. No. 151 108.R1011 Contig ID 5'-most EST uC-zmflmo17326d04a1 BLASTN Method NCBI GI q22091 BLAST score 168 1.0e-89 E value Match length 325 % identity 87 NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein 258634 Seq. No. Contig ID 151 111.R1011 LIB3068-035-Q1-K1-A3 5'-most EST Method BLASTN q22091 NCBI GI BLAST score 225 E value 1.0e-123 294 Match length 94 % identity NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein Seq. No. 258635 151 117.R1011 Contig ID uC-zmflmo17301b08a1 5'-most EST BLASTN Method NCBI GI g22091 BLAST score 196

1.0e-106 E value 245 Match length 95 % identity

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

258636 Seq. No.

151 118.R1011 Contig ID uC-zmflmo17248b03a1 5'-most EST



Method BLASTN
NCBI GI g22091
BLAST score 254
E value 1.0e-141
Match length 295
% identity 97

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 258637

Contig ID 151\_120.R1011 5'-most EST uC-zmflmo17009f03a1

5'-most EST uC-zmflmo17009f Method BLASTN

NCBI GI g257040
BLAST score 137
E value 2.0e-71
Match length 168
% identity 96

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 258638

Contig ID 151\_126.R1011

5'-most EST uC-zmflmo17395g06a1

Method BLASTN
NCBI GI g4007864
BLAST score 62
E value 2.0e-26
Match length 145

% identity 86

NCBI Description Zea mays HRGP gene, AC1503 line

Seq. No. 258639

Contig ID 151\_127.R1011

5'-most EST uC-zmflmo17129f02a1

Method BLASTN
NCBI GI g22091
BLAST score 184
E value 3.0e-99
Match length 241
% identity 94

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 258640

Contig ID 151\_130.R1011

5'-most EST uC-zmflmo17248b06a1

Method BLASTN
NCBI GI g22091
BLAST score 88
E value 4.0e-42
Match length 188
% identity 87

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 258641

Contig ID 151\_136.R1011 5'-most EST uC-zmflb73411a02a1

Method BLASTN NCBI GI g257040



```
BLAST score
                  116
                  6.0e-59
E value
Match length
                  139
% identity
                  96
                  hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
NCBI Description
Seq. No.
                  258642
Contig ID
                  152 1.R1011
                  LIB3066-006-Q1-K1-C7
5'-most EST
                  BLASTX
Method
NCBI GI
                  g2129753
BLAST score
                  952
                  1.0e-103
E value
Match length
                  237
                  76
% identity
                  threonine synthase (EC 4.2.99.2) precursor - Arabidopsis
NCBI Description
                  thaliana (fragment) > gi 1448917 (L41666) threonine synthase
                   [Arabidopsis thaliana]
                   258643
Seq. No.
Contig ID
                  153 1.R1011
5'-most EST
                  uC-zmflb73141b02b1
Method
                  BLASTX
NCBI GI
                   g2130091
BLAST score
                   2186
                   0.0e+00
E value
Match length
                   439
% identity
                   96
NCBI Description
                   aspartate aminotransferase - proso millet
                   >qi 633095 dbj BAA08106 (D45076) plastidic aspartate
                   aminotransferase [Panicum miliaceum]
                   258644
Seq. No.
                   153 2.R1011
Contig ID
                   LIB3150-108-P2-K1-D3
5'-most EST
Method
                   BLASTX
                   g2130091
NCBI GI
                   287
BLAST score
E value
                   1.0e-25
Match length
                   55
                   96
% identity
                   aspartate aminotransferase - proso millet
NCBI Description
                   >gi 633095 dbj BAA08106 (D45076) plastidic aspartate
                   aminotransferase [Panicum miliaceum]
                   258645
Seq. No.
                   154 1.R1011
Contig ID
5'-most EST
                   CPR962_700268092_FL
Method
                   {\tt BLASTX}
```

Method BLASTX
NCBI GI g2828012
BLAST score 1302
E value 1.0e-160
Match length 281
% identity 100

NCBI Description (AF036891) starch synthase I precursor [Zea mays]

Seq. No. 258646

35713

```
155 1.R1011
Contig ID
5'-most EST
                  CPR9730:2F700213266consensus FL
                  BLASTX
Method
NCBI GI
                  q1946364
BLAST score
                  1151
                  1.0e-126
E value
                  424
Match length
                  55
% identity
                  (U93215) lipase isolog [Arabidopsis thaliana]
NCBI Description
                  258647
Seq. No.
                  157 1.R1011
Contig ID
5'-most EST
                  CPR9742consensus_FL
Method
                  BLASTX
                  q2245136
NCBI GI
                  714
BLAST score
E value
                  2.0e-75
                  214
Match length
% identity
                  61
                  (Z97344) trehalose-6-phosphate synthase homolog
NCBI Description
                  [Arabidopsis thaliana]
                  258648
Seq. No.
Contig ID
                  158 1.R1011
                  CPR17405:2F700282409PROFILIN1.con_FL
5'-most EST
Method
                  BLASTX
                  q464466
NCBI GI
                  590
BLAST score
E value
                  2.0e-60
Match length
                  204
                  63
% identity
NCBI Description PROFILIN 1 >gi 422031 pir S35796 profilin 1 - maize
                  >gi_313138_emb_CAA51718_ (X73279) profilin 1 [Zea mays]
                  258649
Seq. No.
Contig ID
                  158 2.R1011
5'-most EST
                  LIB3066-018-Q1-K1-A7
Method
                  BLASTX
NCBI GI
                  q464466
BLAST score
                   699
E value
                  8.0e-74
                  131
Match length
                  100
% identity
NCBI Description PROFILIN 1 >gi 422031 pir S35796 profilin 1 - maize
                  >gi 313138 emb CAA51718 (X73279) profilin 1 [Zea mays]
                  258650
Seq. No.
                  158 3.R1011
Contig ID
                  LIB3075-054-Q1-K1-B7
5'-most EST
```

Method BLASTX NCBI GI g464466 BLAST score 281 7.0e-25 E value Match length 54 % identity 100

NCBI Description PROFILIN 1 >gi\_422031\_pir\_\_S35796 profilin 1 - maize >gi 313138 emb CAA51718 (X73279) profilin 1 [Zea mays]



```
Seq. No.
                   258651
                   158 4.R1011
"Contig ID
                   LIB3066-010-Q1-K1-H12
 5'-most EST
                   BLASTN
Method
NCBI GI
                   q313137
BLAST score
                   164
                   4.0e-87
E value
                   272
Match length
                   95
 % identity
NCBI Description
                   Z.mays ZmPRO1 mRNA for profilin
 Seq. No.
                   258652
                   158 5.R1011
 Contig ID
 5'-most EST
                   bdu700382235.h1
Method
                   BLASTX
                   q464466
NCBI GI
BLAST score
                   489
                   3.0e-49
E value
Match length
                   102
                   92
 % identity
                   PROFILIN 1 >gi 422031 pir S35796 profilin 1 - maize
NCBI Description
                   >gi 313138 emb CAA51718 (X73279) profilin 1 [Zea mays]
                   258653
 Seq. No.
                   159 1.R1011
 Contig ID
                   LIB3066-027-Q1-K1-D2
 5'-most EST
Method
                   BLASTX
NCBI GI
                   g3901094
 BLAST score
                   857
                   1.0e-91
 E value
                   257
Match length
 % identity
                   64
                   (Z27090) pollen allergen Phl pI [Phleum pratense]
 NCBI Description
                   258654
 Seq. No.
 Contig ID
                   159 4.R1011
 5'-most EST
                   LIB148-047-Q1-E1-F1
                   BLASTX
 Method
 NCBI GI
                   q1911582
                   222
 BLAST score
 E value
                    4.0e-18
 Match length
                   70
                   57
 % identity
 NCBI Description
                   (S83343) Cyn d 1=major allergen [Cynodon dactylon=Bermuda
                   grass, pollen, Peptide Partial, 246 aa] [Cynodon dactylon]
 Seq. No.
                   258655
 Contig ID
                   159 5.R1011
 5'-most EST
                   LIB3066-032-Q1-K1-D1
 Method
                   BLASTX
 NCBI GI
```

Method BLASTX
NCBI GI g1171008
BLAST score 268
E value 2.0e-23

Match length 90 % identity 62

NCBI Description POLLEN ALLERGEN PHL P 1 PRECURSOR (PHL P I)

```
>gi 629812 pir S44182 allergen Phl p I - common timothy
>gi 473360_emb_CAA55390_ (X78813) Phl p I allergen [Phleum
pratense]
```

258656 Seq. No. Contig ID 159 6.R1011

5'-most EST LIB148-066-Q2-E1-C9

Method BLASTX NCBI GI g1911582 BLAST score 175 E value 2.0e-16 Match length 84

55 % identity

NCBI Description (S83343) Cyn d 1=major allergen [Cynodon dactylon=Bermuda grass, pollen, Peptide Partial, 246 aa] [Cynodon dactylon]

Seq. No. 258657 Contig ID 161 1.R1011

5'-most EST LIB3066-025-Q1-K1-A9

Method BLASTX NCBI GI q3894172 BLAST score 169 E value 1.0e-23 Match length 150 % identity 42

NCBI Description (ACO05312) putative cinnamoyl-CoA reductase [Arabidopsis

thaliana]

Seq. No. 258658 Contig ID 161 2.R1011

5'-most EST LIB148-066-Q2-E1-H9

258659 Seq. No. Contig ID 161 3.R1011

5'-most EST uC-zmflb73262a01a2

Method BLASTN NCBI GI g2626751 BLAST score 53 E value 7.0e-21 Match length 157 % identity 83

NCBI Description Triticum aestivum retrotransposon Tarl, partial sequence

Seq. No. 258660 Contig ID 161 4.R1011

5'-most EST uC-zmflmo17244c09a1

Method BLASTX NCBI GI g3894172 BLAST score 432 E value 2.0e-42 Match length 169 % identity 46

(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis NCBI Description

thaliana]

Seq. No. 258661 Contig ID 163 1.R1011



RA012A10\_700336827 FL 5'-most EST Method BLASTX NCBI GI g4204288 BLAST score 617 4.0e-76 E value Match length 412 % identity 42 NCBI Description (AC003027) lcl prt seq No definition line found [Arabidopsis thaliana] 258662 Seq. No. Contig ID 165 1.R1011 5'-most EST ntr700074680.h1 Method BLASTX NCBI GI g3790587 BLAST score 858 7.0e-92 E value Match length 354 54 % identity (AF079182) RING-H2 finger protein RHF2a [Arabidopsis NCBI Description thaliana] Seq. No. 258663 165 2.R1011 Contig ID 5'-most EST LIB3075-032-Q1-K1-A8 Seq. No. 258664 Contig ID 165 3.R1011 5'-most EST wty700165881.h1 Method BLASTX NCBI GI q3790587 BLAST score 153 E value 3.0e-1474 Match length % identity 66 NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana] Seq. No. 258665 Contig ID 165 4.R1011 5'-most EST nbm700477612.h1 Method BLASTX NCBI GI g3790587 BLAST score 415 E value 1.0e-40 Match length 86 88 % identity NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No. 258666 Contig ID 166\_1.R1011

5'-most EST uC-zmflMo17092d01b1

MethodBLASTXNCBI GIg862650BLAST score506E value7.0e-51



```
Match length
                  198
% identity
                  53
                  (U20193) MADS-box protein AGL12 [Arabidopsis thaliana]
NCBI Description
                  258667
Seq. No.
                  166 2.R1011
Contig ID
5'-most EST
                  uC-zmflb73186e10b1
Method
                  BLASTX
NCBI GI
                  g862650
BLAST score
                  296
                  1.0e-26
E value
Match length
                  76
% identity
                  68
                  (U20193) MADS-box protein AGL12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  258668
Contiq ID
                  166 3.R1011
5'-most EST
                  uC-zmroteosinte085a11b1
Method
                  BLASTX
NCBI GI
                  q862650
BLAST score
                  297
                  8.0e-27
E value
Match length
                  76
% identity
                  70
                  (U20193) MADS-box protein AGL12 [Arabidopsis thaliana]
NCBI Description
                  258669
Seq. No.
Contig ID
                  166 4.R1011
5'-most EST
                  uC-zmflb73097b01a2
                  258670
Seq. No.
Contig ID
                  166 5.R1011
5'-most EST
                  uC-zmromo17107e01a1
                  258671
Seq. No.
                  167 1.R1011
Contig ID
5'-most EST
                  clt700044153.f1
Method
                  BLASTX
NCBI GI
                  g1553133
BLAST score
                  179
E value
                   2.0e-12
                  192
Match length
% identity
                  12
NCBI Description (U64722) actin-fragmin kinase [Physarum polycephalum]
                   258672
Seq. No.
Contig ID
                  167 4.R1011
5'-most EST
                  nwy700444883.hl
Seq. No.
                   258673
                  168 1.R1011
Contig ID
```

5'-most EST RA012B12\_700347284\_FL

Method BLASTX NCBI GI g2865394 BLAST score 889 1.0e-95 E value Match length 301

```
% identity
                   60
NCBI Description
                   (AF036949) basic leucine zipper protein [Zea mays]
                  258674
Seq. No.
                  171 1.R1011
Contig ID
                  RA012B6 700344331 FL
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1304266
                  323
BLAST score
                  1.0e-29
E value
                  117
Match length
% identity
                  61
                  (D64051) HALF-1 [Triticum aestivum]
NCBI Description
Seq. No.
                  258675
                  173 1.R1011
Contig ID
                  uwc700152704.h1
5'-most EST
Method
                  BLASTX
                   q3738230
NCBI GI
                   273
BLAST score
                  2.0e-23
E value
                  223
Match length
% identity
                  32
                  (AB007790) DREB2A [Arabidopsis thaliana]
NCBI Description
                  >gi 4126706 dbj BAA36705 (AB016570) DREB2A [Arabidopsis
                  thaliana]
Seq. No.
                  258676
                  174 1.R1011
Contig ID
                  LIB3069-023-Q1-K1-H5
5'-most EST
                  BLASTX
Method
NCBI GI
                   q1753085
BLAST score
                   325
                  8.0e-30
E value
                  157
Match length
                   53
% identity
NCBI Description
                 (U25283) leucine zipper protein [Oryza sativa]
Seq. No.
                   258677
Contig ID
                   174 2.R1011
5'-most EST
                  LIB3067-042-Q1-K1-B12
Method
                  BLASTX
                  g1753085
NCBI GI
BLAST score
                   249
E value
                   9.0e-24
                   93
Match length
% identity
                   65
NCBI Description (U25283) leucine zipper protein [Oryza sativa]
Seq. No.
                   258678
```

Contig ID 175 1.R1011

RA012C7\_700350520\_FL 5'-most EST

Method BLASTX NCBI GI g2145356 BLAST score 3031 E value 0.0e+00Match length 789



% identity 75 (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi\_3132474 NCBI Description (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana] 258679 Seq. No. 175 2.R1011 Contig ID LIB3279-008-P1-K1-H7 5'-most EST BLASTX Method g2145356 NCBI GI BLAST score 212 6.0e-17 E value 49 Match length 76 % identity (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi 3132474 NCBI Description (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana] 258680 Seq. No. 175 6.R1011 Contig ID nbm700471323.h1 5'-most EST Method BLASTX g2145358 NCBI GI BLAST score 342 E value 2.0e-45 127 Match length 77 % identity (Y10922) HD-Zip protein [Arabidopsis thaliana] NCBI Description Seq. No. 258681 176\_1.R1011 Contig ID uC-zmflb73001e04b1 5'-most EST Method BLASTX g2911067 NCBI GI BLAST score 1432 0.0e + 00E value 641 Match length 76 % identity (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis NCBI Description thaliana] 258682 Seq. No. 176 2.R1011 Contig ID xyt700344948.hl 5'-most EST BLASTX Method g2911067 NCBI GI 500 BLAST score 2.0e-50 E value 123 Match length % identity (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis NCBI Description thaliana]

258683 Seq. No.

Contig ID

RT001A12FL\_700076615\_FL 5'-most EST

178 1.R1011

258684 Seq. No. Contig ID 179\_1.R1011

BLAST score

E value Match length 281 2.0e-24

104



```
5'-most EST
                  LIB3151-026-Q1-K1-D12
                  258685
Seq. No.
                  180 1.R1011
Contig ID
                  LIB3152-016-P1-K1-B2
5'-most EST
                  BLASTX
Method
                  g2224899
NCBI GI
                  281
BLAST score
                  2.0e-24
E value
                  195
Match length
                  38
% identity
                  (U67133) DNA-binding protein PcMYB1 [Petroselinum crispum]
NCBI Description
                  258686
Seq. No.
Contig ID
                  180 2.R1011
5'-most EST
                  LIB3151-023-Q1-K1-F1
                  BLASTX
Method
NCBI GI
                  g2224901
                  217
BLAST score
                  2.0e-17
E value
                  68
Match length
                  60
% identity
                  (U67134) PcMYB1 protein [Petroselinum crispum]
NCBI Description
                  258687
Seq. No.
                  181 1.R1011
Contig ID
                  xsy700209975.hl
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1705594
BLAST score
                   238
                  2.0e-19
E value
                  220
Match length
% identity
                   33
                  PEROXISOME ASSEMBLY PROTEIN CAR1 (PEROXIN-2)
NCBI Description
                  >gi_2133320_pir__A56730 car1 protein - Podospora anserina
                  >gi 1360119 emb CAA60739 (X87329) peroxisome assembly
                   factor [Podospora anserina]
                   258688
Seq. No.
                  182 1.R1011
Contig ID
                  RT001E1_700023190_FL
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1432058
BLAST score
                   492
E value
                   4.0e-49
Match length
                   236
                   48
% identity
NCBI Description (U58540) WRKY2 [Petroselinum crispum]
Seq. No.
                   258689
Contig ID
                  182_2.R1011
                   qw1700613365.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                   q1432058
```

35721

% identity 61

NCBI Description (U58540) WRKY2 [Petroselinum crispum]

5'-most EST uC-zmflb73177e04b1

Seq. No. 258691
Contig ID 183 1.R1011

5'-most EST RT001E2 700025985 FL

Seq. No. 258692 Contig ID 184\_1.R1011

5'-most EST RT001E3FL\_700026214\_FL

Method BLASTX
NCBI GI g122772
BLAST score 1211
E value 1.0e-133
Match length 329
% identity 76

NCBI Description TRANSCRIPTION FACTOR HBP-1B >gi 100809 pir S15347

transcription factor HBP-1b - wheat >gi\_21635\_emb\_CAA40102\_

(X56782) HBP-1b [Triticum aestivum]

Seq. No. 258693 Contig ID 185\_1.R1011

5'-most EST RT001F6\_700028403\_FL

Method BLASTX
NCBI GI g1168546
BLAST score 298
E value 2.0e-26
Match length 151
% identity 49

NCBI Description HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-5 (HD-ZIP PROTEIN

ATHB-5) >gi\_629504\_pir\_\_S47135 homeotic protein Athb-5 - Arabidopsis thaliana >gi\_499160 emb CAA47426 (X67033)

Athb-5 [Arabidopsis thaliana]

Seq. No. 258694 Contig ID 186\_1.R1011

5'-most EST RT001G10FL 700104561 FL

Method BLASTX
NCBI GI g2194132
BLAST score 833
E value 4.0e-89
Match length 375
% identity 50

NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]

Seq. No. 258695 Contig ID 187\_1.R1011

5'-most EST RT001G11\_700106005\_FL

Method BLASTX
NCBI GI g3047106
BLAST score 1397
E value 1.0e-155
Match length 410

NCBI GI

```
% identity
                   68
N∈BI Description
                   (AF058919) Arabidopsis thaliana homeodomain protein AHDP
                   (SP:P93041) [Arabidopsis thaliana]
                   258696
Seq. No.
                   188 1.R1011
Contig ID
5'-most EST
                   RT001G1 700030417 FL
Seq. No.
                   258697
Contig ID
                   189_1.R1011
5'-most EST
                   fC-zmst1700333259f1
                   BLASTX
Method
NCBI GI
                   g1899060
BLAST score
                   1576
E value
                   1.0e-176
Match length
                   328
% identity
                   91
                  (U79669) endosperm C-24 sterol methyltransferase [Zea mays]
NCBI Description
                   258698
Seq. No.
Contig ID
                   189 2.R1011
5'-most EST
                   uwc700155621.h1
Method
                   BLASTX
NCBI GI
                   g1899060
BLAST score
                   184
                   1.0e-26
E value
Match length
                   81
% identity
                   80
                  (U79669) endosperm C-24 sterol methyltransferase [Zea mays]
NCBI Description
Seq. No.
                   258699
Contig ID
                   190 1.R1011
5'-most EST
                   gwl700612536.h1
Method
                   BLASTX
NCBI GI
                   g3168840
BLAST score
                   284
E value
                   8.0e-25
Match length
                   65
% identity
                   82
NCBI Description
                  (U88711) copper homeostasis factor [Arabidopsis thaliana]
Seq. No.
                   258700
Contig ID
                   191 1.R1011
5'-most EST
                   RT001G7_700099947_FL
Method
                   BLASTX
NCBI GI
                   g551535
BLAST score
                   263
E value
                   2.0e-22
Match length
                   175
% identity
                   29
NCBI Description
                  (U14134) transcription factor IIIA [Homo sapiens]
Seq. No.
                   258701
                   192 1.R1011
Contig ID
5'-most EST
                   RT001H1_700086694 FL
Method
                   BLASTX
```

35723

g2642154



```
BLAST score
                  282
                  1.0e-24
E value
Match length
                  135
% identity
                  50
                  (AC003000) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3790595 (AF079186) RING-H2 finger protein RHC2a
                   [Arabidopsis thaliana]
                  258702
Seq. No.
                  193 1.R1011
Contig ID
```

5'-most EST hbs701180711.h1
Method BLASTX
NCBI GI g1747310
BLAST score 538
E value 2.0e-54
Match length 212
% identity 49

NCBI Description (D58424) Myb-like DNA binding protein [Arabidopsis

thaliana]

 Seq. No.
 258703

 Contig ID
 193\_2.R1011

 5'-most EST
 kem700611496.h1

5'-most EST RT001H5\_700088489\_FL

Method BLASTX
NCBI GI g2317905
BLAST score 285
E value 7.0e-25
Match length 325
% identity 26

NCBI Description (U89959) bZIP-like protein [Arabidopsis thaliana]

 Seq. No.
 258705

 Contig ID
 195\_2.R1011

5'-most EST LIB3150-116-P2-K1-F12

Method BLASTX
NCBI GI g2146866
BLAST score 152
E value 2.0e-09
Match length 169
% identity 25

NCBI Description gene C35D10.10 protein - Caenorhabditis elegans >gi\_687889

(U21324) weak similarity to aa 31-55 of A. thaliana

thioredoxine [Caenorhabditis elegans]

Seq. No. 258706 Contig ID 196\_1.R1011

5'-most EST LIB3156-016-Q1-K1-B6

Method BLASTX
NCBI GI g1345644
BLAST score 1830
E value 0.0e+00
Match length 473
% identity 72



NCBI Description CYTOCHROME P450 86A1 (CYPLXXXVI) >gi\_940446\_emb\_CAA62082\_ (X90458) cytochrome p450 [Arabidopsis thaliana]

Seq. No. 258707 Contig ID 204\_1.R1011

5'-most EST uC-zmflb73272h04b1

Method BLASTX
NCBI GI g3142291
BLAST score 298
E value 2.0e-26
Match length 136
% identity 45

NCBI Description (AC002411) Contains similarity to adenylate cyclase

gb AF012921 from Magnaporthe grisae. EST gb Z24512 comes

from this gene. [Arabidopsis thaliana]

Seq. No. 258708 Contig ID 205 1.R1011

5'-most EST LIB3066-042-Q1-K1-D9

Method BLASTX
NCBI GI g1399277
BLAST score 1439
E value 1.0e-160
Match length 477
% identity 59

NCBI Description (U31836) calmodulin-domain protein kinase CDPK isoform 7

[Arabidopsis thaliana]

Seq. No. 258709 Contig ID 205\_2.R1011

5'-most EST LIB148-040-Q1-E1-B8

Method BLASTX
NCBI GI g1871195
BLAST score 152
E value 3.0e-09
Match length 56
% identity 55

NCBI Description (U90439) Ca++ dependent protein kinase isolog [Arabidopsis

thaliana] >gi\_2335093 (AC002339) putative calcium-dependent

protein kinase [Arabidopsis thaliana]

Seq. No. 258710 Contig ID 206 1.R1011

5'-most EST fC-gmst700662785 FL

Method BLASTX
NCBI GI g2462749
BLAST score 256
E value 6.0e-22
Match length 85
% identity 66

NCBI Description (AC002292) Putative Serine/Threonine protein kinase

[Arabidopsis thaliana]

5'-most EST fC-zmf1700354473f2

Method BLASTX

```
g2832691
NCBI GI
BLAST score
                   695
E value
                  7.0e-92
Match length
                  328
                  52
% identity
                  (AL021713) polygalacturonase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  258712
Seq. No.
Contig ID
                  208 1.R1011
                  uC-zmflmo17076d02a1
5'-most EST
Method
                  BLASTX
NCBI GI
                  g1155255
BLAST score
                  499
                  4.0e-50
E value
                  242
Match length
% identity
                  42
                 (U39228) beta-glucosidase [Prunus avium]
NCBI Description
Seq. No.
                  258713
                  208 2.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte106g09b2
Method
                  BLASTX
NCBI GI
                  g1155255
                  235
BLAST score
                  8.0e-32
E value
Match length
                  133
% identity
                  52
NCBI Description (U39228) beta-glucosidase [Prunus avium]
                  258714
Seq. No.
Contig ID
                  209 1.R1011
5'-most EST
                  fC-zmf1700338026_FL
Method
                  BLASTX
NCBI GI
                  q2642640
BLAST score
                   451
E value
                   1.0e-44
Match length
                  111
                   77
% identity
                  (AF032473) ADP-glucose pyrophosphorylase large subunit 2
NCBI Description
                   [Citrullus lanatus]
Seq. No.
                   258715
Contig ID
                   210 1.R1011
5'-most EST
                  fC-zmf1700338726 FL
Seq. No.
                  258716
Contig ID
                  211 1.R1011
5'-most EST
                  LIB3088-046-Q1-K1-F12
Method
                  BLASTX
NCBI GI
                  q231707
BLAST score
                  730
E value
                  2.0e-77
Match length
                  154
% identity
                  89
                  CELL DIVISION CONTROL PROTEIN 2 HOMOLOG 2
NCBI Description
```

>gi 100668 pir S22441 protein kinase (EC 2.7.1.37) cdc2



homolog 2 - rice >gi\_20345\_emb\_CAA42923\_ (X60375) Rcdc2-2 [Oryza sativa] >gi\_228925\_prf\_\_1814443B cdc2

protein: ISOTYPE=cdc20s-2 [Oryza sativa]

 Seq. No.
 258717

 Contig ID
 212\_1.R1011

 5'-most EST
 nbm700478009.h1

Method BLASTX
NCBI GI g3800878
BLAST score 1799
E value 0.0e+00
Match length 494
% identity 70

NCBI Description (AF096281) threonine dehydratase/deaminase [Arabidopsis

thaliana]

Seq. No. 258718 Contig ID 212 2.R1011

5'-most EST uC-zmrob73002f07a1

Seq. No. 258719 Contig ID 212\_3.R1011

5'-most EST uC-zmflb73304f01a1

 Seq. No.
 258720

 Contig ID
 213\_1.R1011

 5'-most EST
 ymt700220010.h1

Method BLASTX
NCBI GI g3790587
BLAST score 250
E value 6.0e-21
Match length 59
% identity 75

NCBI Description (AF079182) RING-H2 finger protein RHF2a [Arabidopsis

thaliana]

5'-most EST fC-zmf1700341881 FL

Method BLASTX
NCBI GI g4154279
BLAST score 534
E value 2.0e-54
Match length 145
% identity 65

NCBI Description (AF082346) C13 endopeptidase NP1 precursor [Hordeum

vulgare]

Seq. No. 258722 Contig ID 215\_1.R1011

5'-most EST LIB3150-019-Q1-N1-H3

Method BLASTX
NCBI GI g4582459
BLAST score 516
E value 5.0e-52
Match length 226
% identity 50

35727



```
NCBI Description
                   (AC007071) putative RanBP7/importin protein [Arabidopsis
                  thaliana]
Seq. No.
                  258723
Contig ID
                  215 2.R1011
5'-most EST
                  uC-zmflmo17016f02a1
Seq. No.
                  258724
Contig ID
                  216_1.R1011
```

5'-most EST fC-zmf1700342726 FL Method BLASTX NCBI GI q3021268 197 BLAST score 5.0e-15 E value

Match length 112 % identity 39

NCBI Description (AL022347) putative protein [Arabidopsis thaliana]

Seq. No. 258725 Contig ID 217 1.R1011

5'-most EST fC-zmf1700342745\_FL

Method BLASTX NCBI GI q2465923 BLAST score 627 3.0e-65 E value Match length 248 % identity 54

NCBI Description (AF024648) receptor-like serine/threonine kinase

[Arabidopsis thaliana]

Seq. No. 258726 Contig ID 218 1.R1011 5'-most EST kem700612112.h1

Method BLASTX NCBI GI q3309066 BLAST score 2208 E value 0.0e + 00Match length 429 % identity 97

NCBI Description (AF073488) bifunctional dihydrofolate reductase-thymidylate

synthase [Zea mays]

Seq. No. 258727 Contig ID 218 2.R1011

5'-most EST LIB3067-002-Q1-K1-D10

Method BLASTX NCBI GI g3309066 BLAST score 354 E value 2.0e-33 Match length 68 97 % identity

NCBI Description (AF073488) bifunctional dihydrofolate reductase-thymidylate

synthase [Zea mays]

258728 Seq. No. Contig ID 219 1.R1011 5'-most EST uC-zmflb73245e04b2

35728



```
Method
                  BLASTX
                  g3047123
NCBI GI
BLAST score
                  415
                  3.0e-40
E value
                  169
Match length
                  48
% identity
                  (AF058919) similar to the family of glycosyl hydrolases
NCBI Description
                   [Arabidopsis thaliana]
                  258729
Seq. No.
                  219 2.R1011
Contig ID
5'-most EST
                  LIB3067-030-Q1-K1-C3
Method
                  BLASTX
                  g3047123
NCBI GI
BLAST score
                  727
                   4.0e-77
E value
                  204
Match length
% identity
                   62
                  (AF058919) similar to the family of glycosyl hydrolases
NCBI Description
                   [Arabidopsis thaliana]
                   258730
Seq. No.
Contig ID
                   220 1.R1011
                  LIB3137-003-Q1-K1-F4
"5'-most EST
Method
                  BLASTX
NCBI GI
                  g3176669
BLAST score
                   487
E value
                   1.0e-48
Match length
                   213
% identity
                   48
                  (AC004393) End is cut off. [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   258731
                   221 1.R1011
Contig ID
                   fC-zmf1700343886 FL
5'-most EST
                   BLASTX
Method
                   g4580398
NCBI GI
BLAST score
                   746
                   6.0e-79
E value
                   198
Match length
                   71
% identity
                   (AC007171) putative protein kinase APK1A [Arabidopsis
NCBI Description
                   thaliana]
                   258732
Seq. No.
                   222_1.R1011
Contig ID
5'-most EST
                   fC-zmf1700344343 FL
Method
                   BLASTX
NCBI GI
                   g3482921
BLAST score
                   264
E value
                   2.0e-22
                   79
Match length
% identity
                   62
```

Seq. No. 258733 Contig ID 223 1.R1011

NCBI Description

35729

(AC003970) Unknown protein [Arabidopsis thaliana]



```
5'-most EST
                   fC-zmf1700344346: FL
                   258734
Seq. No.
Contig ID
                   224 1.R1011
5'-most EST
                   LIB3061-007-Q1-K1-F5
Method
                   BLASTX
NCBI GI
                   q1076318
BLAST score
                   1110
E value
                   1.0e-121
Match length
                   332
% identity
                   66
NCBI Description
                  dihydrolipoamide S-acetyltransferase (EC 2.3.1.12)
                   precursor - Arabidopsis thaliana (fragment)
                   >gi_559395_emb_CAA86300_ (Z46230) dihydrolipoamide
                   acetyltransferase (E2) subunit of PDC [Arabidopsis
                   thalianal
                   258735
Seq. No.
Contig ID
                   225 1.R1011
5'-most EST
                   uwc700153592.h1
Method
                   BLASTX
NCBI GI
                   g1076486
BLAST score
                   628
E value
                   4.0e-65
Match length
                   215
% identity
                   55
NCBI Description
                  cim1 protein - soybean >gi 555616 (U03860) cytokinin
                   induced message [Glycine max]
Seq. No.
                   258736
Contig ID
                   226 1.R1011
5'-most EST
                   LIB83-005-Q1-E1-C1
Method
                   BLASTX
NCBI GI
                   q3122357
BLAST score
                   747
E value
                   3.0e-79
Match length
                   224
% identity
                   63
NCBI Description
                  PUTATIVE LIPOATE-PROTEIN LIGASE B (LIPOATE BIOSYNTHESIS
                   PROTEIN B) >gi 2494127 (AC002376) Contains similarity to
                   Mycobacterium LIPB gene (gb_Q104041). [Arabidopsis
                  thaliana]
Seq. No.
                   258737
Contig ID
                  227 1.R1011
5'-most EST
                  LIB143-064-Q1-E1-B9
Method
                  BLASTX
NCBI GI
                  q3786005
BLAST score
                  1542
E value
                  1.0e-172
Match length
                  365
```

% identity 80 NCBI Description

(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No. 258738 Contig ID 227 2.R1011

% identity

NCBI Description

77

```
5'-most EST
                    ymt700224159.h1
Method
                    BLASTX
NCBI GI
                    g3786005
BLAST score
                    462
E value
                    2.0e-46
Match length
                    100
% identity
                    87
NCBI Description
                   (AC005499) putative phosphoethanolamine
                   cytidylyltransferase [Arabidopsis thaliana]
Seq. No.
                    258739
Contig ID
                    228 1.R1011
5'-most EST
                    fC-zmle700445521a1
Method
                   BLASTX
NCBI GI
                   g1708236
BLAST score
                   756
E value
                    3.0e-80
Match length
                   236
% identity
                   63
NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
                    (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                   >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase
                    (EC 4.1.3.5) - Arabidopsis thaliana
                   >gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
                   >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA
                   synthase [Arabidopsis thaliana]
Seq. No.
                   258740
Contig ID
                   228 2.R1011
5'-most EST
                   LIB3075-014-Q1-K1-F9
Method
                   BLASTX
NCBI GI
                   g1708236
BLAST score
                   257
E value
                   5.0e-22
Match length
                   86
% identity
                   60
NCBI Description HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE)
                   (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE)
                   >gi_2129617_pir JC4567 hydroxymethylglutaryl-CoA synthase
                   (EC 4.1.3.5) - Arabidopsis thaliana
                   >gi_1143390_emb_CAA58763_ (X83882)
hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana]
                   >gi_1586548_prf 2204245A hydroxy methylglutaryl CoA
                   synthase [Arabidopsis thaliana]
Seq. No.
                   258741
Contig ID
                   228 3.R1011
5'-most EST
                   LIB3180-048-P2-C12
Method
                   BLASTX
NCBI GI
                   g4098521
BLAST score
                   1422
E value
                   1.0e-158
Match length
                   343
```

35731

(U79160) HMG-CoA synthase [Arabidopsis thaliana] >gi\_4098523 (U79161) HMG-CoA synthase [Arabidopsis



## thaliana]

```
      Seq. No.
      258742

      Contig ID
      228_4.R1011

      5'-most EST
      LIB3136-016-Q1-K1-A12
```

Seq. No. 258743 Contig ID 229 1.R1011

5'-most EST fC-zmfl700352002\_FL Method BLASTX

NCBI GI g585593
BLAST score 220
E value 3.0e-17
Match length 188
% identity 27

NCBI Description NUCLEAR PORE GLYCOPROTEIN P62 (NUCLEOPORIN P62)

>gi\_432654\_emb\_CAA41411\_ (X58521) nucleoporin p62 [Homo

sapiens]

5'-most EST fC-zmf1700345914\_FL

Method BLASTN
NCBI GI g2911359
BLAST score 118
E value 2.0e-59
Match length 367
% identity 89

NCBI Description Zea mays NADPH HC toxin reductase (hml) gene, hml-Pr

allele, complete cds

Seq. No. 258745 Contig ID 231\_1.R1011

5'-most EST LIB3062-039-Q1-K1-F3

Seq. No. 258746 Contig ID 232\_1.R1011

5'-most EST LIB3075-008-Q1-K1-A5

Method BLASTX
NCBI GI g2498077
BLAST score 761
E value 6.0e-81
Match length 149
% identity 98

NCBI Description NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)

(PP18) >gi\_1777930 (U55019) nucleoside diphosphate kinase

[Saccharum officinarum]

Seq. No. 258747 Contig ID 233\_1.R1011

5'-most EST uC-zmflb73158e10b2

Method BLASTX
NCBI GI g3201626
BLAST score 1204
E value 1.0e-132
Match length 287
% identity 78



NCBI Description (AC004669) putative protein kinase MAP3K [Arabidopsis thalianal 258748 Seq. No. 234 1.R1011 Contig ID fC-zmf1700348029: FL 5'-most EST 258749 Seq. No. Contig ID 234\_3.R1011 hvj700621656.hl 5'-most EST Seq. No. 258750 235\_1.R1011 Contig ID uC-zmflb73091c01b2 5'-most EST Method BLASTX q267196 NCBI GI 2070 BLAST score E value 0.0e + 00Match length 575 68 % identity GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR NCBI Description  $\verb|\gi_66574_pir_YUPOY ADPglucose--starch glucosyltransferase|\\$ (EC 2.4.1.21) precursor - potato >gi\_21471\_emb\_CAA41359 (X58453) glycogen (starch) synthase [Solanum tuberosum] 258751 Seq. No. 235 2.R1011 Contig ID uC-zmflb73143a08b1 5'-most EST BLASTX Method NCBI GI q3688123 BLAST score 423 E value 8.0e-69 Match length 244 59 % identity NCBI Description (AJ006293) granule-bound starch synthase [Antirrhinum majus] 258752 Seq. No. Contig ID 235 3.R1011 5'-most EST fC-zmst700454550f1 258753 Seq. No. 235 4.R1011 Contig ID 5'-most EST uC-zmflb73100g10b1 Method BLASTX NCBI GI q267196

Method BLASTX
NCBI GI g267196
BLAST score 223
E value 6.0e-18
Match length 54
% identity 78

NCBI Description GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR

>gi\_66574\_pir\_\_YUPOY ADPglucose--starch glucosyltransferase
(EC 2.4.1.21) precursor - potato >gi\_21471\_emb\_CAA41359\_
(X58453) glycogen (starch) synthase [Solanum tuberosum]



```
5'-most EST
                   fC-zmle700422033 FL
Seq. No.
                   258755
                   237 1.R1011
Contig ID
5'-most EST
                  fC-zmf1700349253 FL
Method
                  BLASTX
NCBI GI
                  q126334
BLAST score
                  257
E value
                   1.0e-21
Match length
                  277
% identity
                   32
NCBI Description
                  LIPASE PRECURSOR (TRIACYLGLYCEROL LIPASE)
                  >gi_79925_pir__A24075 lipase precursor - Staphylococcus
                  hyicus >gi_47136_emb_CAA26602_ (X02844) precursor
                   [Staphylococcus hyicus]
Seq. No.
                   258756
Contig ID
                  238 1.R1011
5'-most EST
                  fC-zmf1700350038 FL
Method
                  BLASTX
NCBI GI
                  q1495802
BLAST score
                  2024
E value
                  0.0e + 00
Match length
                   626
% identity
                   60
NCBI Description (X96405) 13-lipoxygenase [Solanum tuberosum]
                  258757
Seq. No.
Contig ID
                  238 2.R1011
5'-most EST
                  uC-zmflMo17009h06b1
Method
                  BLASTX
NCBI GI
                  g1495802
BLAST score
                  536
E value
                  2.0e-80
Match length
                  280
% identity
                  56
NCBI Description (X96405) 13-lipoxygenase [Solanum tuberosum]
Seq. No.
                   258758
                  238 3.R1011
Contig ID
5'-most EST
                  LIB189-001-Q1-E1-G4
Method
                  BLASTX
NCBI GI
                  g2826842
BLAST score
                  349
E value
                  8.0e-33
Match length
                  106
% identity
                   61
NCBI Description (AJ002236) loxc homologue [Lycopersicon pimpinellifolium]
Seq. No.
                  258759
Contig ID
                  238 4.R1011
5'-most EST
                  LIB3060-028-Q1-K1-F9
```

 Seq. No.
 258760

 Contig ID
 238\_5.R1011

 5'-most EST
 pwr700452561.h1

Method BLASTX

```
NCBI GI
                   q2826842
BLAST score
                   365
E value
                   9.0e-35
Match length
                   137
% identity
NCBI Description
                  (AJ002236) loxc homologue [Lycopersicon pimpinellifolium]
                   258761
Seq. No.
Contig ID
                   238 6.R1011
5'-most EST
                   uC-zmflmo17420g06a1
Method
                   BLASTX
NCBI GI
                   q626032
BLAST score
                   429
E value
                   2.0e-42
Match length
                   121
% identity
NCBI Description lipoxygenase L-2 - rice
                   258762
Seq. No.
Contig ID
                   239_1.R1011
                   fC-zmf1700351139_FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   q2827715
BLAST score
                   817
E value
                   3.0e-87
Match length
                   237
                   69
% identity
                  (AL021684) receptor protein kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   258763
Contig ID
                   240 1.R1011
5'-most EST
                   fC-zmf1700351266 FL
Method
                   BLASTX
NCBI GI
                   g4263791
BLAST score
                   476
E value
                   1.0e-47
Match length
                   147
% identity
                   59
                   (AC006068) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   258764
Seq. No.
Contig ID
                   240 2.R1011
5'-most EST
                   uC-zmflb73233h08a1
                   258765
Seq. No.
                   241 1.R1011
Contig ID
                   uC-zmflb73013h07b1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g1154889
BLAST score
                   2010
E value
                   0.0e+00
Match length
                   566
% identity
                   74
NCBI Description
                  (Z68504) 3-hydroxy-3-methylglutaryl-CoA reductase [Oryza
```

sativa] >gi 1171364 (U43961) 3-hydroxy-3-methylglutaryl=CoA



## reductase [Oryza sativa]

Seq. No. 258766 Contig ID 241\_2.R1011

5'-most EST uC-zmflm017209d08b1

Method BLASTX
NCBI GI g1154889
BLAST score 178
E value 1.0e-12
Match length 58
% identity 64

NCBI Description (Z68504) 3-hydroxy-3-methylglutaryl-CoA reductase [Oryza

sativa] >gi\_1171364 (U43961) 3-hydroxy-3-methylglutaryl=CoA

reductase [Oryza sativa]

Seq. No. 258767 Contig ID 241 3.R1011

5'-most EST uC-zmflm017209f12b1

Method BLASTX
NCBI GI g1154889
BLAST score 1067
E value 1.0e-117
Match length 237
% identity 87

NCBI Description (Z68504) 3-hydroxy-3-methylglutaryl-CoA reductase [Oryza

sativa] >gi\_1171364 (U43961) 3-hydroxy-3-methylglutaryl=CoA

reductase [Oryza sativa]

Seq. No. 258768 Contig ID 241 4.R1011

5'-most EST uC-zmroteosinte064b12b1

Method BLASTX
NCBI GI g520582
BLAST score 1292
E value 1.0e-143
Match length 342
% identity 69

NCBI Description (D37796) Ids3 [Hordeum vulgare]

Seq. No. 258770 Contig ID 243\_1.R1011

5'-most EST LIB3118-003-Q1-K1-F3

Method BLASTX
NCBI GI g1911822
BLAST score 476
E value 2.0e-47
Match length 217
% identity 46

NCBI Description (S83425) glycosylasparaginase alpha beta {EC 3.5.1.26}

[Spodoptera frugiperda, Sf9, Peptide, 320 aa] [Spodoptera

frugiperda]

Seq. No. 258771



Contig ID 243 3.R1011

5'-most EST uC-zmflb73250e07a2

Seq. No. 258772 Contig ID 245 1.R1011

5'-most EST uC-zmflmo17022h09b1

Seq. No. 258773 Contig ID 245\_2.R1011

5'-most EST uC-zmflb73213d03b1

Method BLASTX
NCBI GI g3879734
BLAST score 259
E value 6.0e-22
Match length 230
% identity 33

NCBI Description (Z93388) predicted using Genefinder; cDNA EST EMBL:D70912

comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST

EMBL:D74229 comes from this gene; cDNA EST EMBL:D727

Seq. No. 258774 Contig ID 245\_3.R1011

5'-most EST uC-zmroteosinte074c09b1

Seq. No. 258775 Contig ID 245\_4.R1011

5'-most EST LIB3067-026-Q1-K1-D3

Seq. No. 258777 Contig ID 245 6.R1011

5'-most EST uC-zmflmo17204h02b1

Seq. No. 258779

Contig ID 245 11.R1011

5'-most EST uC-zmflb73130h10a1

Method BLASTX
NCBI GI g3879734
BLAST score 149
E value 9.0e-10
Match length 48
% identity 62

NCBI Description (Z93388) predicted using Genefinder; cDNA EST EMBL:D70912

comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST

EMBL:D74229 comes from this gene; cDNA EST EMBL:D727

Seq. No. 258780

Contig ID 245 12.R1011

Seq. No.



```
5'-most EST
                   nwy700447484.h1
Seq. No.
                   258781
                   247 1.R1011
Contig ID
                   wen \overline{7}00336979.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g4544432
BLAST score
                   1381
E value
                   1.0e-153
Match length
                   395
% identity
                   69
NCBI Description
                   (AC006955) putative mannose-1-phosphate quanyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                   258782
                   247 2.R1011
Contig ID
5'-most EST
                   uC-zmflmo17375b08a1
Seq. No.
                   258783
Contig ID
                   248 1.R1011
5'-most EST
                   fC-zmf1700352293 FL
Method
                   BLASTX
NCBI GI
                   g127112
BLAST score
                   450
E value
                   4.0e-44
Match length
                   175
% identity
                   51
                  MAK16 PROTEIN >gi_73269 pir_ BVBYK6 MAK16 protein - yeast
NCBI Description
                   (Saccharomyces cerevisiae) >gi 171880 (J03852) MAK16
                   protein [Saccharomyces cerevisiae] >gi 595561 (U12980)
                   Mak16p: putative nuclear protein [Saccharomyces cerevisiae]
Seq. No.
                   258784
                   249 1.R1011
Contig ID
                   wty700169932.h1
5'-most EST
Method
                   BLASTX
NCBI GI
                   g629561
BLAST score
                   615
E value
                   1.0e-63
Match length
                   348
                   42
% identity
NCBI Description
                  SRG1 protein - Arabidopsis thaliana
                   >gi_479047 emb CAA55654 (X79052) SRG1 [Arabidopsis
                   thaliana]
                   258785
Seq. No.
                   249 2.R1011
Contig ID
5'-most EST
                   gct701176519.h1
Method
                  BLASTX
NCBI GI
                   q4454018
BLAST score
                   389
                   2.0e-37
E value
Match length
                   226
                   43
% identity
NCBI Description
                  (AL035396) SRG1-like protein [Arabidopsis thaliana]
```



```
250 1.R1011
Contig ID
5'-most EST
                   fC-zmf1700353002 FL
```

Method BLASTX NCBI GI g2245066 BLAST score 589 E value 2.0e-60 Match length 269 % identity 47

NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 258787 Contig ID 251 1.R1011

5'-most EST LIB3075-023-Q1-K1-E7

Method BLASTX NCBI GI q3355471 BLAST score 851 E value 3.0e-91 Match length 270 % identity 58

NCBI Description (AC004218) putative lysophospholipase [Arabidopsis

thaliana]

Seq. No. 258788 Contig ID 252 1.R1011

5'-most EST LIB3137-043-Q1-K1-D7

Method BLASTX NCBI GI q2829275 BLAST score 796 E value 7.0e-85 Match length 237 % identity 67

NCBI Description

(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi 3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi\_4539375\_emb\_CAB40069.1\_

(AL049525) nucleoside diphosphate kinase 3 (ndpk3)

[Arabidopsis thaliana]

258789 Seq. No. 252 2.R1011 Contig ID

5'-most EST LIB3066-025-Q1-K1-H9

Method BLASTX NCBI GI g2829275 BLAST score 373 E value 1.0e-35 78 Match length % identity

NCBI Description (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi 3513740 (AF080118) contains similarity to

nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi 4539375 emb CAB40069.1

(AL049525) nucleoside diphosphate kinase 3 (ndpk3)

[Arabidopsis thaliana]

Seq. No. 258790 Contig ID 252 3.R1011

5'-most EST uC-zmflmo17192h08b1



Method BLASTX
NCBI GI g2829275
BLAST score 225
E value 2.0e-18
Match length 116
% identity 48

NCBI Description (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi\_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi 4539375 emb CAB40069.1

(AL049525) nucleoside diphosphate kinase 3 (ndpk3)

[Arabidopsis thaliana]

Seq. No. 258791 Contig ID 252 5.R1011

Method BLASTX
NCBI GI g2829275
BLAST score 304
E value 8.0e-28
Match length 64
% identity 88

NCBI Description (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis

thaliana] >gi\_35,13740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi\_4539375\_emb\_CAB40069.1\_

(AL049525) nucleoside diphosphate kinase 3 (ndpk3)

[Arabidopsis thaliana]

 Seq. No.
 258792

 Contig ID
 253\_1.R1011

5'-most EST fC-zmf1700353723: FL

Method BLASTX
NCBI GI g169705
BLAST score 831
E value 5.0e-89
Match length 183
% identity 87

NCBI Description (M64737) ATP:pyruvate phosphotransferase [Ricinus communis]

 Seq. No.
 258793

 Contig ID
 253\_2.R1011

5'-most EST uC-zmflmo17313a07b1

Method BLASTX
NCBI GI g2497539
BLAST score 1411
E value 1.0e-157
Match length 311
% identity 88

NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi\_169703

(M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No. 258794 Contig ID 254\_1.R1011

Method BLASTX NCBI GI g1899175



600 BLAST score E value 7.0e-62 Match length 179 % identity 68

(U90262) calcium-dependent calmodulin-independent protein NCBI Description

kinase CDPK [Cucurbita pepo]

Seq. No. 258795 Contig ID 255 1.R1011

5'-most EST LIB3150-032-Q1-N1-C6

Method BLASTX NCBI GI q1587206 BLAST score 2454 E value 0.0e + 00Match length 533 89 % identity

NCBI Description T complex protein [Cucumis sativus]

Seq. No. 258796 255 2.R1011 Contig ID

5'-most EST LIB3150-027-Q1-N1-D6

Method BLASTX NCBI GI g1587206 BLAST score 282 E value 4.0e-25 Match length 59 % identity 88

NCBI Description T complex protein [Cucumis sativus]

Seq. No. 258797 255 3.R1011 Contig ID

uC-zmroteosinte001a02b1 5'-most EST

Method BLASTX NCBI GI q1587206 BLAST score 374 E value 6.0e-36 Match length 82

85 % identity

NCBI Description T complex protein [Cucumis sativus]

Seq. No. 258798 Contig ID 255 4.R1011 ymt700220262.h1 5'-most EST Method BLASTX

NCBI GI g1587206 BLAST score 488 E value 3.0e-49Match length 107 93 % identity

NCBI Description T complex protein [Cucumis sativus]

258799 Seq. No. 255\_5.R1011 Contig ID 5'-most EST cat700017202.rl

Seq. No. 258800 Contig ID 256 1.R1011



```
5'-most EST
                   LIB3066-030-Q1-K1-D3
Method
                   BLASTX
                   g548493
NCBI GI
BLAST score
                   1170
                   1.0e-128
E value
                   414
Match length
                   55
% identity
                   EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi_629854_pir__S30067 polygalacturonase - maize
                   >gi 288612 emb CAA47052 (X66422) polygalacturonase [Zea
                   mays]
                   258801
Seq. No.
                   256 2.R1011
Contig ID
                   uC-zmflmo17218b05a1
5'-most EST
Method
                   BLASTX
                   g3193292
NCBI GI
                   294
BLAST score
                   9.0e-36
E value
Match length
                   136
% identity
                   63
                   (AF069298) similar to ATPases associated with various
NCBI Description
                   cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
Seq. No.
                   258802
                   256 3.R1011
Contig ID
5'-most EST
                   LIB148-050-Q1-E1-B11
Method
                   BLASTX
NCBI GI
                   g22422
BLAST score
                   301
E value
                   2.0e-27
Match length
                   95
                   60
% identity
                   (X57743) polygalacturonase [Zea mays]
NCBI Description
                   258803
Seq. No.
                   256 5.R1011
Contig ID
5'-most EST
                   LIB148-028-Q1-E1-B10
Method
                   BLASTX
NCBI GI
                   q548493
BLAST score
                   213
                   4.0e-17
E value
Match length
                   116
% identity
                   41
NCBI Description
                   EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                    (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi_629854_pir__S30067 polygalacturonase - maize
>gi_288612_emb_CAA47052_(X66422) polygalacturonase [Zea
                   mays]
                   258804
Seq. No.
```

3.5

257 1.R1011

BLASTN

g429006

fC-zmf1700354921 FL

Contig ID

NCBI GI

5'-most EST Method



```
BLAST score
                   39
E value
                   3.0e-12
Match length
                   95
% identity
                  85
NCBI Description Rice mRNA for MCM3 (gene name SS300), partial cds
                  258805
Seq. No.
                  257_2.R1011
Contig ID
5'-most EST
                  yyf700352534.h1
Seq. No.
                  258806
Contig ID
                  257_3.R1011
5'-most EST
                  uC-zmflMo17005g11b1
Seq. No.
                  258807
                  257 4.R1011
Contig ID
                  LIB3137-020-Q1-K1-D2
5'-most EST
Method
                  BLASTN
                  g429006
NCBI GI
BLAST score
                  39
                  2.0e-12
E value
Match length
                  95
% identity
                  85
NCBI Description Rice mRNA for MCM3 (gene name SS300), partial cds
                  258808
Seq. No.
                  257 5.R1011
Contig ID
5'-most EST
                  xyt700345654.h1
                  258809
Seq. No.
Contig ID
                  258 1.R1011
5'-most EST
                  pmx700091042.h1
Method
                  BLASTX
NCBI GI
                   q4107009
BLAST score
                  2217
E value
                   0.0e + 00
Match length
                   499
% identity
NCBI Description (D82039) OSK1 [Oryza sativa]
Seq. No.
                   258810
                  258 2.R1011
Contig ID
5'-most EST
                  uC-zmflmo17407b11a1
Seq. No.
                   258811
Contig ID
                   259 1.R1011
5'-most EST
                   fC-zmf1700355774: FL
                  258812
Seq. No.
                  260 1.R1011
Contig ID
                  LIB3075-019-Q1-K1-C10
```

5'-most EST LIB\(\bar{3}\)075-01 Method BLASTX NCBI GI g2501850

BLAST score 1893 E value 0.0e+00 Match length 433 % identity 82



```
NCBI Description (AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
Seq. No.
                  258813
                  261 1.R1011
Contig ID
5'-most EST
                  uC-zmflb73051e09a2
Method
                  BLASTX
NCBI GI
                  g2146739
BLAST score
                  1595
E value
                  1.0e-178
Match length
                  457
% identity
                  68
NCBI Description
                  hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi 881521
                  (U28214) hexokinase 1 [Arabidopsis thaliana]
Seq. No.
                  258814
                  262 1.R1011
Contig ID
5'-most EST
                  LIB3136-011-Q1-K1-A10
Method
                  BLASTX
NCBI GI
                  g1170871
BLAST score
                  1573
E value
                  1.0e-176
Match length
                  399
% identity
                  75
NCBI Description
                  MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
                  (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
                  >gi_1076749_pir__S46499 NADP-dependent malic enzyme - rice
                  >gi 415315_dbj_BAA03949_ (D16499) NADP-dependent malic
                  enzyme [Oryza sativa]
Seq. No.
                  258815
                  264 1.R1011
Contig ID
                  pmx700083149.h1
5'-most EST
Method
                  BLASTX
NCBI GI
                  q3402722
BLAST score
                  1200
E value
                  0.0e + 00
Match length
                  502
                  77
% identity
                 (AC004261) CPDK-related protein [Arabidopsis thaliana]
NCBI Description
                  258816
Seq. No.
                  264 2.R1011
Contig ID
5'-most EST
                  uC-zmroteosinte004f11b1
Method
                  BLASTX
NCBI GI
                  g3402722
BLAST score
                  823
E value
                  2.0e-88
Match length
                  181
% identity
NCBI Description
                  (AC004261) CPDK-related protein [Arabidopsis thaliana]
```

Seq. No. 258817 Contig ID 264 4.R1011

5'-most EST LIB3067-055-Q1-K1-G12

Method BLASTX NCBI GI g3402722 BLAST score 433



E value 1.0e-42 Match length 101 % identity 76

NCBI Description (AC004261) CPDK-related protein [Arabidopsis thaliana]

 Seq. No.
 258818

 Contig ID
 265\_1.R1011

 5'-most EST
 zuv700353218.h1

 Method
 BLASTX

Method BLASTX
NCBI GI g2911042
BLAST score 1553
E value 1.0e-173
Match length 394
% identity 77

NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein

[Arabidopsis thaliana]

Seq. No. 258819 Contig ID 265 2.R1011

5'-most EST uC-zmflb73152c03b1

Method BLASTX
NCBI GI g2911042
BLAST score 201
E value 1.0e-32
Match length 103
% identity 71

NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein

[Arabidopsis thaliana]

Seq. No. 258820 Contig ID 266 1.R1011

5'-most EST fC-zmf1700378034\_FL

Method BLASTX
NCBI GI g2645170
BLAST score 1618
E value 0.0e+00
Match length 382
% identity 81

NCBI Description (D50576) YY2 protein [Oryza sativa]

Seq. No. 258821 Contig ID 267\_1.R1011 5'-most EST xdb700341886.h1

 Seq. No.
 258822

 Contig ID
 269 1.R1011

 5'-most EST
 afb700381131.h1

Method BLASTX
NCBI GI g3342242
BLAST score 1840
E value 0.0e+00
Match length 463
% identity 72

NCBI Description (AF030421) cell wall invertase; beta-fructofuranosidase;

fructosidase [Triticum aestivum]

Seq. No. 258823

```
270 1.R1011
Contig ID
                   clt700045156.fl
5'-most EST
                   BLASTX
Method
                   q3057120
NCBI GI
                   1686
BLAST score
                   0.0e + 00
E value
                   393
Match length
                   78
% identity
                   (AF023159) starch synthase DULL1 [Zea mays]
NCBI Description
                   258824
Seq. No.
                   271_1.R1011
Contig ID
                   uC-zmflb73131e07b2
5'-most EST
                   BLASTX
Method
                   g2224915
NCBI GI
BLAST score
                   909
                   6.0e-98
E value
                   243
Match length
                   67
% identity
                   (U95968) beta-expansin [Oryza sativa]
NCBI Description
                   258825
Seq. No.
                   271 2.R1011
Contig ID
                   uC-zmflb73188b07b1
5'-most EST
                   BLASTX
Method
                   g2224915
NCBI GI
BLAST score
                   924
                   1.0e-99
E value
                   243
Match length
                   67
% identity
                   (U95968) beta-expansin [Oryza sativa]
NCBI Description
                   258826
Seq. No.
                   271_3.R1011
Contig ID
                   uC-zmflb73280a12b2
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2224915
                   902
BLAST score
                   3.0e-97
E value
                   231
Match length
% identity
                   71
                   (U95968) beta-expansin [Oryza sativa]
NCBI Description
Seq. No.
                   258827
                   271 4.R1011
Contig ID
5'-most EST
                   uC-zmflmo17335d10b1
Method
                   BLASTX
NCBI GI
                   g2224915
BLAST score
                   491
E value
                   2.0e-49
                   147
Match length
% identity
                   (U95968) beta-expansin [Oryza sativa]
NCBI Description
Seq. No.
                   258828
```

271 6.R1011

uC-zmflmo17398h09a1

Contig ID

5'-most EST



```
258829
Seq. No.
                  272 1.R1011
Contig ID
                  fC-zmf1700381459 FL
5'-most EST
                  BLASTX
Method
                  g3287857
NCBI GI
                  703
BLAST score
                  6.0e-74
E value
                  252
Match length
                  56
% identity
                  3-HYDROXYBUTYRYL-COA DEHYDROGENASE (BETA-HYDROXYBUTYRYL-COA
NCBI Description
                  DEHYDROGENASE) (BHBD) >gi_1209052 (U32229) HbdA
                  [Bradyrhizobium japonicum]
                  258830
Seq. No.
                  272 2.R1011
Contig ID
                  pmx700081915.h1
5'-most EST
Method
                  BLASTX
                  g2501578
NCBI GI
                  1298
BLAST score
                  1.0e-143
E value
Match length
                  313
                  83
% identity
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047
NCBI Description
                  ethylene-responsive protein 1 - Para rubber tree
                  >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                  258831
Seq. No.
                  272 3.R1011
Contig ID
                  LIB3059-058-Q1-K1-E10
5'-most EST
                  BLASTX
Method
                  q3287857
NCBI GI
BLAST score
                  267
                   3.0e-23
E value
                  142
Match length
                   44
% identity
                  3-HYDROXYBUTYRYL-COA DEHYDROGENASE (BETA-HYDROXYBUTYRYL-COA
NCBI Description
                   DEHYDROGENASE) (BHBD) >gi_1209052 (U32229) HbdA
                   [Bradyrhizobium japonicum]
                   258832
Seq. No.
                   273 1.R1011
Contig ID
                   uC-zmflb73213e03a1
5'-most EST
                   BLASTX
Method
NCBI GI
                   g2129550
BLAST score
                   1948
E value
                   0.0e + 00
Match length
                   466
% identity
                   calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
NCBI Description
                   Arabidopsis thaliana >gi_2129554_pir S71901
                   calcium-dependent protein kinase 6 - Arabidopsis thaliana
                   >gi 836940 (U20623) calcium-dependent protein kinase
```

[Arabidopsis thaliana] >gi\_836944 (U20625)

calcium-dependent protein kinase [Arabidopsis thaliana] >gi 4454034 emb\_CAA23031.1\_ (AL035394) calcium-dependent



## protein kinase (CDPK6) [Arabidopsis thaliana]

 Seq. No.
 258833

 Contig ID
 273\_2.R1011

 5'-most EST
 nbm700477567.h1

Seq. No. 258834 Contig ID 274\_1.R1011

5'-most EST uC-zmflmo17136b11b1

Method BLASTX
NCBI GI g135060
BLAST score 4041
E value 0.0e+00
Match length 802
% identity 97

NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)

(SHRUNKEN-1) >gi\_66570\_pir\_\_YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi\_22486\_emb\_CAA26247\_ (X02400) sucrose

synthase [Zea mays] >gi\_22488\_emb\_CAA26229\_ (X02382)

sucrose synthase [Zea mays]

 Seq. No.
 258835

 Contig ID
 274\_2.R1011

 5'-most EST
 ymt700221147.h1

Method BLASTX
NCBI GI g1351136
BLAST score 4302
E value 0.0e+00
Match length 816
% identity 100

NCBI Description SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)

>gi 514946 (L22296) UDP-glucose:D-fructose

2-glucosyl-transferase [Zea mays] >gi\_533252 (L33244)

sucrose synthase 2 [Zea mays]

 Seq. No.
 258836

 Contig ID
 274\_3.R1011

5'-most EST LIB143-002-Q1-E1-H2

Method BLASTX
NCBI GI g584706
BLAST score 1952
E value 0.0e+00
Match length 404
% identity 93

NCBI Description ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)

>gi\_2130066\_pir\_\_JC5124 aspartate transaminase (EC
2.6.1.1), cytoplasmic - rice >gi\_287298\_dbj\_BAA03504\_
(D14673) aspartate aminotransferase [Oryza sativa]

 Seq. No.
 258837

 Contig ID
 274\_4.R1011

 5'-most EST
 cjh700194011.h1

Method BLASTX
NCBI GI g584706
BLAST score 308
E value 1.0e-40
Match length 140

Match length

% identity

50



```
% identity
                    ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
NCBI Description
                    >gi_2130066_pir__JC5124 aspartate transaminase (EC
                    2.6.1.1), cytoplasmic - rice >gi 287298 dbj BAA03504
                    (D14673) aspartate aminotransferase [Oryza sativa]
                    258838
Seq. No.
                    274 6.R1011
Contig ID
5'-most EST
                    uC-zmflmo17289d04b1
Method
                    BLASTX
NCBI GI
                    q135060
BLAST score
                    294
                    2.0e-26
E value
Match length
                    56
% identity
                    98
                    SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
NCBI Description
                    (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose
                    synthase [Zea mays] >gi 22488 emb CAA26229 (X02382)
                    sucrose synthase [Zea mays]
                    258839
Seq. No.
Contig ID
                    274 7.R1011
5'-most EST
                    xsy700208695.h1
Method
                    BLASTN
NCBI GI
                    a533251
                    254
BLAST score
                    1.0e-140
E value
Match length
                    340
% identity
NCBI Description
                    Zea mays (clone pSM8) sucrose synthase 2 (Sus1) gene,
                    complete cds
                    258840
Seq. No.
Contig ID
                    274 8.R1011
5'-most EST
                    uC-zmflmo17198q09b1
Method
                    BLASTX
NCBI GI
                    g135060
BLAST score
                    360
E value
                    4.0e-34
Match length
                    82
% identity
                    90
                    SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
NCBI Description
                    (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose
                    synthase [Zea mays] >gi 22488 emb CAA26229 (X02382)
                    sucrose synthase [Zea mays]
                    258841
Seq. No.
                    274 30.R1011
Contig ID
                    uwc700155657.h1
5'-most EST
                    BLASTX
Method
NCBI GI
                    g741983
BLAST score
                    264
E value
                    2.0e-23
```

Method

NCBI GI

E value

BLAST score

BLASTX

293 2.0e-26

q4512664



```
NCBI Description sucrose synthase: ISOTYPE=2 [Zea mays]
Seq. No.
                  258842
                  275 1.R1011
Contig ID
                  fC-zmf1700381963: FL
5'-most EST
Method
                  BLASTX
                  q4097094
NCBI GI
BLAST score
                  561
E value
                  3.0e-57
Match length
                  263
                  49
% identity
                  (U45447) vacuolar proton-ATPase subunit D [Oryctolagus
NCBI Description
                  cuniculus]
                  258843
Seq. No.
                  275 2.R1011
Contig ID
5'-most EST
                  qmh700026412.fl
Seq. No.
                  258844
                  275 3.R1011
Contig ID
5'-most EST
                  LIB3078-056-Q1-K1-C12
Seq. No.
                  258845
                  275 4.R1011
Contig ID
5'-most EST
                  LIB148-017-Q1-E1-C8
Method
                  BLASTX
NCBI GI
                  q731097
BLAST score
                  274
E value
                  4.0e-24
Match length
                  114
                  52
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT)
NCBI Description
                   (V-ATPASE 28 KD ACCESSORY PROTEIN) >gi_1083086 pir A55910
                  subunit D vacuolar H(+)-ATPase - bovine >gi_517446 (U11927)
                  vacuolar H-ATPase subunit D [Bos gaurus]
                  258846
Seq. No.
                  276 1.R1011
Contig ID
                  LIB3279-059-P1-K1-G7
5'-most EST
Method
                  BLASTX
NCBI GI
                  g4512664
BLAST score
                  1252
E value
                  1.0e-138
Match length
                  311
% identity
                  (AC006931) putative ribose phosphate pyrophosphokinase
NCBI Description
                   [Arabidopsis thaliana]
                  >gi_4544471_gb_AAD22378.1_AC006580 10 (AC006580) putative
                  ribose phosphate pyrophosphokinase [Arabidopsis thaliana]
                  258847
Seq. No.
Contig ID
                  276 2.R1011
5'-most EST
                  fC-zmle700578607f1
```



132

65

Match length % identity

```
84
Match length
                  70
% identity
NCBI Description
                   (AC006931) putative ribose phosphate pyrophosphokinase
                   [Arabidopsis thaliana]
                  >gi 4544471 gb AAD22378.1 AC006580 10 (AC006580) putative
                  ribose phosphate pyrophosphokinase [Arabidopsis thaliana]
                  258848
Seq. No.
                  276 3.R1011
Contig ID
5'-most EST
                  LIB3137-015-Q1-K1-B2
                  BLASTX
Method
NCBI GI
                  g4512664
BLAST score
                  495
                  4.0e-50
E value
                  116
Match length
% identity
                  81
                   (AC006931) putative ribose phosphate pyrophosphokinase
NCBI Description
                   [Arabidopsis thaliana]
                  >gi 4544471 gb AAD22378.1 AC006580 10 (AC006580) putative
                  ribose phosphate pyrophosphokinase [Arabidopsis thaliana]
Seq. No.
                  258849
                  277 1.R1011
Contig ID
5'-most EST
                  LIB148-012-Q1-E1-H2
                  258850
Seq. No.
                  278 1.R1011
Contig ID
5'-most EST
                  LIB3075-045-Q1-K1-H12
Method
                  BLASTX
NCBI GI
                  q3885492
BLAST score
                  1128
E value
                  1.0e-126
Match length
                  228
% identity
                  97
                  (AF063865) tapetum specific protein [Zea mays]
NCBI Description
Seq. No.
                  258851
                  279 1.R1011
Contig ID
5'-most EST
                  cyk700052056.f1
Method
                  BLASTX
NCBI GI
                   g3367596
BLAST score
                   1289
E value
                   1.0e-142
Match length
                   370
% identity
                   70
NCBI Description
                  (AL031135) putative protein [Arabidopsis thaliana]
Seq. No.
                   258852
Contig ID
                  280 1.R1011
                  LIB3066-014-Q1-K1-G10
5'-most EST
Method
                  BLASTX
NCBI GI
                  g626029
BLAST score
                  475
                  2.0e-47
E value
```

NCBI Description pollen allergen Lol p XI - perennial ryegrass



>gi 1582249 prf 2118270A allergen Lol p XI [Lolium perenne]

258853 Seq. No. 280 2.R1011 Contig ID ymy700282545.h25'-most EST Method BLASTX

NCBI GI g626029 BLAST score 504 7.0e-51 E value Match length 131 70 % identity

pollen allergen Lol p XI - perennial ryegrass NCBI Description

>gi 1582249 prf 2118270A allergen Lol p XI [Lolium

perenne]

258854 Seq. No. 281 1.R1011 Contig ID

5'-most EST LIB3062-025-Q1-K1-D4

Method BLASTX NCBI GI g3355626 BLAST score 892 E value 1.0e-168 Match length 362

% identity 79

(Y09204) histidinol-phosphate aminotransferase [Nicotiana NCBI Description

tabacum]

258855 Seq. No. 282 1.R1011 Contig ID 5'-most EST xjt700095261.h1

Method BLASTX NCBI GI g4426627 BLAST score 1146 E value 1.0e-126 Match length 267

75 % identity

(AF099969) sterol-C5(6)-desaturase homolog [Nicotiana NCBI Description

tabacum]

258856 Seq. No. 282 3.R1011 Contig ID 5'-most EST yne700378507.h1

Method BLASTX NCBI GI g4426627 BLAST score 310 E value 3.0e-28 Match length 62 % identity

NCBI Description (AF099969) sterol-C5(6)-desaturase homolog [Nicotiana

tabacum]

258857 Seq. No. Contig ID 282 5.R1011

5'-most EST LIB3137-014-Q1-K1-A8

Seq. No. 258858



```
Contig ID
                   283 1.R1011
5'-most EST
                   fC-zmf1700550995 FL
Method
                   BLASTX
NCBI GI
                   q1705463
BLAST score
                   182
E value
                   2.0e-13
Match length
                   41
% identity
                   88
NCBI Description BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir_ S71201
                   biotin sythase - Arabidopsis thaliana >gi 10453\overline{16} (\overline{U2}4147)
                   biotin sythase [Arabidopsis thaliana] >gi 1403662 (U31806)
                   BIO2 protein [Arabidopsis thaliana] >gi 1769457 (L34413)
                   biotin synthase [Arabidopsis thaliana] >gi_2288983
                   (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana]
                   >gi_1589016_prf__2209438A biotin synthase [Arabidopsis
                   thaliana]
                   258859
Seq. No.
Contig ID
                   284 1.R1011
5'-most EST
                   uC-zmroteosintel18a10b1
Method
                   BLASTX
                   q1806142
NCBI GI
BLAST score
                   935
E value
                   1.0e-101
Match length
                   219
% identity
                   76
NCBI Description (X97315) cdc2MsD [Medicago sativa]
Seq. No.
                   258860
Contig ID
                   285_1.R1011
5'-most EST
                   fC-zmf1700553370 FL
Method
                   BLASTX
NCBI GI
                   g2352084
BLAST score
                   370
E value
                   2.0e-35
Match length
                   110
% identity
                   70
NCBI Description (U96613) serine/threonine kinase [Arabidopsis thaliana]
Seq. No.
                   258861
Contig ID
                   285 2.R1011
5'-most EST
                   LIB189-008-Q1-E1-E5
Method
                   BLASTX
NCBI GI
                   g2352084
BLAST score
                   651
E value
                   2.0e-68
Match length
                  137
% identity
NCBI Description (U96613) serine/threonine kinase [Arabidopsis thaliana]
```

Seq. No. 258862 Contig ID 286 1.R1011

5'-most EST LIB3075-047-Q1-K1-A5

Method BLASTX NCBI GI g584777 BLAST score 298 E value 9.0e-27





Match length % identity

NCBI Description

PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR

(PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP

SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE

SYNTHASE 1)

Seq. No. Contig ID 258863

287 16.R1011

5'-most EST

LIB3066-010-Q1-K1-C10

Seq. No.

258864

Contig ID

287 17.R1011

5'-most EST

uC-zmflMo17086c02b1

Seq. No.

258865

Contig ID 5'-most EST

287 19.R1011 xjt700095025.h1

Seq. No.

258866

Contig ID

287 20.R1011

5'-most EST

uC-zmflb73178f04b1

Seq. No.

258867

Contig ID

287 21.R1011

5'-most EST

LIB3066-038-Q1-K1-E12

Seq. No.

Contig ID

287 22.R1011

5'-most EST

uC-zmflb73413b09a1

Seq. No.

258869

Contig ID 5'-most EST

287 23.R1011 hvj700619653.h1

Seq. No.

258870

Contig ID

287 24.R1011

5'-most EST

LIB3061-044-Q1-K1-H5

Seq. No.

258871

Contig ID

287\_25.R1011

5'-most EST

 $\mathtt{wty}\overline{7}\mathtt{00169279.h1}$ 

Seq. No.

258872

Contig ID

287\_26.R1011

5'-most EST

uC-zmflb73214g09a1

Method NCBI GI

BLASTN g4416300

BLAST score

92

E value Match length 2.0e-44

% identity

261 45

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No.

258873

Contig ID

287 27.R1011





5'-most EST wty700163043.hl

Seq. No. 258874

Contig ID 287 28.R1011

5'-most EST dyk700105488.hl

 Seq. No.
 258875

 Contig ID
 287\_29.R1011

 5'-most EST
 uC-zmrob73044h06a1

Method BLASTN
NCBI GI 94416300
BLAST score 200
E value 1.0e-108
Match length 330
% identity 48

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

5'-most EST LIB3075-025-Q1-K1-F9

Seq. No. 258877

Contig ID 287 31.R1011

5'-most EST LIB3066-011-Q1-K1-D10

Seq. No. 258878

Contig ID 287 32.R1011

5'-most EST LIB3078-024-Q1-K1-D5

Seq. No. 258879 Contig ID 287\_33.R1011

5'-most EST uC-zmflMo17016a02b1

Seq. No. 258881

Contig ID 287 35.R1011

5'-most EST uC-zmflmo17132g06b1

Seq. No. 258882 Contig ID 287 36.R1011

5'-most EST LIB3061-005-Q1-K1-D9 Method BLASTN

Method BLASTN
NCBI GI g4185305
BLAST score 267
E value 1.0e-148
Match length 641
% identity 81

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 258883



287 37.R1011

5'-most EST uC-zmflb73171e05b1

Method BLASTN NCBI GI g4416300 BLAST score 77

E value 4.0e-35 Match length 129 % identity 46

Contig ID

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 258884 Contig ID 287 38.R1011 5'-most EST LIB3150-091-P1-N1-G1

Seq. No. 258885 Contig ID 287 39.R1011

5'-most EST LIB3068-010-Q1-K1-H12

Seq. No. 258886 Contig ID 287 40.R1011

5'-most EST LIB3156-013-Q1-K1-C6

Seq. No. 258887 Contig ID -287 41.R1011

5'-most EST LIB3066-049-Q1-K1-G1

Method BLASTN NCBI GI g4416300 BLAST score 160 E value 1.0e-84 Match length 429 % identity 46

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 258888 Contig ID 287 42.R1011

5'-most EST LIB3060-004-Q1-K1-B10 Method

BLASTN NCBI GI g3452299 BLAST score 67 3.0e-29 E value Match length 192 % identity 86

NCBI Description Zea mays retrotransposon Ji-6 3' LTR, partial sequence

Seq. No. 258889 Contig ID 287 43.R1011

5'-most EST zuv700354930.h1

Seq. No. 258890 Contig ID

287 44.R1011 5'-most EST LIB189-027-Q1-E1-F9

Seq. No. 258891 Contig ID 287 45.R1011

5'-most EST LIB36-003-Q1-E1-H3





```
Seq. No.
                   258892
Contig ID
                   287 46.R1011
5'-most EST
                   LIB3066-048-Q1-K1-B1
Seq. No.
                   258893
Contig ID
                   287 47.R1011
5'-most EST
                   wyr700240233.h1
Seq. No.
                   258894
Contig ID
                   287 48.R1011
5'-most EST
                   LIB3060-016-Q1-K1-B3
Method
                   BLASTN
NCBI GI
                   g4416300
BLAST score
                   70
E value
                   6.0e-31
Match length
                   118
% identity
                   45
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster
                   region, complete sequence
Seq. No.
                   258895
Contig ID
                   287 49.R1011
5'-most EST
                  LIB3116-010-Q1-K1-A1
Seq. No.
                  258896
Contig ID
                  287 50.R1011
5'-most EST
                  LIB148-033-01-E1-B9
Method
                  BLASTN
NCBI GI
                  g433038
BLAST score
                  61
E value
                  9.0e-26
Match length
                  81
% identity
                  94
NCBI Description Zea mays W-22 clone cDNA7 retroelement PREM-1-containing
                  mRNA
Seq. No.
                  258897
Contig ID
                  287 51.R1011
5'-most EST
                  LIB3066-014-Q1-K1-B11
Method
```

Method BLASTN
NCBI GI g2832242
BLAST score 428
E value 0.0e+00
Match length 460
% identity 13

% identity

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 258898 Contig ID 287 52.R1011 5'-most EST wyr700238654.hl Method BLASTN NCBI GI g1244652 BLAST score 152 E value 6.0e-80 Match length 244

46





```
NCBI Description Zea mays copia-type retroelement PREM-2 gag gene, complete
 Seq. No.
                   258899
 Contig ID
                   287 53.R1011
 5'-most EST
                   LIB3060-034-Q1-K1-C8
Seq. No.
                   258900
Contig ID
                   287 54.R1011
5'-most EST
                   LIB148-028-Q1-E1-F2
Method
                   BLASTN
NCBI GI
                   g433044
BLAST score
                   144
E value
                   5.0e-75
Match length
                   176
% identity
                   95
NCBI Description Zea mays W-22 clone PREM-1D retroelement PREM-1, partial
                   sequence
Seq. No.
                   258901
                   287 55.R1011
Contig ID
5'-most EST
                   uer700579605.h1
Seq. No.
                   258902
Contig ID
                   287 56.R1011
5'-most EST
                   uC-zmflmo17263f12b1
Seq. No.
                   258903
Contig ID
                   287 57.R1011
5'-most EST
                  uC-zmflmo17220g10b1
Seq. No.
                   258904
Contig ID
                   287 58.R1011
5'-most EST
                  LIB148-022-Q1-E1-E2
Seq. No.
                   258905
Contig ID
                  287 59.R1011
5'-most EST
                  LIB3075-028-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2429087
BLAST score
                  322
E value
                  5.0e-30
Match length
                  113
% identity
                   58
NCBI Description (L37358) lipoxygenase 2 [Hordeum vulgare]
Seq. No.
                  258906
Contig ID
                  287 60.R1011
5'-most EST
                  uer700577816.h1
Method
                  BLASTX
NCBI GI
                  g2506825
                  287
                  5.0e-26
```

BLAST score E value Match length 92 % identity 63

NCBI Description LIPOXYGENASE 1 >gi\_532572 (L35931) lipoxygenase 1 [Hordeum vulgare] >gi\_1094924\_prf\_\_2107185A lipoxygenase [Hordeum



## vulgare]

Seq. No. 258907 Contig ID 287 61.R1011 5'-most EST  $uC-\overline{z}mflmo17341a04b1$ Method BLASTN

NCBI GI g4416300 BLAST score 54 E value 2.0e-21 Match length 104 % identity 45

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 258908 Contig ID 287 62.R1011 5'-most EST xsy700207329.h1

Seq. No. 258909 Contig ID 287 63.R1011

5'-most EST LIB3066-013-Q1-K1-C7

Seq. No. 258910 Contig ID 287 64.R1011

5'-most EST uC-zmflb73195e06b1

Method BLASTN NCBI GI g22447 BLAST score 37 E value 2.0e-11 Match length 37

% identity 100

NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein

Seq. No. 258911 Contig ID 287 65.R1011

5'-most EST LIB3059-035-Q1-K1-E10

Seq. No. 258912 Contig ID 287 66.R1011 5'-most EST

uC-zmflB73025f11b2

Seq. No. 258913 Contig ID 287 67.R1011

5'-most EST LIB3136-002-P1-K1-H7

Method BLASTX NCBI GI g126401 BLAST score 373 E value 3.0e-36 Match length 87 % identity 79

LIPOXYGENASE L-2 >gi\_100690\_pir\_\_S23454 lipoxygenase (EC 1.13.11.12) L-2 - rice >gi\_20267\_emb\_CAA45738\_ (X64396) NCBI Description

lipoxygenase [Oryza sativa]

Seq. No. 258914

Contig ID 287 68.R1011

uC-zmflmo17125b02b1 5'-most EST





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Seq. No.
                   258915
Contig ID
                   287 69.R1011
5'-most EST
                  LIB36-021-Q1-E1-C1
Seq. No.
                   258916
                  287 70.R1011
Contig ID
5'-most EST
                  uC-zmflmo17069f07b1
Seq. No.
                  258917
Contig ID
                  287 71.R1011
5'-most EST
                  fwa700098016.h1
Seq. No.
                  258918
Contig ID
                  287_72.R1011
5'-most EST
                  wyr700241024.hl
                  BLASTN
                  g4416300
```

Method NCBI GI BLAST score 118 E value 1.0e-59 Match length 250 % identity 44

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 258919 Contig ID 287\_73.R1011 5'-most EST mwy700439844.h1

Seq. No. 258920 Contig ID 287 74.R1011

5'-most EST uC-zmflmo17289h10b1

Method BLASTN NCBI GI q433041 BLAST score 127 E value 7.0e-65 Match length 323 % identity 92

NCBI Description Zea mays W-22 clone PREM-1B retroelement PREM-1, partial

sequence

Seq. No. 258921 Contig ID 287 75.R1011

5'-most EST LIB3150-072-P2-K1-D1

Method BLASTN NCBI GI q433038 BLAST score 131 E value 2.0e-67 Match length 203 % identity 91

NCBI Description Zea mays W-22 clone cDNA7 retroelement PREM-1-containing

mRNA

Seq. No. 258922

Contig ID 287 76.R1011

5'-most EST uC-zmflmo17022g07b1



8

Seq. No. 258923
Contig ID 287\_77.R1011
5'-most EST ntr700075965.h1
Method BLASTX
NCBI GI 33204159

NCBI GI g3204159 BLAST score 285 E value 3.0e-66 Match length 184 % identity 63

NCBI Description (AJ006523) coatomer, beta-prime subunit [Drosophila melanogaster] >gi\_3204161\_emb\_CAA07085\_ (AJ006524)

coatomer, beta-prime subunit [Drosophila melanogaster]

Seq. No. 258924 Contig ID 287\_78.R1011

5'-most EST uC-zmflb73278a03b1

 Seq. No.
 258925

 Contig ID
 287\_79.R1011

 5'-most EST
 mwy700440461.h1

Method BLASTX
NCBI GI g2506825
BLAST score 187
E value 8.0e-14
Match length 40
% identity 85

NCBI Description LIPOXYGENASE 1 >gi\_532572 (L35931) lipoxygenase 1 [Hordeum

vulgare] >gi\_1094924\_prf\_\_2107185A lipoxygenase [Hordeum

vulgare]

Seq. No. 258926 Contig ID 287\_80.R1011

5'-most EST LIB3067-039-Q1-K1-G7

Method BLASTX
NCBI GI g3645899
BLAST score 325
E value 4.0e-30
Match length 76
% identity 80

NCBI Description (U68408) 5' end not determined experimentally [Zea mays]

Seq. No. 258927

Contig ID 287\_81.R1011

5'-most EST fC-zmle700421516:\_FL

Seq. No. 258928

Contig ID 287\_82.R1011

5'-most EST LIB84-006-Q1-E1-A8

Seq. No. 258929

Contig ID 287\_83.R1011 5'-most EST nbm700470175.h1

Seq. No. 258930

Contig ID 287\_84.R1011 5'-most EST nbm700477431.h1



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Seq. No.
                   258931
Contig ID
                   287_85.R1011
5'-most EST
                   uC-zmflmo17159a03b1
Method
                   BLASTN
NCBI GI
                   g4416300
BLAST score
                   109
E value
                   3.0e-54
Match length
                   270
% identity
                   47
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster
                   region, complete sequence
Seq. No.
                   258932
Contig ID
                   287 86.R1011
5'-most EST
                   uC-zmflmo17054b08b1
Seq. No.
                   258933
Contig ID
                   287 87.R1011
5'-most EST
                   uC-zmflmo17044c05b1
Method
                  BLASTN
NCBI GI
                   q22447
BLAST score
                  85
E value
                   1.0e-39
Match length
                   307
% identity
                   89
NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein
Seq. No.
                  258934
Contig ID
                  287 88.R1011
5'-most EST
                  LIB3060-032-Q1-K1-B3
Method
                  BLASTN
NCBI GI
                  g433038
BLAST score
                  139
E value
                  6.0e-72
Match length
                  199
% identity
                  92
NCBI Description Zea mays W-22 clone cDNA7 retroelement PREM-1-containing
                  mRNA
Seq. No.
                  258935
Contig ID
                  287 89.R1011
5'-most EST
                  LIB148-030-Q1-E1-B9
Seq. No.
                  258936
                  287 90.R1011
Contig ID
5'-most EST
                  mwy700441301.h1
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  63
```

E value 1.0e-26

Match length 106 % identity 91

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 258937 Contig ID 287 91.R1011



LIB3060-042-Q1-K1-G9 Seq. No. 258938

Contig ID 287 92.R1011 5'-most EST LIB3136-018-Q1-K1-H12

Method BLASTN NCBI GI q4416300 BLAST score 117 E value 7.0e-59 Match length 195 % identity 45

5'-most EST

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 258939 Contig ID 287 93.R1011 5'-most EST pwr700450135.h1

Method BLASTN NCBI GI q22447 BLAST score 213 E value 1.0e-116 Match length 344 % identity 91

NCBI Description Zea mays ZMPMS2 gene for 19 kDa zein protein

Seq. No. 258940 Contig ID 287\_94.R1011

5'-most EST uC-zmflmo17257b02b1

Method BLASTN NCBI GI g433043 BLAST score 89 E value 3.0e-42Match length 177 % identity 88

NCBI Description Zea mays W-22 clone PREM-1E retroelement PREM-1, partial

sequence

Seq. No. 258941 Contig ID 287 95.R1011

5'-most EST LIB143-040-Q1-E1-A10

Method BLASTN NCBI GI g4416300 BLAST score 95 E value 8.0e-46

Match length 131 % identity 47

Zea mays chromosome 4 22 kDa zein-associated intercluster NCBI Description

region, complete sequence

Seq. No. 258942

Contig ID 287 96.R1011 5'-most EST mwy700440838.h1

Seq. No. 258943 Contig ID

287 97.R1011

5'-most EST  $uC-\overline{z}mflm017211f10b1$ 

Method BLASTN



NCBI GI q433043 BLAST score 94 E value 3.0e-45Match length 125 % identity 95

NCBI Description Zea mays W-22 clone PREM-1E retroelement PREM-1, partial

sequence

Seq. No. 258944 Contig ID 287 98.R1011 uer700577023.hl 5'-most EST

Seq. No. 258945

Contig ID 287\_99.R1011

5'-most EST uC-zmflB73042b12b1

Seq. No. 258946

Contig ID 287 100.R1011 5'-most EST ntr700076363.h1

Seq. No. 258947

Contig ID 287\_101.R1011 5'-most EST wty700170905.h1

Seq. No. 258948

Contig ID 287\_102.R1011

5'-most EST uC-zmflm017209f06b1

88

Method BLASTN NCBI GI g717080 BLAST score 150 E value 1.0e-78 Match length 293 % identity

NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (GapC4)

gene, promoter region

Seq. No. 258949

Contig ID 287 103.R1011 5'-most EST cyk700050287.f1

Method BLASTN NCBI GI g433038 BLAST score 171 E value 3.0e-91 Match length 227 % identity 94

NCBI Description Zea mays W-22 clone cDNA7 retroelement PREM-1-containing

mRNA

Seq. No. 258950

Contig ID 287 104.R1011 5'-most EST wty700163395.h1

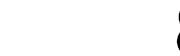
Seq. No. 258951

Contig ID 287 105.R1011

5'-most EST LIB148-047-Q1-E1-B11

Seq. No. 258952





Contig ID 287 106.R1011 5'-most EST LIB3068-041-Q1-K1-F8 Seq. No. 258953 Contig ID 287 107.R1011 5'-most EST LIB3066-016-Q1-K1-B3 Seq. No. 258954 Contig ID 287 108.R1011 5'-most EST dyk700104303.h1 Seq. No. 258955 Contig ID 288\_1.R1011 5'-most EST fC-zmle700421615 FL BLASTX Method NCBI GI g2191136

BLAST score 157 E value 6.0e-11 Match length 75 % identity 48

NCBI Description (AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A.

thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

Seq. No. 258956 Contig ID 289 1.R1011

5'-most EST LIB3157-013-Q1-K1-B12

Method BLASTX NCBI GI g1838961 BLAST score 301 E value 5.0e-27 Match length 117 % identity

NCBI Description (Y10994) acyl carrier protein [Casuarina glauca]

Seq. No. 258957 Contig ID 290 1.R1011

5'-most EST fC-zmle700421740\_FL

Method BLASTX NCBI GI g4127688 BLAST score 264 E value 4.0e-30 Match length 100 % identity 64

NCBI Description (AJ006065) isochorismate synthase [Catharanthus roseus]

Seq. No. 258958 Contig ID 291 1.R1011 5'-most EST

fC-zmle700421804 FL

Seq. No. 258959 Contig ID 292 1.R1011 5'-most EST

fC-zmle700421971: FL

Method BLASTX NCBI GI g3236253 BLAST score 539





E value 5.0e-55 Match length 215 % identity

(AC004684) receptor-like protein kinase [Arabidopsis NCBI Description

thaliana]

Seq. No. 258960 Contig ID 293 1.R1011

5'-most EST fC-zmle700422028: FL

Seq. No. 258961 Contig ID 295 1.R1011

5'-most EST uC-zmflmo17277d11a1

Method BLASTX NCBI GI q1706082 BLAST score 908 E value 1.0e-133 Match length 312 % identity 75

NCBI Description SERINE CARBOXYPEPTIDASE II-3 PRECURSOR (CP-MII.3)

>gi\_629787\_pir\_\_S44191 serine-type carboxypeptidase (EC
3.4.16.1) II-3 - barley >gi\_619350\_bbs\_153536

CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley,

cv. Alexis, aleurone, Peptide, 516 aa]

>gi\_474392\_emb\_CAA55478\_ (X78877) serine carboxylase II-3

[Hordeum vulgare]

Seq. No. 258962 Contig ID 295 2.R1011 5'-most EST vux700160383.h1

Method BLASTN NCBI GI g474391 BLAST score 47 E value 2.0e-17 Match length 115 % identity 85

NCBI Description H.vulgare L. (Alexis) Serine carboxypeptidase II-3 mRNA

Seq. No. 258963 Contig ID 296 1.R1011

5'-most EST uC-zmroteosinte102f12b2

Method BLASTX NCBI GI g1477480 BLAST score 363 E value 3.0e-34 Match length 109 % identity 66

NCBI Description (U40341) carbamoyl phosphate synthetase large chain

[Arabidopsis thaliana]

Seq. No. 258964 297 1.R1011 Contig ID

5'-most EST fC-zmle700423970 FL

Method BLASTX NCBI GI g2586083 BLAST score 225 E value 3.0e-18



8

c

Match length 118 % identity 40

NCBI Description (U72725) receptor kinase-like protein [Oryza

longistaminata]

Seq. No. 258965 Contig ID 298\_1.R1011

5'-most EST uC-zmflb73080g04b2

Method BLASTX
NCBI GI g4587513
BLAST score 1126
E value 1.0e-123
Match length 329
% identity 64

NCBI Description (AC007060) Contains eukaryotic protein kinase domain

PF\_00069. [Arabidopsis thaliana]

Seq. No. 258966 Contig ID 298 2.R1011

5'-most EST uC-zmflb73061a05b1

Method BLASTX
NCBI GI g4539330
BLAST score 175
E value 3.0e-12
Match length 144
% identity 34

NCBI Description (AL035679) putative receptor-like protein kinase (fragment)

[Arabidopsis thaliana]

Seq. No. 258967 Contig ID 298\_4.R1011 5'-most EST fdz701160622.h1

Seq. No. 258968 Contig ID 299\_1.R1011

5'-most EST uC-zmflmo17020g10b1

Method BLASTX
NCBI GI g3695005
BLAST score 1883
E value 0.0e+00
Match length 364
% identity 100

NCBI Description (AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2

[Zea mays]

Seq. No. 258969 Contig ID 299\_2.R1011

5'-most EST uC-zmflb73191c10b1

Method BLASTX
NCBI GI g2117355
BLAST score 1557
E value 1.0e-174
Match length 499
% identity 62

NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) alpha-II

chain precursor - potato >gi\_587562\_emb\_CAA56520\_ (X80236) mitochondrial processing peptidase [Solanum tuberosum]

BLAST score

1055





```
Seq. No.
                   258970
Contig ID
                   299 4.R1011
5'-most EST
                   LIB3136-003-Q1-K1-C8
Method
                   BLASTX
NCBI GI
                   g3929545
BLAST score
                   289
E value
                   8.0e-26
Match length
                   76
% identity
                   79
NCBI Description
                  (AF067194) S-adenosylmethionine decarboxylase [Oryza
                   sativa]
Seq. No.
                   258971
                   299 5.R1011
Contig ID
5'-most EST
                   xmt700263855.h1
Method
                   BLASTX
NCBI GI
                   g4220446
BLAST score
                   337
E value
                   2.0e-31
Match length
                   91
% identity
                   73
NCBI Description
                  (AC006216) Strong similarity to gi_2062155 T02004.2
                   mitochondrial processing peptidase alpha subunit precusor
                   isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs
                   gb_Z18504 and gb_AA395715 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   258972
Contig ID
                  300 1.R1011
5'-most EST
                  tzu700201602.h1
Method
                  BLASTX
NCBI GI
                  g3242708
BLAST score
                  729
E value
                   6.0e-77
Match length
                  291
% identity
                  50
NCBI Description (AC003040) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  258973
Contig ID
                  301_1.R1011
5'-most EST
                  fC-zmle700426373:_FL
Method
                  BLASTX
NCBI GI
                  g1418990
BLAST score
                  180
E value
                  6.0e-13
Match length
                  68
% identity
NCBI Description (Z75524) unknown [Lycopersicon esculentum]
Seq. No.
                  258974
Contig ID
                  302 1.R1011
5'-most EST
                  uC-zmflmo17053c04b1
Method
                  BLASTX
NCBI GI
                  g1085973
```



E value 1.0e-115 Match length 228 % identity 85

NCBI Description isopentyl pyrophosphate isomerase - Clarkia breweri (fragment) >gi\_572635\_emb\_CAA57947 (X82627) isopentenyl

pyrophosphate isomerase [Clarkia breweri]

5'-most EST LIB3066-042-Q1-K1-E8

Method BLASTX
NCBI GI g1213442
BLAST score 306
E value 2.0e-27
Match length 93
% identity 69

NCBI Description (U48961) isopentenyl pyrophosphate isomerase [Arabidopsis

thaliana]

Seq. No. 258976 Contig ID 302\_3.R1011

5'-most EST uC-zmflmo17047c05a1

Method BLASTX
NCBI GI g1085973
BLAST score 564
E value 8.0e-58
Match length 125
% identity 83

NCBI Description isopentyl pyrophosphate isomerase - Clarkia breweri

(fragment) >gi\_572635\_emb\_CAA57947 (X82627) isopentenyl

pyrophosphate isomerase [Clarkia breweri]

Seq. No. 258977 Contig ID 303\_1.R1011

5'-most EST uC-zmroteosinte045h11b2

Method BLASTX
NCBI GI g4006829
BLAST score 596
E value 2.0e-61
Match length 182
% identity 65

NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

5'-most EST LIB3136-003-Q1-K1-E10

Method BLASTX
NCBI GI g1168470
BLAST score 307
E value 9.0e-52
Match length 144
% identity 77

NCBI Description PROTEIN KINASE APK1A >gi\_282877\_pir\_\_S28615 protein kinase,

tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi\_217829\_dbj\_BAA02092 (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis

thaliana]

NCBI GI

BLAST score





```
Seq. No.
                     258979
  Contig ID
                     304 1.R1011
  5'-most EST
                     fC-zmle700426721:_FL
  Seq. No.
                     258980
  Contig ID
                     306 1.R1011
  5'-most EST
                     fC-zmst700623122a1
  Method
                    BLASTX
  NCBI GI
                     q4538976
  BLAST score
                    384
  E value
                     9.0e-37
  Match length
                    156
  % identity
                     49
                    (AL049487) sucrose-phosphate synthase-like protein
  NCBI Description
                     [Arabidopsis thaliana]
  Seq. No.
                     258981
  Contig ID
                    307_1.R1011
  5'-most EST
                    fC-zmle700427304:_FL
 Method
                    BLASTX
 NCBI GI
                    g2997591
 BLAST score
                    554
 E value
                    1.0e-56
 Match length
                    147
  % identity
                    71
NCBI Description
                   (AF020814) glucose-6-phosphate/phosphate-translocator
                    precursor [Pisum sativum]
 Seq. No.
                    258982
 Contig ID
                    308 1.R1011
 5'-most EST
                    tzu700201874.h1
 Method
                    BLASTX
 NCBI GI
                    g2462834
 BLAST score
                    333
 E value
                    1.0e-30
 Match length
                    142
 % identity
                    47
 NCBI Description
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    258983
 Contig ID
                    308 2.R1011
 5'-most EST
                    vux700158343.h1
 Method
                    BLASTX
 NCBI GI
                    g2462834
 BLAST score
                    333
 E value
                    8.0e-31
 Match length
                    145
 % identity
                    46
 NCBI Description
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    258984
 Contig ID
                    309 1.R1011
 5'-most EST
                    uC-zmflmo17134b09a1
 Method
                    BLASTX
```

35770

q3256035





```
9.0e-24
E value
Match length
                   90
% identity
                   56
NCBI Description
                   (Y14274) putative serine/threonine protein kinase [Sorghum
                   bicolor]
Seq. No.
                   258985
Contig ID
                   310 1.R1011
5'-most EST
                   LIB<u>1</u>43-012-Q1-E1-B6
Method
                   BLASTX
NCBI GI
                   g2688828
BLAST score
                   648
E value
                   2.0e-67
Match length
                   334
% identity
                   42
NCBI Description (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus
                   armeniaca]
Seq. No.
                   258986
Contig ID
                   311 1.R1011
5'-most EST
                   LIB3180-015-P2-M1-B3
Method
                   BLASTX
NCBI GI
                 g1616661
BLAST score
                   2380
E value
                   0.0e+00
Match length
                   484
% identity
                   95
NCBI Description (U49388) adenylosuccinate synthetase [Zea mays]
Seq. No.
                   258987
                   312 1.R1011
Contig ID
5'-most EST
                   fC-zmle700578414_FL
Method
                  BLASTX
NCBI GI
                   g1903357
BLAST score
                  326
E value
                   4.0e-30
Match length
                  134
% identity
                   47
NCBI Description (AC000104) Strong similarity to Arabidopsis 2A6
                   (gb_X83096). [Arabidopsis thaliana]
Seq. No.
                   258988
Contig ID
                   313 1.R1011
5'-most EST
                  uC-zmflb73407f11a2
Method
                  BLASTX
NCBI GI
                  q2245077
BLAST score
                  238
E value
                  6.0e-20
Match length
                  57
% identity
NCBI Description (Z97343) glucanase homolog [Arabidopsis thaliana]
Seq. No.
                  258989
```

Seq. No. 258989

Contig ID 314\_1.R1011

5'-most EST "C-zmflh732

5'-most EST uC-zmflb73205g09b2

Method BLASTX NCBI GI g2632252



```
BLAST score
                   1.0e-177
E value
Match length
                   330
% identity
                  (Y12464) serine/threonine kinase [Sorghum bicolor]
NCBI Description
                  258990
Seq. No.
                  314_2.R1011
Contig ID
5'-most EST
                  uC-zmflB73008e08b1
                  BLASTX
Method
NCBI GI
                  q2632254
BLAST score
                   373
                   1.0e-35
E value
Match length
                  89
% identity
NCBI Description
                  (Y12465) serine/threonine kinase [Sorghum bicolor]
                  258991
Seq. No.
                  314 4.R1011
Contig ID
5'-most EST
                  xtd700282379.h2
                  BLASTX
Method
                   q2632254
NCBI GI
BLAST score
                   352
E value
                   3.0e - 33
Match length
                  82
% identity
NCBI Description (Y12465) serine/threonine kinase [Sorghum bicolor]
Seq. No.
                   258992
Contig ID
                   315 1.R1011
5'-most EST
                  LIB84-008-Q1-E1-H4
Method
                  BLASTX
NCBI GI
                   g1362021
BLAST score
                   182
E value
                   6.0e-13
Match length
                   69
                   58
% identity
NCBI Description
                  zink finger protein 7 - Arabidopsis thaliana >qi 790685
```

(L39650) zinc finger protein [Arabidopsis thaliana] >gi 2213609 (AC000103) F21J9.3 [Arabidopsis thaliana]

Seq. No. 258993

315 2.R1011 Contig ID

5'-most EST LIB3078-039-Q1-K1-D7

Method BLASTX NCBI GI g1362017 BLAST score 149 E value 2.0e-09 58 Match length 53 % identity

NCBI Description zinc finger protein 4 - Arabidopsis thaliana >gi 790679 (L39647) zinc finger protein [Arabidopsis thaliana]

Seq. No. 258994 Contig ID 316 1.R1011 wyr700244154.hl 5'-most EST BLASTX Method



NCBI GI g4314378
BLAST score 678
E value 6.0e-71
Match length 280
% identity 46

NCBI Description (AC006232) putative lipase [Arabidopsis thaliana]

Seq. No. 258995 Contig ID 316\_2.R1011

5'-most EST LIB3062-022-Q1-K1-G12

5'-most EST uC-zmflmo17221b01a1

Seq. No. 258997 Contig ID 316 4.R1011

5'-most EST LIB3150-012-Q1-N1-H11

5'-most EST fC-zmro700451410 FL

Method BLASTN
NCBI GI g4416300
BLAST score 88
E value 1.0e-41
Match length 336
% identity 84

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 258999 Contig ID 317 2.R1011

5'-most EST uC-zmflb73056g01b1

Method BLASTN
NCBI GI g4416300
BLAST score 95
E value 1.0e-45
Match length 383
% identity 84

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 259000 Contig ID 318\_1.R1011

5'-most EST fC-zmro700570160 FL

Method BLASTX
NCBI GI g2493493
BLAST score 301
E value 5.0e-27
Match length 117
% identity 48

NCBI Description SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1)

>gi\_619352\_bbs\_153538\_CP-MII.1=serine\_carboxypeptidase

[Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324

aa]





```
259001
Seq. No.
                   318 2.R1011
Contig ID
5'-most EST
                   fC-zmro700451901:_FL
Method
                   BLASTX
NCBI GI
                   g3738328
BLAST score
                   414
E value
                   3.0e-40
Match length
                   149
                   50
% identity
                  (AC005170) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   259002
                   319 1.R1011
Contig ID
5'-most EST
                   fC-zmro700452834: FL
Method
                   BLASTX
NCBI GI
                   g2507246
BLAST score
                   355
E value
                   6.0e-34
Match length
                   66
% identity
                   100
NCBI Description COMPLEMENT FACTOR D PRECURSOR (C3 CONVERTASE ACTIVATOR)
                   (PROPERDIN FACTOR D) (ADIPSIN) (ENDOGENOUS VASCULAR
                   ELASTASE) >gi_2118079_pir__I55608 endogenous vascular elastase - rat >gi_693722_bbs_157144 (S73894) endogenous
                   vascular elastase, EVE=serine proteinase adipsin homolog
                   [rats, Sprague-Dawley, pulmonary arteries, Peptide, 263 aa]
                   [Rattus sp.]
                   259003
Seq. No.
                   320 1.R1011
Contig ID
5'-most EST
                   rv1700456136.h1
                   BLASTX
Method
NCBI GI
                   q1619300
BLAST score
                   305
                   2.0e-27
E value
Match length
                   153
% identity
                   40
NCBI Description (X95269) LRR protein [Lycopersicon esculentum]
Seq. No.
                   259004
Contig ID
                   321_1.R1011
5'-most EST
                   fC-zmro700569668 FL
Method
                   BLASTX
NCBI GI
                   q4038030
BLAST score
                   696
                   3.0e-73
E value
                   172
Match length
% identity
NCBI Description (AC005936) putative protein kinase, 5' partial [Arabidopsis
                   thaliana]
```

Seq. No. 259005 Contig ID 323 1.R1011 5'-most EST xsy700211828.h1 Method BLASTX

NCBI GI q2914710



```
BLAST score
E value
                  1.0e-110
Match length
                  358
% identity
                  56
NCBI Description (AC003974) putative beta-D-galactosidase [Arabidopsis
                  thaliana]
Seq. No.
                  259006
Contig ID
                  324 1.R1011
5'-most EST
                  uC-zmflmo17403e01a1
Method
                  BLASTX
NCBI GI
                  q2809262
BLAST score
                  464
                  3.0e-47
E value
                  216
Match length
                  49
% identity
NCBI Description (AC002560) F21B7.31 [Arabidopsis thaliana]
```

Seq. No. 259007 Contig ID 325 1.R1011 5'-most EST uwc700151077.h1 Method BLASTX NCBI GI g3913182 BLAST score 935 E value 1.0e-101 Match length 251 74 % identity

NCBI Description CINNAMYL-ALCOHOL DEHYDROGENASE (CAD)

>gi\_2239258\_emb\_CAA74070\_ (Y13733) cinnamyl alcohol

dehydrogenase [Zea mays]

259008 Seq. No. Contig ID 325 2.R1011

5'-most EST fC-zmro700570469 FL

Method BLASTN NCBI GI q3097280 BLAST score 295 E value 1.0e-165 Match length 353 % identity 99

NCBI Description Zea mays mRNA for cinnamyl alcohol dehydrogenase

Seq. No. 259009 Contig ID 325 3.R1011

5'-most EST uC-zmflb73369d05a1

Method BLASTX NCBI GI q3097281 BLAST score 448 E value 3.0e-44Match length 120 78 % identity

NCBI Description (AJ005702) cinnamyl alcohol dehydrogenase [Zea mays]

Seq. No. 259010 Contig ID 326 1.R1011 5'-most EST

fC-zmro700570704r1

Method BLASTX



NCBI GI q1175395 BLAST score 185 E value 2.0e-13 Match length 131 % identity 31

NCBI Description HYPOTHETICAL 14.1 KD PROTEIN C31A2.02 IN CHROMOSOME I

>gi\_2130413\_pir\_\_S58099 hypothetical protein SPAC31A2.02 -

fission yeast (Schizosaccharomyces pombe) >gi\_914880\_emb\_CAA90460\_ (Z50113) unknown

[Schizosaccharomyces pombe]

Seq. No. 259011 Contig ID 327 1.R1011

5'-most EST LIB3059-054-Q1-K1-E11

Method BLASTX NCBI GI g3775995 BLAST score 716 E value 2.0e-75 Match length 190 % identity 66

NCBI Description (AJ010461) RNA helicase [Arabidopsis thaliana]

Seq. No. 259012 Contig ID -327 2.R1011 5'-most EST nbm700478039.h1

Seq. No. 259013 Contig ID 328 1.R1011

5'-most EST fC-zmro700571573 FL

Method BLASTX NCBI GI g4538947 BLAST score 983 E value 1.0e-106 Match length 288 % identity 42

NCBI Description (AL049483) putative mitochondrial carrier protein

[Arabidopsis thaliana]

Seq. No. 259014 Contig ID 329 1.R1011

5'-most EST LIB3059-030-Q1-K1-B11

Method BLASTX NCBI GI g1706695 BLAST score 210 E value 5.0e-16 Match length 284 % identity 28

NCBI Description PHOSPHOMEVALONATE KINASE >gi 1362436 pir S57588

phosphomevalonate kinase (EC 2.7.4.2) - yeast (Saccharomyces cerevisiae) >gi 887601 emb CAA90191

(Z49939) Erg8p [Saccharomyces cerevisiae]

Seq. No. 259015 Contig ID 329 2.R1011

5'-most EST LIB3137-029-Q1-K1-H9

Method BLASTX NCBI GI q1706695

35776



```
BLAST score
E value
                   5.0e-11
Match length
                   103
% identity
                   39
NCBI Description PHOSPHOMEVALONATE KINASE >gi_1362436_pir__S57588
                   phosphomevalonate kinase (EC^{-}2.7.4.2) - \overline{\text{ye}}ast
                   (Saccharomyces cerevisiae) >gi 887601 emb CAA90191
                   (Z49939) Erg8p [Saccharomyces cerevisiae]
Seq. No.
                   259016
Contig ID
                   329 3.R1011
5'-most EST
                   fC-zmf1700341257b1
Seq. No.
                   259017
Contig ID
                   330 1.R1011
                   fC-zmro700571850 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   q3688209
BLAST score
                   361
E value
                   5.0e-34
Match length
                   114
% identity
                   61
NCBI Description (AJ010093) MAP3K beta 1 protein kinase [Brassica napus]
Seq. No.
                   259018
Contiq ID
                   331 1.R1011
                   fC-zmro700572286 FL
5'-most EST
Method
                   BLASTX
NCBI GI
                   g2655031
BLAST score
                   324
E value
                   8.0e-30
Match length
                   64
% identity
NCBI Description (AF019297) starch synthase isoform zSTSII-2 [Zea mays]
Seq. No.
                   259019
Contig ID
                   331 2.R1011
5'-most EST
                   uC-zmflb73212b10a1
Method
                   BLASTX
NCBI GI
                   g2655031
BLAST score
                   626
E value
                   4.0e-65
Match length
                   121
% identity
NCBI Description
                  (AF019297) starch synthase isoform zSTSII-2 [Zea mays]
Seq. No.
                   259020
Contig ID
                   332 1.R1011
5'-most EST
                   fC-zmro700572502 FL
Method
                   BLASTX
NCBI GI
                   g629602
BLAST score
                   155
                   6.0e-10
E value
Match length
                   55
% identity
                   49
NCBI Description
```

>gi\_488787\_emb\_CAA55893\_ (X79330) putative imbibition

probable imbibition protein - wild cabbage



## protein [Brassica oleracea]

259021 Seq. No. Contig ID 333 1.R1011

5'-most EST fC-zmro700572669\_FL

Method BLASTX NCBI GI g4539330 BLAST score 568 E value 1.0e-69 Match length 193 70 % identity

(AL035679) putative receptor-like protein kinase (fragment) NCBI Description

[Arabidopsis thaliana]

Seq. No. 259022 Contig ID 334 1.R1011 5'-most EST xmt700258227.h1

Method BLASTX NCBI GI q4417286 BLAST score 644 E value 6.0e-67 Match length 206 % identity 62

NCBI Description (AC007019) putative shikimate kinase [Arabidopsis thaliana]

Seq. No. 259023 Contig ID 334 2.R1011

5'-most EST uC-zmflb73062d01b1

Method BLASTX NCBI GI g114200 BLAST score 169 E value 1.0e-11 Match length 48 % identity 67

NCBI Description SHIKIMATE KINASE PRECURSOR >gi\_100253\_pir\_\_S21584 shikimate kinase precursor - tomato >gi\_19349\_emb\_CAA45121\_ (X63560)

shikimate kinase precursor [Lycopersicon esculentum]

Seq. No. 259024 334 3.R1011 Contig ID

5'-most EST LIB3116-014-Q1-K1-D1

Method BLASTN NCBI GI g3821794 BLAST score 39 E value 2.0e-12 Match length 51 % identity 94

NCBI Description Zea mays gene encoding protein kinase CK2 alpha subunit

Seq. No. 259025 334 5.R1011 Contig ID

5'-most EST LIB189-029-Q1-E1-A12

Seq. No. 259026 Contig ID 334 6.R1011

 $uC-\overline{z}mflmo17331c04a1$ 5'-most EST

Method BLASTX



NCBI GI g4417286 BLAST score 153 E value 5.0e-10 Match length 63 % identity 51

NCBI Description (AC007019) putative shikimate kinase [Arabidopsis thaliana]

Seq. No. 259027 Contig ID 335\_1.R1011

5'-most EST LIB3150-107-P2-K1-E5

 Seq. No.
 259028

 Contig ID
 335\_2.R1011

5'-most EST uC-zmflb73080b12a1

Seq. No. 259029 Contig ID 335\_4.R1011

5'-most EST uC-zmflmo17257c08b1

Seq. No. 259030 Contig ID 335\_5.R1011

5'-most EST uC-zmflMo17084h05b1

Seq. No. 259031 Contig ID 335 6.R1011

5'-most EST uC-zmroteosinte022d04b1

Seq. No. 259032 Contig ID 335 9.R1011

5'-most EST LIB3067-055-Q1-K1-G7

 Seq. No.
 259033

 Contig ID
 335\_10.R1011

5'-most EST LIB3157-019-Q1-K1-D7

Seq. No. 259034 Contig ID 336 1.R1011

5'-most EST uC-zmflb73242f04b1

Method BLASTX
NCBI GI g1815681
BLAST score 1048
E value 1.0e-114
Match length 223

% identity 85

NCBI Description (U85246) expansin [Oryza sativa]

 Seq. No.
 259035

 Contig ID
 336\_2.R1011

 5'-most EST
 LIB36-007-Q1-E1-G3

Method BLASTX

NCBI GI g1815681 BLAST score 691 E value 1.0e-72 Match length 263 % identity 86

NCBI Description (U85246) expansin [Oryza sativa]



 Seq. No.
 259036

 Contig ID
 336\_3.R1011

 5'-most EST
 LIB3069-017-Q1-K1-B3

 Method
 BLASTX

 NCBI GI
 g1041702

NCBI GI g1041702 BLAST score 437 E value 5.0e-43 Match length 122 % identity 67

NCBI Description (U30476) expansin At-EXP1 [Arabidopsis thaliana]

Seq. No. 259037 Contig ID 336\_4.R1011

5'-most EST LIB3062-059-Q1-K1-G3

Seq. No. 259038 Contig ID 336\_5.R1011

5'-most EST uC-zmflb73130b02a1

Seq. No. 259039 Contig ID 336 6.R1011

5'-most EST LIB3062-057-Q1-K1-D11

Method BLASTX
NCBI GI g1041710
BLAST score 950
E value 1.0e-103
Match length 281
% identity 65

NCBI Description (U30477) expansin Os-EXP2 [Oryza sativa]

Seq. No. 259040 Contig ID 336 7.R1011

5'-most EST uC-zmflmo17291h04a1

Seq. No. 259041 Contig ID 336 8.R1011

5'-most EST fC-zmf1700550656a1

Method BLASTX
NCBI GI g3747132
BLAST score 350
E value 8.0e-33
Match length 99
% identity 65

NCBI Description (AF096776) expansin [Lycopersicon esculentum]

Seq. No. 259042 Contig ID 337\_1.R1011

5'-most EST fC-zmro700573083\_FL

Method BLASTX
NCBI GI g2494417
BLAST score 397
E value 4.0e-38
Match length 198
% identity 86

NCBI Description FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi\_1364071\_pir\_\_S57717 fructose-1, 6-bisphosphatase (EC





3.1.3.11) - sugarcane hybrid H65-7052 >gi\_895909\_emb\_CAA61409.1\_ (X89006) fructose-1, 6-bisphosphatase [Saccharum hybrid cultivar H65-7052]

Seq. No. 259043 Contig ID 337\_2.R1011

5'-most EST uC-zmroB73020b07b1

Method BLASTX NCBI GI q3913640 BLAST score 819 E value 1.0e-126 Match length 248 % identity 91

NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC

(D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)

>gi\_3041775\_dbj\_BAA25422\_ (AB007193)

fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No. 259044 Contig ID 338\_1.R1011

5'-most EST uC-zmflmo17312b01b1

Method BLASTX NCBI GI q1362162 BLAST score 2167 E value 0.0e + 00Match length 478 % identity 82

beta-glucosidase BGQ60 precursor - barley >gi 804656 NCBI Description

(L41869) beta-glucosidase [Hordeum vulgare]

Seq. No. 259045 Contig ID 338 2.R1011 5'-most EST xsy700213883.h1

Method BLASTX NCBI GI q122087 BLAST score 589 E value 8.0e-61 Match length 136 % identity 88

[Medicago sativa] >gi\_19609 emb\_CAA31965 (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi\_21797 emb\_CAA25451 (X00937) H3 histone [Triticum aesti $\overline{v}$ um] > $\overline{g}$ i 488565 (U09459) histone H3.1 [Medicago sativa] >gi\_2565419 (AF026803)

histone H3 [Onobrychis viciifolia]

Seq. No. 259046 338 3.R1011 Contig ID 5'-most EST cat700017682.r1

Method BLASTX NCBI GI q122085 BLAST score 589 E value 8.0e-61 Match length 136 % identity 88



NCBI Description HISTONE H3 >gi\_81641\_pir\_\_S06250 histone H3 - Arabidopsis thaliana >gi\_82482\_pir\_\_S04099 histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969 (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi\_20253\_emb\_CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi\_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi 168495 (M13378) histone H3 [Zea mays] >gi\_168497 (M13379) histone H3 [Zea mays] >gi 168506  $(M3\overline{5}388)$  histone H3 [Zea mays]  $>gi_169655$   $(M7\overline{7}493)$  histone H3 [Petroselinum crispum] >gi\_169657 (M77494) histone H3 [Petroselinum crispum] >gi\_169659 (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi\_886738\_emb\_CAA59111 (X84377) histone 3 [Zea mays]  $>gi_1\overline{040764}$  (M35 $\overline{387}$ ) histone H3 [Arabidopsis thaliana] >gi\_1314779 (U54827) histone H3 homolog [Brassica napus] >gi 1531754 emb CAA57811 (X82414) Histone H3 [Asparagus officinalis] >gi\_1667592 (U77296) histone 3 [Oryza sativa] >gi\_3249101 (AC003114) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb\_H76511 gb\_H76255, gb\_AA712452, gb N65260 and gb\_T42306 come from this gene. [Arabidopsis thaliana] >gi\_225459\_prf\_\_1303352A histone H3 [Helicoverpa zea] >gi\_225839\_prf\_\_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 259047 Contig ID 338 4.R1011 5'-most EST LIB3069-004-01-K1-H5 Method BLASTX NCBI GI g122087 BLAST score 589 8.0e-61

E value Match length 136 % identity 88

NCBI Description

(X00937) H3 histone [Triticum aestivum]  $> \overline{gi}$  488565 (U09459)

histone H3.1 [Medicago sativa] >gi\_2565419 (AF026803)

histone H3 [Onobrychis viciifolia]

Seq. No. 259048

338 5.R1011 Contig ID 5'-most EST xsy700209683.hl

Method BLASTX NCBI GI g122087 BLAST score 536 E value 2.0e-54 Match length 127 % identity

NCBI Description

HISTONE H3 >gi\_81849\_pir\_\_S04520 histone H3 (clone pH3c-1) - alfalfa >gi\_82609\_pir\_\_A26014 histone H3 - wheat >gi\_19607\_emb\_CAA31964 (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi\_19609\_emb\_CAA31965\_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi\_21797\_emb\_CAA25451\_





(X00937) H3 histone [Triticum aestivum] >gi\_488565 (U09459) histone H3.1 [Medicago sativa] >gi\_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No. 259049 Contig ID 338 6.R1011

5'-most EST LIB3150-043-Q1-N1-H5

Method BLASTX NCBI GI g417103 BLAST score 623 E value 4.0e-65 Match length 124 % identity 100

NCBI Description HISTONE H3.2, MINOR >gi\_282871\_pir\_\_\$24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >qi 488563 (U09458) histone H3.2 [Medicago sativa]  $>gi_488567$  ( $\overline{U}09460$ ) histone H3.2 [Medicago sativa] >gi\_488569 ( $\overline{U}$ 09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2

[Medicago sativa]  $>gi_488577$  (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi  $1\overline{4}351\overline{5}7$  emb CA $\overline{A}58445$  (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218 (AB015760) histone H3 [Nicotiana

tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 259050 Contig ID 338 7.R1011 5'-most EST

LIB3076-036-Q1-K1-E4

Method BLASTX NCBI GI g122087 BLAST score 589 E value 7.0e-61 Match length 136 % identity

NCBI Description

HISTONE H3 >gi\_81849\_pir\_\_S04520 histone H3 (clone pH3c-1) - alfalfa >gi\_82609\_pir\_\_A26014 histone H3 - wheat >gi\_19607\_emb\_CAA31964 (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi\_19609\_emb\_CAA31965 (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi\_21797\_emb\_CAA25451 (X00937) H3 histone [Triticum aesti $\overline{v}$ um] > $\overline{g}i_4\overline{8}8565$  (U0 $\overline{9}459$ )

histone H3.1 [Medicago sativa] >gi\_2565419 (AF026803)

histone H3 [Onobrychis viciifolia]

Seq. No. 259051 Contig ID

338 8.R1011 5'-most EST ntr700074133.h1

Method BLASTX NCBI GI q417103 BLAST score 679



6.0e-71E value Match length 270 % identity 100 NCBI Description

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone H3.3-like protein - Arabidopsis thaliana >gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563

(U09458) histone H3.2 [Medicago sativa] >gi 488567 ( $\overline{\text{U}}$ 09460) histone H3.2 [Medicago sativa]  $>gi_488569$  ( $\overline{U}09461$ ) histone H3.2 [Medicago sativa]  $>gi_488575$  (U09464) histone H3.2

[Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911 emb\_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi\_1435157 emb\_CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 259052 Contig ID 338 9.R1011

5'-most EST uC-zmroteosinte086d05b1

Method BLASTX NCBI GI q122087 BLAST score 673 E value 1.0e-70 Match length 136 % identity 100

NCBI Description

HISTONE H3 >gi\_81849\_pir\_ S04520 histone H3 (clone pH3c-1) - alfalfa >gi\_82609\_pir\_ A26014 histone H3 - wheat >gi\_19607\_emb\_CAA31964\_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi\_19609\_emb\_CAA31965\_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi\_21797\_emb\_CAA25451\_ (X00037) H3 histone [Tritigure and interpretations] (X00937) H3 histone [Triticum aestivum]  $> \overline{g}i_488565$  (U0 $\overline{9}459$ )

histone H3.1 [Medicago sativa] >gi\_2565419 (AF026803)

histone H3 [Onobrychis viciifolia]

Seq. No. 259053

Contig ID 338 10.R1011

5'-most EST uC-zmflb73069e07b1

Method BLASTX NCBI GI g417103 BLAST score 665 E value 1.0e-69 Match length 133 % identity 100

NCBI Description HISTONE H3.2, MINOR >qi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 ( $\overline{\text{U}}$ 09460) histone H3.2 [Medicago sativa] >gi 488569 (U09461) histone

% identity





H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2 [Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911 emb\_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi\_1435157 emb\_CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1 (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 259054 Contig ID 338 11.R1011 5'-most EST LIB3279-011-P1-K1-G5 Method BLASTX NCBI GI q122085 BLAST score 446 E value 2.0e-44 Match length 90

100

NCBI Description HISTONE H3 >gi\_81641\_pir\_\_S06250 histone H3 - Arabidopsis thaliana >gi 82482 pir 504099 histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969\_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi\_20253 emb\_CAA31970\_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi 168493 (M36658) histone H3 (H3C3) [Zea mays] >gi\_168495 (M13378) histone H3 [Zea mays] >gi\_168497 (M13379) histone H3 [Zea mays] >gi\_168506  $(M3\overline{5}388)$  histone H3 [Zea mays] >gi\_169655  $(M7\overline{7}493)$  histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi\_169659 (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi\_886738\_emb\_CAA59111\_ (X84377) histone 3 [Zea mays]  $>gi_1\overline{040764}$  (M35 $\overline{387}$ ) histone H3 [Arabidopsis thaliana] >gi\_1314779 (U54827) histone H3 homolog [Brassica napus] >gi\_1531754\_emb\_CAA57811 (X82414) Histone H3 [Asparagus officinalis] >\overline{\text{gi}}\_1\overline{1667592} (U\overline{77296}) histone 3 [Oryza sativa] >gi\_3249101 (AC003114) Match to histone H3 gene gb\_M17131 and gb M35387 from A. thaliana. ESTs gb\_H76511 gb\_H76255, gb\_AA712452, gb\_N65260 and gb\_T42306 come from this gene. [Arabidopsis thaliana] >gi\_225459\_prf\_\_1303352A histone H3 [Helicoverpa zea]
>gi\_225839\_prf\_\_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 259055

Contig ID 338 16.R1011

5'-most EST LIB3067-010-Q1-K1-C10

Method BLASTX
NCBI GI g122085
BLAST score 585
E value 2.0e-60
Match length 136
% identity 87

NCBI Description HISTONE H3 >gi\_81641\_pir\_\_S06250 histone H3 - Arabidopsis





thaliana >gi\_82482\_pir\_\_S04099 histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_ S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969\_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi\_20253\_emb\_CAA31970\_ (X13680) histone H3 (AA 1-136) [Oryza  $\overline{sativa}$ ] >g $\overline{i}$ \_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi\_168495 (M13378) histone H3 [Zea mays] >gi\_168497 (M13379) histone H3 [Zea mays] >gi 168506 (M35388) histone H3 [Zea mays] >gi 169655 (M77493) histone H3 [Petroselinum crispum] >gi\_169657 (M77494) histone H3 [Petroselinum crispum]  $>gi_169659$  (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi\_886738 emb CAA59111 (X84377) histone 3 [Zea mays] >gi 1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi 1314779 (U54827) histone H3 homolog [Brassica napus] >gi\_1531754 emb CAA57811 (X82414) Histone H3 [Asparagus officinalis] >gi 1667592 (U77296) histone 3 [Oryza sativa]  $>gi_3249101$  ( $\overline{A}C003114$ ) Match to histone H3 gene gb M17131 and gb M35387 from A. thaliana. ESTs gb\_H76511 gb\_H76255, gb\_AA712452, gb\_N65260 and gb T42306 come from this gene. [Arabidopsis thaliana] >gi\_225459\_prf\_\_1303352A histone H3 [Helicoverpa zea] >gi\_225839\_prf\_\_1314298B histone H3 [Arabidopsis thaliana]

Seq. No.
Contig ID
5'-most EST
Method
NCBI GI
BLAST score
E value
Match length
% identity
NCBI Description

259056 338\_17.R1011 uC-zmroteosinte036b03b1 BLASTX g122085 670 2.0e-70 136 99

HISTONE H3 >gi\_81641\_pir\_\_S06250 histone H3 - Arabidopsis thaliana >gi\_82482\_pir\_\_\_S04099 histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_\_S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969 (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi\_20253\_emb\_CAA31970\_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi\_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi\_168495 (M13378) histone H3 [Zea mays] >gi\_168497 (M13379) histone H3 [Zea mays] >gi\_168506  $(M3\overline{5}388)$  histone H3 [Zea mays]  $>gi_169655$   $(M7\overline{7}493)$  histone H3 [Petroselinum crispum] >gi\_169657 (M77494) histone H3 [Petroselinum crispum] >gi\_169659 (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi\_886738\_emb\_CAA59111\_ (X84377) histone 3 [Zea mays] >gi\_1040764 (M35 $\overline{3}$ 87) histone H3 [Arabidopsis thaliana] >gi\_1314779 (U54827) histone H3 homolog [Brassica napus] >gi\_1531754\_emb CAA57811 (X82414) Histone H3 [Asparagus officinalis]  $>\overline{g}i_1\overline{1667592}$  (U $\overline{77296}$ ) histone 3 [Oryza sativa]  $>gi_3249101$  ( $\overline{A}C003114$ ) Match to histone H3 gene gb\_M17131 and gb\_M35387 from A. thaliana. ESTs gb\_H76511 gb\_ $\overline{\text{H}}$ 76255, gb AA7 $\overline{\text{1}}$ 2452, gb\_N65260 and gb\_T42306 come from this gene. [Arabidopsis thaliana] >gi\_225459\_prf\_\_1303352A histone H3 [Helicoverpa zea]
>gi\_225839\_prf\_\_1314298B histone H3 [Arabidopsis thaliana]



Seq. No. 259057 Contig ID 338 18.R1011 5'-most EST pmx700086563.h1 Method BLASTX NCBI GI g122085 BLAST score 661 E value 3.0e-69 Match length 136 % identity

NCBI Description HISTONE H3 >gi 81641 pir\_\_S06250 histone H3 - Arabidopsis thaliana >gi\_82482\_pir\_\_S04099 histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_S57626 histone H3 - maize >gi\_20251 emb\_CAA31969 (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi\_20253\_emb\_CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi\_168493 (M36658) histone H3 (H3C3) [Zea mays]  $>gi_168495$  (M13378) histone H3 [Zea mays]  $>gi_168497$  (M13379) histone H3 [Zea mays]  $>gi_168506$ (M35388) histone H3 [Zea mays] >gi\_169655 (M77493) histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi\_169659 (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3

[Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi\_886738\_emb\_CAA59111\_ (X84377) histone 3 [Zea mays]  $>gi_1\overline{040764}$  (M35 $\overline{387}$ ) histone H3 [Arabidopsis thaliana] >gi\_1314779 (U54827) histone H3 homolog [Brassica napus]  $> gi_1531754$  emb CAA57811 (X82414) Histone H3 [Asparagus officinalis]  $> \overline{gi}$  1667592 (U77296) histone 3 [Oryza sativa] >gi\_3249101 (AC003114) Match to histone H3 gene gb\_M17131 and gb M35387 from A. thaliana. ESTs gb\_H76511 gb\_H76255, gb AA712452, gb N65260 and gb\_T42306 come from this gene. [Arabidopsis thaliana]

>gi\_225459\_prf\_\_1303352A histone H3 [Helicoverpa zea]
>gi\_225839\_prf\_\_1314298B histone H3 [Arabidopsis thaliana]

Seq. No. 259058 Contig ID 338 19.R1011 5'-most EST LIB3069-039-Q1-K1-A11 Method BLASTX NCBI GI g122087 BLAST score 585 E value 2.0e-60

Match length 135 % identity

NCBI Description

HISTONE H3 >gi\_81849\_pir\_\_S04520 histone H3 (clone pH3c-1) - alfalfa >gi\_82609\_pir\_\_A26014 histone H3 - wheat >gi\_19607\_emb\_CAA31964\_(X13673) histone H3 (AA 1-136) [Medicago sativa] >gi\_19609\_emb\_CAA31965\_(X13674) histone H3 (AA 1-136) [Medicago sativa] >gi\_21797\_emb\_CAA25451\_(X13673) H3 (AA 1-136) [Medicago sativa] (X00937) H3 histone [Triticum aesti $\overline{v}$ um] > $\overline{g}$ i  $4\overline{8}8565$  (U0 $\overline{9}459$ ) histone H3.1 [Medicago sativa] >gi\_2565419 (AF026803)

histone H3 [Onobrychis viciifolia]

Seq. No. 259059 Contig ID 338 20.R1011 LIB3150-035-Q1-N1-E2 5'-most EST Method BLASTX



NCBI GI g122085
BLAST score 670
E value 2.0e-70
Match length 136
% identity 99
NCBI Description HISTONE

HISTONE H3 >gi\_81641 pir S06250 histone H3 - Arabidopsis thaliana >gi\_82482\_pir\_\_S04099 histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969\_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi\_20253 emb CAA31970 (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi\_168493 (M36658) histone H3 (H3C3) [Zea mays]  $>gi_168495$  (M13378) histone H3 [Zea mays] >gi\_168497 (M13379) histone H3 [Zea mays] >gi 168506  $(M3\overline{5}388)$  histone H3 [Zea mays] >gi\_169655 (M7 $\overline{7}493$ ) histone H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3 [Petroselinum crispum] >gi\_169659 (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi\_886738\_emb CAA59111 (X84377) histone 3 [Zea mays] >gi\_1 $\overline{040764}$  (M35 $\overline{387}$ ) histone H3 [Arabidopsis thaliana] >gi\_1314779 (U54827) histone H3 homolog [Brassica napus] >gi\_1531754 emb CAA57811 (X82414) Histone H3 [Asparagus officinalis] >\overline{\text{gi}}\_1\overline{1667592} (U\overline{77296}) histone 3 [Oryza sativa]  $>gi_3249101$  ( $\overline{A}C003114$ ) Match to histone H3 gene gb\_M17131 and gb\_M35387 from A. thaliana. ESTs gb\_H76511 gb\_H76255, gb\_AA712452, gb N65260 and gb\_T42306 come from this gene. [Arabidopsis thaliana] >gi\_225459\_prf\_\_1303352A histone H3 [Helicoverpa zea]
>gi\_225839\_prf\_\_1314298B histone H3 [Arabidopsis thaliana]

 Seq. No.
 259060

 Contig ID
 338\_21.R1011

 5'-most EST
 LIB3069-044-Q1-K1-G9

 Method
 BLASTX

 NCBI GI
 g417103

 BLAST score
 478

 E value
 1.0e-54

BLAST score 478
E value 1.0e-54
Match length 142
% identity 84
NCBI Description HISTONE

HISTONE H3.2, MINOR >gi\_282871\_pir\_\_S24346 histone
H3.3-like protein - Arabidopsis thaliana
>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563
(U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460)
histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone
H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2
[Medicago sativa] >gi\_488577 (U09465) histone H3.2
[Medicago sativa] >gi\_488577 (U09465) histone H3.2
[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone
H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)
histone H3 variant H3.3 [Lycopersicon esculentum]
>gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana
tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa]
>gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia
coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_





## (AL035708) Histon H3 [Arabidopsis thaliana]

 Seq. No.
 259061

 Contig ID
 338\_22.R1011

 5'-most EST
 LIB3070-015-Q1-N1-B12

 Mathod
 DIAGRA

Method BLASTX
NCBI GI g122085
BLAST score 580
E value 8.0e-60
Match length 134

% identity NCBI Description

NCBI Description HISTONE H3 >gi\_81641\_pir\_\_S06250 histone H3 - Arabidopsis thaliana  $>gi_8\overline{2}482$   $pir_8\overline{5}04099$  histone H3 (variant H3R-21) - rice >gi\_1362194\_pir\_\_S57626 histone H3 - maize >gi\_20251\_emb\_CAA31969\_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi\_20253\_emb\_CAA31970\_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >g $\overline{1}$ \_168493 (M36658) histone H3 (H3C3) [Zea mays]  $>gi_168495$  (M13378) histone H3 [Zea mays] >gi\_168497 (M13379) histone H3 [Zea mays] >gi\_168506 (M35388) histone H3 [Zea mays] >gi\_169655 (M77493) histone H3 [Petroselinum crispum] >gi\_169657 (M77494) histone H3 [Petroselinum crispum] >gi\_169659 (M77495) histone H3 [Petroselinum crispum] >gi\_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi\_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi\_886738\_emb\_CAA59111\_ (X84377) histone 3 [Zea mays]  $>gi_1\overline{040764}$  (M35 $\overline{3}87$ ) histone H3 [Arabidopsis thaliana]  $> \overline{gi}_1 1314779$  (U54827) histone H3 homolog [Brassica napus] >gi\_1531754\_emb\_CAA57811\_ (X82414) Histone H3 [Asparagus officinalis]  $> \overline{gi}_1 \overline{1667592}$  (U $\overline{7}7296$ ) histone 3 [Oryza sativa] >gi\_3249101 (AC003114) Match to histone H3 gene gb\_M17131 and gb M35387 from A. thaliana. ESTs gb\_H76511 gb\_H76255, gb AA712452, gb N65260 and gb\_T42306 come from this gene. [Arabidopsis thaliana] >gi\_225459\_prf\_\_1303352A histone H3 [Helicoverpa zea]
>gi\_225839\_prf\_\_1314298B histone H3 [Arabidopsis thaliana]

 Seq. No.
 259062

 Contig ID
 338\_28.R1011

5'-most EST uC-zmroteosinte100a03b2

Method BLASTX
NCBI GI g1362162
BLAST score 437
E value 2.0e-62
Match length 125
% identity 93

NCBI Description beta-glucosidase BGQ60 precursor - barley >gi 804656

(L41869) beta-glucosidase [Hordeum vulgare]

 Seq. No.
 259063

 Contig ID
 339\_1.R1011

 5'-most EST
 wty700169889.h1

 Method
 BLASTX

 NCBI GI
 g3024122

BLAST score 1910 E value 0.0e+00 Match length 434 % identity 92





NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >qi 1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa] Seq. No. 259064 Contig ID 339 2.R1011 5'-most EST uwc700150248.h1 Method BLASTX NCBI GI g3024122 BLAST score 1889 E value 0.0e+00Match length 392 % identity 92 NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821

(U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No. 259065 Contig ID 339 3.R1011 5'-most EST uC-zmflb73126e10b1 Method BLASTX

NCBI GI q4204265 BLAST score 919 E value 7.0e-99 Match length 449 % identity 48

NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 259066 Contig ID 339 4.R1011

5'-most EST uC-zmflb73347d11a1

Method BLASTX NCBI GI g1076389 BLAST score 2717 E value 0.0e + 00Match length 587 % identity 89

NCBI Description protein phosphatase 2A pDF1 - Arabidopsis thaliana

>gi\_683502\_emb\_CAA57528\_ (X82002) protein phosphatase 2A 65

kDa regulatory subunit [Arabidopsis thaliana]

Seq. No. 259067 Contig ID 339 5.R1011

5'-most EST LIB189-026-Q1-E1-H12

Method BLASTX NCBI GI q1709000 BLAST score 418 E value 2.0e-40 Match length 86 % identity 93

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi\_960357\_dbj\_BAA09895\_ (D63835) S-adenosylmethionine

synthetase [Hordeum vulgare]

Seq. No. 259068 Contig ID 339 6.R1011



```
5'-most EST
                    LIB3150-112-P2-K1-A1
Method
                    BLASTX
NCBI GI
                    q1076389
BLAST score
                    1008
E value
                    1.0e-109
Match length
                    230
% identity
                    24
NCBI Description
                    protein phosphatase 2A pDF1 - Arabidopsis thaliana
                    >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65
                    kDa regulatory subunit [Arabidopsis thaliana]
Seq. No.
                    259069
Contig ID
                    339_7.R1011
5'-most EST
                    uC-zmflb73086e11b2
Method
                    BLASTX
NCBI GI
                    q3024122
BLAST score
                    713
E value
                    2.0e-75
Match length
                    140
% identity
                    96
NCBI Description
                   S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                    ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821
                    (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
Seq. No.
                    259070
Contig ID
                   339 8.R1011
5'-most EST
                   LIB84-014-01-E1-D11
Method
                   BLASTX
NCBI GI
                   g461595
BLAST score
                   393
E value
                   9.0e-38
Match length
                   145
% identity
                   56
NCBI Description
                   ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)
                   >gi_479533_pir__S34473 H+-transporting ATP synthase (EC
3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520_
                   (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]
Seq. No.
                   259071
Contig ID
                   339 9.R1011
5'-most EST
                   ymt700219056.h1
Method
                   BLASTX
NCBI GI
                   g4240035
BLAST score
                   497
E value
                   6.0e-50
Match length
                   134
% identity
                   74
NCBI Description (AB018588) ZmGR1b [Zea mays]
```

Seq. No. 259072 Contig ID 339 11.R1011

5'-most EST LIB143-034-Q1-E1-B7

Seq. No. 259073 Contig ID 339\_15.R1011

5'-most EST uC-zmflb73250g06a2

5'-most EST

Method





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Seq. No.
                    259074
 Contig ID
                    339 18.R1011
 5'-most EST
                    LIB36-017-Q1-E1-E6
 Method
                    BLASTN
 NCBI GI
                    g3821780
 BLAST score
                    36
E value
                    1.0e-10
Match length
                    36
 % identity
                    100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                    259075
Contig ID
                    339 19.R1011
5'-most EST
                   LIB3059-014-Q1-K1-D7
Seq. No.
                    259076
Contig ID
                    339 22.R1011
5'-most EST
                    xsy700211827.h1
Method
                    BLASTX
NCBI GI
                    g1709000
BLAST score
                    411
E value
                    4.0e-40
Match length
                    116
% identity
                    73
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                    >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine
                    synthetase [Hordeum vulgare]
   1
Seq. No.
                   259077
Contig ID
                   339 27.R1011
5'-most EST
                   cat 700019427.rl
Method
                   BLASTX
NCBI GI
                   q1076390
BLAST score
                   172
E value
                   4.0e-12
Match length
                   44
% identity
NCBI Description protein phosphatase 2A pDF2 - Arabidopsis thaliana
                   >gi_683504_emb_CAA57529 (X82003) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]
Seq. No.
                   259078
Contig ID
                   339 34.R1011
5'-most EST
                   xsy700207473.h1
Method
                   BLASTN
NCBI GI
                   g4240032
BLAST score
                   70
E value
                   2.0e-31
Match length
                   110
% identity
                   92
NCBI Description Zea mays ZmGR1a mRNA, complete cds
Seq. No.
                   259079
                   340 1.R1011
Contig ID
```

35792

wty700169676.hl

BLASTX



NCBI GI g116054
BLAST score 1254
E value 1.0e-138
Match length 290
% identity 82

NCBI Description CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK)

>gi\_280393\_pir\_\_A43713 calcium-dependent protein kinase (EC
2.7.1.-) - soybean >gi\_169931 (M64987) Glycine max calcium

dependent protein kinase mRNA. [Glycine max]

Seq. No. 259080 Contig ID 341\_1.R1011

Method BLASTX
NCBI GI g2827715
BLAST score 345
E value 5.0e-36
Match length 208
% identity 45

NCBI Description (AL021684) receptor protein kinase - like protein

[Arabidopsis thaliana]

Seq. No. 259081 Contig ID 342 1.R1011

Method BLASTX
NCBI GI g2565305
BLAST score 1856
E value 0.0e+00
Match length 393
% identity 89

NCBI Description (AF024589) glycine decarboxylase P subunit [Hordeum sp. x

Triticum sp.]

 Seq. No.
 259083

 Contig ID
 343\_2.R1011

 5'-most EST
 xjt700095358.h1

Method BLASTX
NCBI GI g710308
BLAST score 523
E value 2.0e-53
Match length 135
% identity 72

NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 259084 Contig ID 344 1.

5'-most EST fC-zmro700575270\_FL

Method BLASTX
NCBI GI g1402918
BLAST score 381
E value 2.0e-36
Match length 101